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(54) Title: PROTEIN KINASES

(57) Abstract: The present invention relates to novel kinase polypeptides, nucleotide sequences encoding the novel kinase polypeptides, as well as various products and methods useful for the diagnosis and treatment of various kinase-related diseases and conditions.

DESCRIPTION

PROTEIN KINASES

FIELD OF THE INVENTION

The present invention relates to novel kinase polypeptides, nucleotide sequences encoding the novel kinase polypeptides, as well as various products and methods useful for the diagnosis and treatment of various kinase-related diseases and conditions.

BACKGROUND OF THE INVENTION

The following description of the background of the invention is provided to aid in understanding the invention, but is not admitted to be or to describe prior art to the invention.

Cellular signal transduction is a fundamental mechanism whereby external stimuli that regulate diverse cellular processes are relayed to the interior of cells. One of the key biochemical mechanisms of signal transduction involves the reversible phosphorylation of proteins, which enables regulation of the activity of mature proteins by altering their structure and function.

Protein phosphorylation plays a pivotal role in biological signal transduction. Among the biological functions controlled by protein phosphorylation are the following: cell division; differentiation and death (apoptosis); cell motility and cytoskeletal structure; control of DNA replication, transcription, splicing and translation; protein translocation events from the endoplasmic reticulum and Golgi apparatus to the membrane and extracellular space; protein nuclear import and export; regulation of metabolic reactions, etc. Abnormal protein phosphorylation is widely recognized to be causally linked to the etiology of many diseases including cancer as well as immunologic, neuronal and metabolic disorders.

The most common phospho-acceptor amino acid residues are serine, threonine and tyrosine. Phosphorylation in histidine has also been observed in bacteria. The presence of a phosphate moeity modulates protein function in multiple ways. A common mechanism includes changes in the catalytic properties (V_{max} and K_m) of an enzyme leading to its activation or inactivation. A second widely recognized mechanism involves promoting protein-protein interactions. An example of this is the tyrosine autophosphorylation of the

ligand-activated EGF receptor tyrosine kinase. This event triggers the high-affinity binding to the phosphotyrosine residue on the receptor's C-terminal intracellular domain to the SH2 motif of the adaptor molecule Grb2. Grb2 in turn binds through its SH3 motif to a second adaptor molecule, such as SHC. The formation of this ternary complex acivates the signaling events that are responsible for the biological effects of EGF. Serine and threonine phosphorylation events have also being recently recognized to exert their biological function through protein-protein interaction events mediated by the high-affinity binding of phosphoserine and phosphothreonine to WW motifs present in a large variety of proteins (Lu, P.J. *et al.* (1999) Science 283:1325-1328). A third important outcome of protein phosphorylation is changes in the subcellular localization of the substrate. As an example, nuclear import and export events in a large diversity of proteins are regulated by protein phosphorylation (Drier E.A. *et al.* (1999) Genes Dev 13: 556-568).

Protein kinases are one of the largest families of eukaryotic proteins with several hundred known members. These proteins share a 250-300 amino acid domain that can be subdivided into 12 distinct subdomains that comprise the common catalytic core structure. These conserved protein motifs have recently been exploited using PCR-based and bioinformatic strategies leading to a significant expansion of the known kinases. Multiple alignment of the sequences in the catalytic domain of protein kinases and subsequent parsimony analysis permits their segregation into a dendrogram reflecting the relatedness of their catalytic domains (Fig. 1). In this manner, related kinases are clustered into distinct branches or subfamilies including: tyrosine kinases, cyclic-nucleotide-dependent kinases, calcium/calmodulin kinases, cyclin-dependent kinases and MAP-kinases, serine-threonine kinase receptors, and several other less defined subfamilies.

We have recently completed a systematic analysis of the protein kinases present in *C. elegans*, the multicellular organism whose entire DNA sequence has been determined. We identified 473 unique kinase profiles including 398 full-length conventional kinases, and 20 additional proteins that may function as atypical protein kinases. (Plowman G.D. *et al.* (1999), Proc. Natl. Acad. Sci. 96:13603-13610).

Using parsimony analysis, the protein kinases may be divided into 4 major groups: AGC, CAMK, CMGC and tyrosine kinases. In addition, there are a number of minor yet distinct families, including the STE and casein kinase 1, families related to worm- or

fungal-specific kinases, and a family designated "other" to represent several smaller families. In addition, we designate an "atypical" family to represent protein kinases whose catalytic domain has little or no primary sequence homology to conventional kinases, including the A6 kinases and PI3 kinases.

The AGC kinases are basic amino acid-directed enzymes that phosphorylate residues found proximal to Arg and Lys. Examples of this group are the cyclic nucleotide-dependent kinases, G protein kinases, NDR or DBF2 and the ribosomal S6 kinases.

The CAMK group kinases are also basic amino acid-directed kinases. They include the Ca2+/calmodulin-regulated and AMP-dependent protein kinases, myosin light chain kinases, checkpoint 2 kinases (CHK2) and EMK-related protein kinases. The EMK family of STK are involved in the control of cell polarity, micotubule stability and cancer. One member of the EMK family, C-TAK1 has been reported to control entry into mitosis by activating Cdc25C which in turn dephosphorylates Cdc2.

CMGC group kinases are "proline-directed" enzymes phosphorylating residues that exist in a proline-rich context. They include the cyclin-dependent kinases (CDKs), mitogen-activated kinases (MAPKs), GSK3s and CLKs. Most CMGC kinases have larger-than-average kinase domains owing to the presence of insertions within subdomains X and XI.

The tyrosine kinase group encompass both cytoplasmic (i.e. src) as well as transmembrane receptor tyrosine kinases (i.e. EGF receptor). These kinases play a pivotal role in the signal transduction processes that mediate cell proliferation, differentiation and apoptotis.

Group members that define smaller, yet distinct phylogenetic branches of conventional kinases include the elongation factor 2 kinases (EIFKs); homologues of the yeast sterile family kinases (STE) which refers to 3 classes of kinases which lie sequentially upstream of the MAPKs; mixed lineage kinases (MLKs); Lim-domain containing kinases (LIMKs); Calcium-calmodulin kinase kinases (CAMKK), dual-specific tyrosine kinases (DYRK), integrin receptor associated kinase (IRAK); testis-specific kinases (TSK); UNC-51 related kinases (UNC); several families that are close homologues to worm (C26C2.1, YQ09, ZC581.9, YFL033c, C24A1.3), Drosophila (SLOB), or yeast (YDOD_sp, YGR262_sc) kinases, and others that are "unique" and don't cluster into any obvious family.

SUMMARY OF THE INVENTION

Through a search of the EST database for homologies to the conserved catalytic kinase domain of protein kinases, hundreds of mammalian members of known and previously unidentified protein kinase families and groups have been identified as part of the present invention. Multiple alignment and parsimony analysis of the catalytic domain reveals that approximately half of these protein kinases cluster into 10 known groups, with the other half perhaps defining novel groups. Classification in this manner has proven highly accurate not only in predicting motifs present in the remaining non-catalytic portion of each protein, but also in their regulation, substrates, and signaling pathways. The present invention includes the partial or complete sequence of new protein kinases, their classification, predicted or deduced protein structure, and a strategy for elucidating their biologic and therapeutic relevance.

Thus, a first aspect of the invention features an isolated, enriched, or purified nucleic acid molecule encoding a kinase polypeptide selected from the group consisting SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,

SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

By "isolated" in reference to nucleic acid is meant a polymer of nucleotides conjugated to each other, including DNA and RNA, that is isolated from a natural source or that is synthesized. The isolated nucleic acid of the present invention is unique in the sense that it is not found in a pure or separated state in nature. Use of the term "isolated" indicates that a naturally occurring sequence has been removed from its normal cellular (*i.e.*, chromosomal) environment. Thus, the sequence may be in a cell-free solution or placed in a different cellular environment. The term does not imply that the sequence is the only nucleotide chain present, but that it is essentially free (about 90 - 95% pure at least) of non-nucleotide material naturally associated with it, and thus is distinguished from isolated chromosomes.

By the use of the term "enriched" in reference to nucleic acid is meant that the specific DNA or RNA sequence constitutes a significantly higher fraction (2 - 5 fold) of the total DNA or RNA present in the cells or solution of interest than in normal or diseased cells or in the cells from which the sequence was taken. This could be caused by a person by preferential reduction in the amount of other DNA or RNA present, or by a preferential increase in the amount of the specific DNA or RNA sequence, or by a combination of the two. However, it should be noted that enriched does not imply that there are no other DNA or RNA sequences present, just that the relative amount of the sequence of interest has been significantly increased. The term "significant" is used to indicate that the level of increase is useful to the person making such an increase, and generally means an increase relative to other nucleic acids of about at least 2 fold, more preferably at least 5 to 10 fold or even more. The term also does not imply that there is no DNA or RNA from other sources. The other source DNA may, for example, comprise DNA from a yeast or bacterial genome, or a cloning vector such as pUC19. This term distinguishes from naturally occurring events, such as viral infection, or tumor type

growths, in which the level of one mRNA may be naturally increased relative to other species of mRNA. That is, the term is meant to cover only those situations in which a person has intervened to elevate the proportion of the desired nucleic acid.

It is also advantageous for some purposes that a nucleotide sequence be in purified form. The term "purified" in reference to nucleic acid does not require absolute purity (such as a homogeneous preparation). Instead, it represents an indication that the sequence is relatively more pure than in the natural environment (compared to the natural level this level should be at least 2-5 fold greater, *e.g.*, in terms of mg/mL). Individual clones isolated from a cDNA library may be purified to electrophoretic homogeneity. The claimed DNA molecules obtained from these clones could be obtained directly from total DNA or from total RNA. The cDNA clones are not naturally occurring, but rather are preferably obtained via manipulation of a partially purified naturally occurring substance (messenger RNA). The construction of a cDNA library from mRNA involves the creation of a synthetic substance (cDNA) and pure individual cDNA clones can be isolated from the synthetic library by clonal selection of the cells carrying the cDNA library. Thus, the process which includes the construction of a cDNA library from mRNA and isolation of distinct cDNA clones yields an approximately 10^6-fold purification of the native message. Thus, purification of at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated.

By a "kinase polypeptide" is meant 10 (preferably 20, more preferably 40, most preferably 75) or more contiguous amino acids set forth in an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,

SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or functional derivatives thereof as described herein. For sequences for which the full-length sequence is not given, the remaining sequences can be determined using methods well-known to those in the art and are intended to be included in the invention. In certain aspects, polypeptides of 100, 200, 300 or more amino acids are preferred. The kinase polypeptide can be encoded by a full-length nucleic acid sequence or any portion of the full-length nucleic acid sequence, so long as a functional activity of the polypeptide is retained. By "functional" domain is meant any region of the polypeptide that may play a regulatory or catalytic role as predicted from amino acid sequence homology to other proteins or by the presence of amino acid sequences that may give rise to specific structural conformations (*i.e.*, coiled-coils). For some purposes, polypeptide domains are preferred, including, but not limited to, N-terminal, catalytic/kinase and C-terminal.

The amino acid sequence will be substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID

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ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 or portions of or the entire corresponding full-length amino acid sequences.

By "identity" is meant a property of sequences that measures their similarity or relationship. Identity is measured by dividing the number of identical residues between two sequences (either full-length or a defined domain) by the total number of residues in the known sequence, or the domain of the known sequence, and multiplying the product by 100. Thus, two copies of exactly the same sequence have 100% identity, but sequences that are less highly conserved, and have replacements and substitutions, have a lower degree of identity. "Gaps" are spaces in an alignment that can result from aligning a novel sequence with a known sequence when the novel sequence has additions or deletions of amino acids in comparison with the known sequence. These gaps do not factor into the assessment of % identity using the above calculation.

Those skilled in the art will recognize that several computer programs are also available for determining sequence identity using standard parameters, for example, Blast (Altschul, *et al.* (1997) Nucleic Acids Res. 25:3389-3402), Blast2 (Altschul, *et al.* (1990) J. Mol. Biol. 215:403-410), and Smith-Waterman (Smith, *et al.* (1981) J. Mol. Biol. 147:195-197).

In preferred embodiments, the invention features isolated, enriched, or purified nucleic acid molecules encoding a kinase polypeptide comprising a nucleotide sequence that: (a) encodes a polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ

ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID

NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID

NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; (b) is the complement of the nucleotide sequence of (a); (c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring kinase polypeptide; (d) encodes a kinase polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID

NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence of SEQ ID

NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of a domain selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; (e) is the complement of the nucleotide sequence of (d); (f) encodes a polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID

NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. (The domain demarcations of the polypeptides of the invention are indicated in Table 2 by reference to the kinase domain.) A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID

NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ

ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; (b) is the complement of the nucleotide sequence of (a); (c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring kinase polypeptide; (d) encodes a kinase polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID ID

NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof.

A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235,

SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to a domain of a polypeptide selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, where the domain is selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; (g) is the complement of the nucleotide sequence of (f); (h) encodes a polypeptide having an amino acid sequence selected from the group consisting

of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148,

SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID

NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; (b) is the complement of the nucleotide sequence of (a); (c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring kinase polypeptide; (d) encodes a kinase polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID

NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,

SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more of the domains selected from the group consisting of a N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; or (i) is the

complement of the nucleotide sequence of (h). The domain demarcations of the polypeptides of the invention are indicated in Table 2 by reference to the kinase domain.

The term "complement" refers to two nucleotides that can form multiple favorable interactions with one another. For example, adenine is complementary to thymine as they can form two hydrogen bonds. Similarly, guanine and cytosine are complementary since they can form three hydrogen bonds. A nucleotide sequence is the complement of another nucleotide sequence if all of the nucleotides of the first sequence are complementary to all of the nucleotides of the second sequence.

The term "domain" refers to a region of a polypeptide that contains a particular function. For instance, N-terminal or C-terminal domains of signal transduction proteins can serve functions including, but not limited to, binding molecules that localize the signal transduction molecule to different regions of the cell or binding other signaling molecules directly responsible for propagating a particular cellular signal. Some domains can be expressed separately from the rest of the protein and function by themselves, while others must remain part of the intact protein to retain function. The latter are termed functional regions of proteins and also relate to domains.

The term "N-terminal domain" refers to the extracatalytic region located between the initiator methionine and the catalytic domain of the protein kinase. The N-terminal domain can be identified following a Smith-Waterman alignment of the protein sequence against the non-redundant protein database to define the N-terminal boundary of the catalytic domain. Depending on its length, the N-terminal domain may or may not play a regulatory role in kinase function. An example of a protein kinase whose N-terminal domain has been shown to play a regulatory role is PAK65, which contains a CRIB motif used for Cdc42 and rac binding (Burbelo, P.D. *et al.* (1995) J. Biol. Chem. 270, 29071-29074). The N-terminal domain of a protein kinase of the invention is that portion of the protein kinase to the amino-terminal side of the kinase domain where the kinase domain is identified in Table 2, herein. Further, in some cases, portions of the N-terminal domains of the protein kinases of the invention have not been identified since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined and using the approaches described herein the N-terminal domain can be identified.

The term "catalytic domain" or "kinase domain" refers to a region of the protein kinase that is typically 25-300 amino acids long and is responsible for carrying out the phosphate transfer reaction from a high-energy phosphate donor molecule such as ATP or GTP to itself (autophosphorylation) or to other proteins (exogenous phosphorylation). The catalytic domain of protein kinases is made up of 12 subdomains that contain highly conserved amino acid residues, and are responsible for proper polypeptide folding and for catalysis. The catalytic domain can be identified following a Smith-Waterman alignment of the protein sequence against the non-redundant protein database. The catalytic/kinase domains of the protein kinases of the invention are identified in Table 2, herein. Further, in some cases, the complete sequence of the catalytic/kinase domains of the protein kinases of the invention may not have been provided since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined, and using the approaches described herein, the catalytic/kinase domain can be identified.

The term "catalytic activity", as used herein, defines the rate at which a kinase catalytic domain phosphorylates a substrate. Catalytic activity can be measured, for example, by determining the amount of a substrate converted to a phosphorylated product as a function of time. Catalytic activity can be measured by methods of the invention by holding time constant and determining the concentration of a phosphorylated substrate after a fixed period of time. Phosphorylation of a substrate occurs at the active-site of a protein kinase. The active-site is normally a cavity in which the substrate binds to the protein kinase and is phosphorylated.

The term "substrate" as used herein refers to a molecule phosphorylated by a kinase of the invention. Kinases phosphorylate substrates on serine/threonine or tyrosine amino acids. The molecule may be another protein or a polypeptide.

The term "C-terminal domain" refers to the region located between the catalytic domain and the carboxy-terminal amino acid residue of the protein kinase. The C-terminal domain can be identified by using a Smith-Waterman alignment of the protein sequence against the non-redundant protein database to define the C-terminal boundary of the catalytic domain or of any functional C-terminal extracatalytic domain. Depending on its length and amino acid composition, the C-terminal domain may or may not play a regulatory role in kinase function. An example of a protein kinase whose C-terminal

domain may play a regulatory role is PAK3 which contains a heterotrimeric G_b subunit-binding site near its C-terminus (Leeuw, T. *et al.* (1998) Nature, 391, 191-195). The C-terminal domain of a protein kinase of the invention is that portion of the protein kinase to the carboxy-terminal side of the kinase domain where the kinase domain is identified in Table 2, herein. In some cases, the C-terminal domains of the protein kinases of the invention have not been provided since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined, and using the approaches described herein, the C-terminal domain can be identified.

The term "signal transduction pathway" refers to the molecules that propagate an extracellular signal through the cell membrane to become an intracellular signal. This signal can then stimulate a cellular response. The polypeptide molecules involved in signal transduction processes are typically receptor and non-receptor protein tyrosine kinases, receptor and non-receptor protein phosphatases, SRC homology 2 and 3 domains, phosphotyrosine binding proteins (SRC homology 2 (SH2) and phosphotyrosine binding (PTB and PH) domain containing proteins), proline-rich binding proteins (SH3 domain containing proteins), nucleotide exchange factors, and transcription factors.

The term "coiled-coil structure region" as used herein, refers to a polypeptide sequence that has a high probability of adopting a coiled-coil structure as predicted by computer algorithms such as COILS (Lupas, A. (1996) Meth. Enzymology 266:513-525). Coiled-coils are formed by two or three amphipathic α-helices in parallel. Coiled-coils can bind to coiled-coil domains of other polypeptides resulting in homo- or heterodimers (Lupas, A. (1991) Science 252:1162-1164). Coiled-coil-dependent oligomerization has been shown to be necessary for protein function including catalytic activity of serine/threonine kinases (Roe, J. *et al.* (1997) J. Biol. Chem. 272:5838-5845). Coiled-coil regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "proline-rich region" as used herein, refers to a region of a protein kinase whose proline content over a given amino acid length is higher than the average content of this amino acid found in proteins (*i.e.*, >10%). Proline-rich regions are easily discernable by visual inspection of amino acid sequences and quantitated by standard computer

sequence analysis programs such as the DNAStar program EditSeq. Proline-rich regions have been demonstrated to participate in regulatory protein -protein interactions. Among these interactions, those that are most relevant to this invention involve the "PxxP" proline rich motif found in certain protein kinases (*i.e.*, human PAK1) and the SH3 domain of the adaptor molecule Nck (Galisteo, M.L. *et al.* (1996) J. Biol. Chem. 271:20997-21000). Other regulatory interactions involving "PxxP" proline-rich motifs include the WW domain (Sudol, M. (1996) Prog. Biophys. Mol. Bio. 65:113-132). Proline rich regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "spacer region" as used herein, refers to a region of the protein kinase located between predicted functional domains. The spacer region has no detectable homology to any amino acid sequence in the database, and can be identified by using a Smith-Waterman alignment of the protein sequence against the non-redundant protein database to define the C- and N-terminal boundaries of the flanking functional domains. Spacer regions may or may not play a fundamental role in protein kinase function. Precedence for the regulatory role of spacer regions in kinase function is provided by the role of the src kinase spacer in inter-domain interactions (Xu, W. *et al.* (1997) Nature 385:595-602). Spacer regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "insert" as used herein refers to a portion of a protein kinase that is absent from a close homolog. Inserts may or may not by the product alternative splicing of exons. Inserts can be identified by using a Smith-Waterman sequence alignment of the protein sequence against the non-redundant protein database, or by means of a multiple sequence alignment of homologous sequences using the DNAStar program Megalign. Inserts may play a functional role by presenting a new interface for protein-protein interactions, or by interfering with such interactions. Insert regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "C-terminal tail" as used herein, refers to a C-terminal domain of a protein kinase, that by homology extends or protrudes past the C-terminal amino acid of its closest homolog. C-terminal tails can be identified by using a Smith-Waterman sequence alignment of the protein sequence against the non-redundant protein database, or by means of a multiple sequence alignment of homologous sequences using the DNAStar program Megalign. Depending on its length, a C-terminal tail may or may not play a regulatory role in kinase function. C-terminal tail regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

Various low or high stringency hybridization conditions may be used depending upon the specificity and selectivity desired. These conditions are well-known to those skilled in the art. Under stringent hybridization conditions only highly complementary nucleic acid sequences hybridize. Preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 20 contiguous nucleotides, more preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 50 contiguous nucleotides, most preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 100 contiguous nucleotides. In some instances, the conditions may prevent hybridization of nucleic acids having more than 5 mismatches in the full-length sequence.

By stringent hybridization assay conditions is meant hybridization assay conditions at least as stringent as the following: hybridization in 50% formamide, 5X SSC, 50 mM NaH_2PO_4, pH 6.8, 0.5% SDS, 0.1 mg/mL sonicated salmon sperm DNA, and 5X Denhart solution at 42 °C overnight; washing with 2X SSC, 0.1% SDS at 45 °C; and washing with 0.2X SSC, 0.1% SDS at 45 °C. Under some of the most stringent hybridization assay conditions, the second wash can be done with 0.1X SSC at a temperature up to 70 °C (pg. 421, Berger *et al.* (1987) Guide to Molecular Cloning Techniques, Meth. Enzym. vol. 152, hereby incorporated by reference herein including any figures, tables, or drawings.). However, other applications may require the use of conditions falling between these sets of conditions. Methods of determining the conditions required to achieve desired hybridizations are well-known to those with ordinary skill in the art, and are based on several factors, including but not limited to, the sequences to be hybridized and the samples to be tested.

In other preferred embodiments, the invention features isolated, enriched, or purified nucleic acid molecules encoding kinase polypeptides, further comprising a vector or promoter effective to initiate transcription in a host cell. The invention also features recombinant nucleic acid, preferably in a cell or an organism. The recombinant nucleic acid may contain a sequence selected from the group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or a functional derivative thereof and a vector or a promoter effective to initiate transcription in a host cell. The recombinant nucleic acid can alternatively contain a transcriptional initiation region functional in a cell, a sequence complementary to an RNA sequence encoding a kinase polypeptide and a transcriptional termination region functional in a cell. Specific

vectors and host cell combinations are discussed herein. The recombinant nucleic acid can also contain the full-length sequence encoding the protein kinase, or a domain, for example.

The term "vector" relates to a single or double-stranded circular nucleic acid molecule that can be transfected into cells and replicated within or independently of a cell genome. A circular double-stranded nucleic acid molecule can be cut and thereby linearized upon treatment with restriction enzymes. An assortment of nucleic acid vectors, restriction enzymes, and the knowledge of the nucleotide sequences cut by restriction enzymes are readily available to those skilled in the art. A nucleic acid molecule encoding a kinase can be inserted into a vector by cutting the vector with restriction enzymes and ligating the two pieces together.

The term "transfecting" defines a number of methods to insert a nucleic acid vector or other nucleic acid molecules into a cellular organism. These methods involve a variety of techniques, such as treating the cells with high concentrations of salt, an electric field, detergent, or DMSO to render the outer membrane or wall of the cells permeable to nucleic acid molecules of interest or use of various viral transduction strategies.

The term "promoter" as used herein, refers to nucleic acid sequence needed for gene sequence expression. Promoter regions vary from organism to organism, but are well known to persons skilled in the art for different organisms. For example, in prokaryotes, the promoter region contains both the promoter (which directs the initiation of RNA transcription) as well as the DNA sequences which, when transcribed into RNA, will signal synthesis initiation. Such regions will normally include those 5'-non-coding sequences involved with initiation of transcription and translation, such as the TATA box, capping sequence, CAAT sequence, and the like.

In preferred embodiments, the isolated nucleic acid comprises, consists essentially of, or consists of a nucleic acid sequence set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35,

SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequence, encodes an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID

NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, a functional derivative thereof, or at least 10, 20, 40, 50, 75, 100, 200, 300 or 500 contiguous amino acids of a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID

NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length sequences or derivatives thereof. The nucleic acid may be isolated from a natural source by cDNA cloning or by subtractive hybridization. The natural source may be mammalian, preferably human, blood, semen, or tissue and the nucleic acid may be synthesized by the triester method or by using an automated DNA synthesizer.

The term "mammal" refers preferably to such organisms as mice, rats, rabbits, guinea pigs, sheep, and goats, more preferably to cats, dogs, monkeys, and apes, and most preferably to humans.

In yet other preferred embodiments, the nucleic acid is a conserved or unique region, for example those useful for: the design of hybridization probes to facilitate identification and cloning of additional polypeptides, the design of PCR probes to facilitate cloning of additional polypeptides, obtaining antibodies to polypeptide regions, and designing antisense oligonucleotides.

By "conserved nucleic acid regions", are meant regions present on two or more nucleic acids encoding a kinase polypeptide, to which a particular nucleic acid sequence can hybridize under lower stringency conditions. Examples of lower stringency conditions suitable for screening for nucleic acid encoding kinase polypeptides are provided in Berger *et al.* (1987) Guide to Molecular Cloning Techniques, Meth. Enzym. vol. 152, hereby incorporated by reference herein in its entirety, including any drawings, figures, or tables. Preferably, conserved regions differ by no more than 5 out of 20 nucleotides, even more preferably 2 out of 20 nucleotides or most preferably 1 out of 20 nucleotides.

By "unique nucleic acid region" is meant a sequence present in a nucleic acid coding for a kinase polypeptide that is not present in a sequence coding for any other naturally occurring polypeptide. Such regions preferably encode 10 (preferably 25, more preferably 50, most preferably 75) or more contiguous amino acids selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,

SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or functional derivatives thereof. In particular, a unique nucleic acid region is preferably of mammalian origin and preferably human.

A second aspect of the invention features a nucleic acid probe for the detection of nucleic acid encoding a kinase polypeptide in a sample, wherein said polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,

SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. Preferably, the nucleic acid probe encodes a kinase polypeptide that is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167,

SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequences. The nucleic acid probe contains a nucleotide base sequence that will hybridize to a sequence selected from the group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ

ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequence, or a functional derivative thereof.

In preferred embodiments, the nucleic acid probe hybridizes to nucleic acid encoding at least 6, 12, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids of a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID

NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or functional derivatives thereof.

Methods for using the probes include detecting the presence or amount of kinase RNA in a sample by contacting the sample with a nucleic acid probe under conditions such that hybridization occurs and detecting the presence or amount of the probe bound to kinase RNA. The nucleic acid duplex formed between the probe and a nucleic acid sequence coding for a kinase polypeptide may be used in the identification of the sequence of the nucleic acid detected (Nelson *et al.*, in Nonisotopic DNA Probe Techniques, Academic Press, San Diego, Kricka, ed., p. 275, 1992, hereby incorporated by reference herein in its entirety, including any drawings, figures, or tables). Kits for performing such methods may be constructed to include a container means having disposed therein a nucleic acid probe.

In a third aspect, the invention describes a recombinant cell or tissue comprising a nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,

SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. In such cells, the nucleic acid may be under the control of the genomic regulatory elements, or may be under the control of exogenous regulatory elements including an exogenous promoter. By "exogenous" it is meant a promoter that is not normally coupled *in vivo* transcriptionally to the coding sequence for the kinase polypeptides.

The polypeptide is preferably a fragment of the protein encoded by an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID

NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence. By "fragment," is meant an amino acid sequence present in a kinase polypeptide. Preferably, such a sequence comprises at least 10, 20, 40, 50, 75, 100, 200, or 300 contiguous amino acids a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,

SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or of the corresponding full-length amino acid sequence, or a functional derivative thereof.

In a fourth aspect, the invention features an isolated, enriched, or purified kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ

ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

By "isolated" in reference to a polypeptide is meant a polymer of amino acids (2 or more amino acids) conjugated to each other, including polypeptides that are isolated from a natural source or that are synthesized. The isolated polypeptides of the present invention are unique in the sense that they are not found in a pure or separated state in nature. Use of the term "isolated" indicates that a naturally occurring sequence has been removed from its normal cellular environment. Thus, the sequence may be in a cell-free solution or placed in a different cellular environment. The term does not imply that the sequence is the only amino acid chain present, but that it is essentially free (about 90 - 95% pure at least) of non-amino acid material naturally associated with it.

By the use of the term "enriched" in reference to a polypeptide is meant that the specific amino acid sequence constitutes a significantly higher fraction (2 - 5 fold) of the total amino acid sequences present in the cells or solution of interest than in normal or diseased cells or in the cells from which the sequence was taken. This could be caused by a person by preferential reduction in the amount of other amino acid sequences present, or by a preferential increase in the amount of the specific amino acid sequence of interest, or by a combination of the two. However, it should be noted that enriched does not imply that there are no other amino acid sequences present, just that the relative amount of the sequence of interest has been significantly increased. The term significant here is used to indicate that the level of increase is useful to the person making such an increase, and generally means an increase relative to other amino acid sequences of about at least 2-fold, more preferably at least 5- to 10-fold or even more. The term also does not imply that there is no amino acid sequence from other sources. The other source of amino acid sequences may, for example, comprise amino acid sequence encoded by a yeast or bacterial genome, or a cloning vector such as pUC19. The term is meant to cover only those situations in which man has intervened to increase the proportion of the desired amino acid sequence.

It is also advantageous for some purposes that an amino acid sequence be in purified form. The term "purified" in reference to a polypeptide does not require absolute purity (such as a homogeneous preparation); instead, it represents an indication that the sequence is relatively purer than in the natural environment. Compared to the natural level

this level should be at least 2-5 fold greater (*e.g.*, in terms of mg/mL). Purification of at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated. The substance is preferably free of contamination at a functionally significant level, for example 90%, 95%, or 99% pure.

In preferred embodiments, the kinase polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequences. Preferably, the kinase polypeptide contains at least 10, 20, 40, 50, 75, 100, 200, or 300 contiguous

amino acids a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or a functional derivative thereof.

In preferred embodiments, the kinase polypeptide comprises an amino acid sequence having (a) an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ

ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221. SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; (b) an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ

ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of a domain selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; (c) an amino acid sequence of a domain of a polypeptide selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,

SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 where the domain is selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; or (d) an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,

SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of the domains selected from the group consisting of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, an insert, and a C-terminal tail. (The domain demarcations of the polypeptides of the invention are indicated in Table 2 by reference to the kinase domain.)

The polypeptide can be isolated from a natural source by methods well-known in the art. The natural source may be mammalian, preferably human, blood, semen, or tissue, and the polypeptide may be synthesized using an automated polypeptide synthesizer. The isolated, enriched, or purified kinase polypeptide is preferably selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ

ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242A.

In some embodiments the invention includes a recombinant kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,

SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. By "recombinant kinase polypeptide" is meant a polypeptide produced by recombinant DNA techniques such that it is distinct from a naturally occurring polypeptide either in its location (*e.g.*, present in a different cell or tissue than found in nature), purity or structure. Generally, such a recombinant polypeptide will be present in a cell in an amount different from that normally observed in nature.

In a fifth aspect, the invention features an antibody (*e.g.*, a monoclonal or polyclonal antibody) having specific binding affinity to a kinase polypeptide or a kinase polypeptide domain or fragment where the polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ

ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. In preferred embodiments, the antibody binds specifically to domains of kinase polypeptides, that are defined *supra*.

By "specific binding affinity" is meant that the antibody binds to the target kinase polypeptide with greater affinity than it binds to other polypeptides under specified conditions. Antibodies or antibody fragments are polypeptides that contain regions that can bind other polypeptides. The term "specific binding affinity" describes an antibody that binds to a kinase polypeptide with greater affinity than it binds to other polypeptides under specified conditions.

The term "polyclonal" refers to antibodies that are heterogenous populations of antibody molecules derived from the sera of animals immunized with an antigen or an antigenic functional derivative thereof. For the production of polyclonal antibodies, various host animals may be immunized by injection with the antigen. Various adjuvants may be used to increase the immunological response, depending on the host species.

"Monoclonal antibodies" are substantially homogenous populations of antibodies to a particular antigen. They may be obtained by any technique which provides for the production of antibody molecules by continuous cell lines in culture. Monoclonal antibodies may be obtained by methods known to those skilled in the art (Kohler *et al.*, Nature 256:495-497, 1975, and U.S. Patent No. 4,376,110, both of which are hereby incorporated by reference herein in their entirety including any figures, tables, or drawings).

The term "antibody fragment" refers to a portion of an antibody, often the hyper variable region and portions of the surrounding heavy and light chains, that displays specific binding affinity for a particular molecule. A hyper variable region is a portion of an antibody that physically binds to the polypeptide target.

Antibodies or antibody fragments having specific binding affinity to a kinase polypeptide or domains of a kinase polypeptide of the invention may be used in methods for detecting the presence and/or amount of kinase polypeptide in a sample by probing the sample with the antibody under conditions suitable for kinase-antibody immunocomplex formation and detecting the presence and/or amount of the antibody conjugated to the

kinase polypeptide. Diagnostic kits for performing such methods may be constructed to include antibodies or antibody fragments specific for the kinase as well as a conjugate of a binding partner of the antibodies or the antibodies themselves.

An antibody or antibody fragment with specific binding affinity to a kinase polypeptide of the invention can be isolated, enriched, or purified from a prokaryotic or eukaryotic organism. Routine methods known to those skilled in the art enable production of antibodies or antibody fragments, in both prokaryotic and eukaryotic organisms. Purification, enrichment, and isolation of antibodies, which are polypeptide molecules, are described above.

Antibodies having specific binding affinity to a kinase polypeptide of the invention may be used in methods for detecting the presence and/or amount of kinase polypeptide in a sample by contacting the sample with the antibody under conditions such that an immunocomplex forms and detecting the presence and/or amount of the antibody conjugated to the kinase polypeptide. Diagnostic kits for performing such methods may be constructed to include a first container containing the antibody and a second container having a conjugate of a binding partner of the antibody and a label, such as, for example, a radioisotope. The diagnostic kit may also include notification of an FDA approved use and instructions therefor.

In a sixth aspect, the invention features a hybridoma which produces an antibody having specific binding affinity to a kinase polypeptide or a kinase polypeptide domain, where the polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID

NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; and where the domains are defined as above. By "hybridoma" is meant an immortalized cell line that is capable of secreting an antibody, for example an antibody to a kinase of the invention. In preferred embodiments, the antibody to the kinase comprises a sequence of amino acids that is able to specifically bind a kinase polypeptide of the invention.

In a seventh aspect, the invention features a kinase polypeptide binding agent able to bind to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,

SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. The binding agent is preferably a purified antibody that recognizes an epitope present on a kinase polypeptide of the invention. Other binding agents include molecules that bind to kinase polypeptides and analogous molecules that bind to a kinase polypeptide. Such binding agents may be identified by using assays that measure kinase binding partner activity, such as those that measure PDGFR activity.

The invention also features a method for screening for human cells containing a kinase polypeptide of the invention or an equivalent sequence. The method involves identifying the novel polypeptide in human cells using techniques that are routine and standard in the art, such as those described herein for identifying the kinases of the invention (*e.g.*, cloning, Southern or Northern blot analysis, in situ hybridization, PCR amplification, etc.).

In an eighth aspect, the invention features methods for identifying a substance that modulates kinase activity comprising the steps of: (a) contacting a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,

SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 with a test substance; (b) measuring the activity of said polypeptide; and (c) determining whether said substance modulates the activity of said polypeptide.

The term "modulates" refers to the ability of a compound to alter the function of a kinase of the invention. A modulator preferably activates or inhibits the activity of a kinase of the invention.

The term "activates" refers to increasing the cellular activity of the kinase. The term inhibit refers to decreasing the cellular activity of the kinase. Kinase activity is preferably the interaction with a natural binding partner.

The term "modulates" also refers to altering the function of kinases of the invention by increasing or decreasing the probability that a complex forms between the kinase and a natural binding partner. A modulator preferably increases the probability that such a complex forms between the kinase and the natural binding partner, more preferably increases or decreases the probability that a complex forms between the kinase and the natural binding partner depending on the concentration of the compound exposed to the

kinase, and most preferably decreases the probability that a complex forms between the kinase and the natural binding partner.

The term "complex" refers to an assembly of at least two molecules bound to one another. Signal transduction complexes often contain at least two protein molecules bound to one another. For instance, a protein tyrosine receptor protein kinase, GRB2, SOS, RAF, and RAS assemble to form a signal transduction complex in response to a mitogenic ligand.

The term "natural binding partner" refers to polypeptides, lipids, small molecules, or nucleic acids that bind to kinases in cells. A change in the interaction between a kinase and a natural binding partner can manifest itself as an increased or decreased probability that the interaction forms, or an increased or decreased concentration of kinase/natural binding partner complex.

The term "contacting" as used herein refers to mixing a solution comprising the test compound with a liquid medium bathing the cells of the methods. The solution comprising the compound may also comprise another component, such as dimethyl sulfoxide (DMSO), which facilitates the uptake of the test compound or compounds into the cells of the methods. The solution comprising the test compound may be added to the medium bathing the cells by utilizing a delivery apparatus, such as a pipet-based device or syringe-based device.

In a ninth aspect, the invention features methods for identifying a substance that modulates kinase activity in a cell comprising the steps of: (a) expressing a kinase polypeptide in a cell, wherein said polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171,

SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; (b) adding a test substance to said cell; and (c) monitoring a change in cell phenotype or the interaction between said polypeptide and a natural binding partner.

The term "expressing" as used herein refers to the production of kinases of the invention from a nucleic acid vector containing kinase genes within a cell. The nucleic acid vector is transfected into cells using well known techniques in the art as described herein.

In a tenth aspect, the invention provides methods for treating a disease or abnormal condition by administering to a patient in need of such treatment a substance that modulates the activity of a polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID

NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. Preferably, the disease is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer. Also included are metabolic disorders, such as diabetes mellitus, and reproductive disorders, such as infertility.

Preferably, the disease or disorder is selected from the group consisting of rheumatoid arthritis, artherosclerosis, autoimmune disorders, and organ transplantation. Preferably the disease or disorder is selected from the group consisting of immune-related diseases and disorders, myocardial infarction, cardiomyopathies, stroke, renal failure, and oxidative stress-related neurodegenerative disorders. Most preferably, the immune-related diseases and disorders are selected from the group consisting of rheumatoid arthritis, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, atherosclerosis, rhinitis, autoimmunity, and organ transplantation.

Substances useful for treatment of disorders or diseases preferably show positive results in one or more in vitro assays for an activity corresponding to treatment of the disease or disorder in question Substances that modulate the activity of the polypeptides

preferably include, but are not limited to, antisense oligonucleotides and inhibitors of protein kinases.

The term "preventing" refers to decreasing the probability that an organism contracts or develops an abnormal condition.

The term "treating" refers to having a therapeutic effect and at least partially alleviating or abrogating an abnormal condition in the organism.

The term "therapeutic effect" refers to the inhibition or activation factors causing or contributing to the abnormal condition. A therapeutic effect relieves to some extent one or more of the symptoms of the abnormal condition. In reference to the treatment of abnormal conditions, a therapeutic effect can refer to one or more of the following: (a) an increase in the proliferation, growth, and/or differentiation of cells; (b) inhibition (*i.e.*, slowing or stopping) of cell death; (c) inhibition of degeneration; (d) relieving to some extent one or more of the symptoms associated with the abnormal condition; and (e) enhancing the function of the affected population of cells. Compounds demonstrating efficacy against abnormal conditions can be identified as described herein.

The term "abnormal condition" refers to a function in the cells or tissues of an organism that deviates from their normal functions in that organism. An abnormal condition can relate to cell proliferation, cell differentiation or cell survival. An abnormal condition may also include irregularities in cell cycle progression, i.e., irregularities in normal cell cycle progression through mitosis and meiosis.

Abnormal cell proliferative conditions include cancers such as fibrotic and mesangial disorders, abnormal angiogenesis and vasculogenesis, wound healing, psoriasis, diabetes mellitus, and inflammation.

Abnormal differentiation conditions include, but are not limited to neurodegenerative disorders, slow wound healing rates, and slow tissue grafting healing rates.

Abnormal cell survival conditions relate to conditions in which programmed cell death (apoptosis) pathways are activated or abrogated. A number of protein kinases are associated with the apoptosis pathways. Aberrations in the function of any one of the protein kinases could lead to cell immortality or premature cell death.

The term "aberration", in conjunction with the function of a kinase in a signal transduction process, refers to a kinase that is over- or under-expressed in an organism, mutated such that its catalytic activity is lower or higher than wild-type protein kinase activity, mutated such that it can no longer interact with a natural binding partner, is no longer modified by another protein kinase or protein phosphatase, or no longer interacts with a natural binding partner.

The term "administering" relates to a method of incorporating a compound into cells or tissues of an organism. The abnormal condition can be prevented or treated when the cells or tissues of the organism exist within the organism or outside of the organism. Cells existing outside the organism can be maintained or grown in cell culture dishes. For cells harbored within the organism, many techniques exist in the art to administer compounds, including (but not limited to) oral, parenteral, dermal, injection, and aerosol applications. For cells outside of the organism, multiple techniques exist in the art to administer the compounds, including (but not limited to) cell microinjection techniques, transformation techniques, and carrier techniques.

The abnormal condition can also be prevented or treated by administering a compound to a group of cells having an aberration in a signal transduction pathway to an organism. The effect of administering a compound on organism function can then be monitored. The organism is preferably a mouse, rat, rabbit, guinea pig, or goat, more preferably a monkey or ape, and most preferably a human.

In an eleventh aspect, the invention features methods for detection the expression of a polypeptide in a sample as a diagnostic tool for diseases or disorders, wherein the method comprises the steps of: (a) contacting the sample with a nucleic acid probe which hybridizes under hybridization assay conditions to a nucleic acid target region of a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ

ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, said probe comprising the nucleic acid sequence encoding the polypeptide, fragments thereof, and the complements of the sequences and fragments; and (b) detecting the presence or amount of the probe:target region hybrid as an indication of the disease.

In preferred embodiments of the invention, the disease or disorder is selected from the group consisting of rheumatoid arthritis, artherosclerosis, autoimmune disorders, organ transplantation, myocardial infarction, cardiomyopathies, stroke, renal failure, oxidative stress-related neurodegenerative disorders, metabolic disorder including diabetes, reproductive disorders including infertility, and cancer.

The kinase "target region" is a nucleotide base sequence selected from the group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID

NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequences, a functional derivative thereof, or a fragment thereof to which the nucleic acid probe will specifically hybridize. Specific hybridization indicates that in the presence of other nucleic acids the probe only hybridizes detectably with the kinase of the invention's target region. Putative target regions can be identified by methods well known in the art consisting of alignment and comparison of the most closely related sequences in the database.

In preferred embodiments the nucleic acid probe hybridizes to a kinase target region encoding at least 6, 12, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids of the sequence set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID

NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or a functional derivative thereof. Hybridization conditions should be such that hybridization occurs only with the kinase genes in the presence of other nucleic acid molecules. Under stringent hybridization conditions only highly complementary nucleic acid sequences hybridize. Preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 20 contiguous nucleotides. Such conditions are defined *supra*.

Hybridization conditions should be such that hybridization occurs only with the genes in the presence of other nucleic acid molecules. Under stringent hybridization conditions only highly complementary nucleic acid sequences hybridize. Preferably, such conditions prevent hybridization of nucleic acids having 1 or 2 mismatches out of 20 contiguous nucleotides. Such conditions are defined *supra*.

The diseases for which detection of kinase genes in a sample could be diagnostic include diseases in which kinase nucleic acid (DNA and/or RNA) is amplified in comparison to normal cells. By "amplification" is meant increased numbers of kinase

DNA or RNA in a cell compared with normal cells. In normal cells, kinases are typically found as single copy genes. In selected diseases, the chromosomal location of the kinase genes may be amplified, resulting in multiple copies of the gene, or amplification. Gene amplification can lead to amplification of kinase RNA, or kinase RNA can be amplified in the absence of kinase DNA amplification.

"Amplification" as it refers to RNA can be the detectable presence of kinase RNA in cells, since in some normal cells there is no basal expression of kinase RNA. In other normal cells, a basal level of expression of kinase exists, therefore in these cases amplification is the detection of at least 1-2-fold, and preferably more, kinase RNA, compared to the basal level.

The diseases that could be diagnosed by detection of kinase nucleic acid in a sample preferably include cancers. The test samples suitable for nucleic acid probing methods of the present invention include, for example, cells or nucleic acid extracts of cells, or biological fluids. The samples used in the above-described methods will vary based on the assay format, the detection method and the nature of the tissues, cells or extracts to be assayed. Methods for preparing nucleic acid extracts of cells are well known in the art and can be readily adapted in order to obtain a sample that is compatible with the method utilized.

Another aspect of the invention involves a method of agonizing (stimulating) or antagonizing a target of the invention and a natural binding partner associated activity in a mammal comprising administering to said mammal an agonist or antagonist to one of the above disclosed polypeptides in an amount sufficient to effect said agonism or antagonism. A method of treating diseases in a mammal with an agonist or antagonist of the protein of the present invention activity comprising administering the agonist or antagonist to a mammal in an amount sufficient to agonize or antagonize associated functions is also encompassed in the present application.

In an effort to discover novel treatments for diseases, biomedical researchers and chemists have designed, synthesized, and tested molecules that inhibit the function of protein polypeptides. Some small organic molecules form a class of compounds that modulate the function of protein polypeptides. Examples of molecules that have been reported to inhibit the function of protein kinases include, but are not limited to, bis monocyclic, bicyclic or heterocyclic aryl compounds (PCT WO 92/20642, published

November 26, 1992 by Maguire *et al.*), vinylene-azaindole derivatives (PCT WO 94/14808, published July 7, 1994 by Ballinari *et al.*), 1-cyclopropyl-4-pyridyl-quinolones (U.S. Patent No. 5,330,992), styryl compounds (U.S. Patent No. 5,217,999), styryl-substituted pyridyl compounds (U.S. Patent No. 5,302,606), certain quinazoline derivatives (EP Application No. 0 566 266 A1), seleoindoles and selenides (PCT WO 94/03427, published February 17, 1994 by Denny *et al.*), tricyclic polyhydroxylic compounds (PCT WO 92/21660, published December 10, 1992 by Dow), and benzylphosphonic acid compounds (PCT WO 91/15495, published October 17, 1991 by Dow *et al*), all of which are incorporated by reference herein, including any drawings.

Compounds that can traverse cell membranes and are resistant to acid hydrolysis are potentially advantageous as therapeutics as they can become highly bioavailable after being administered orally to patients. However, many of these protein inhibitors only weakly inhibit function. In addition, many inhibit a variety of protein kinases and will therefore cause multiple side-effects as therapeutics for diseases.

Some indolinone compounds, however, form classes of acid resistant and membrane permeable organic molecules. WO 96/22976 (published August 1, 1996 by Ballinari *et al.*) describes hydrosoluble indolinone compounds that harbor tetralin, naphthalene, quinoline, and indole substituents fused to the oxindole ring. These bicyclic substituents are in turn substituted with polar groups including hydroxylated alkyl, phosphate, and ether substituents. U.S. Patent Application Serial Nos. 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang et al. (Lyon & Lyon Docket No. 221/187) and 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298) and International Patent Publication WO 96/22976, published August 1, 1996 by Ballinari *et al.*, all of which are incorporated herein by reference in their entirety, including any drawings, describe indolinone chemical libraries of indolinone compounds harboring other bicyclic moieties as well as monocyclic moieties fused to the oxindole ring. Applications 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187), 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon

& Lyon Docket No. 223/298), and WO 96/22976, published August 1, 1996 by Ballinari *et al.* teach methods of indolinone synthesis, methods of testing the biological activity of indolinone compounds in cells, and inhibition patterns of indolinone derivatives, both of which are incorporated by reference herein, including any drawings.

Other examples of substances capable of modulating kinase activity include, but are not limited to, tyrphostins, quinazolines, quinoxolines, and quinolines. The quinazolines, tyrphostins, quinolines, and quinoxolines referred to above include well known compounds such as those described in the literature. For example, representative publications describing quinazolines include Barker et al., EPO Publication No. 0 520 722 A1; Jones et al., U.S. Patent No. 4,447,608; Kabbe et al., U.S. Patent No. 4,757,072; Kaul and Vougioukas, U.S. Patent No. 5, 316,553; Kreighbaum and Comer, U.S. Patent No. 4,343,940; Pegg and Wardleworth, EPO Publication No. 0 562 734 A1; Barker et al., Proc. of Am. Assoc. for Cancer Research 32:327 (1991); Bertino, J.R., Cancer Research 3:293-304 (1979); Bertino, J.R., Cancer Research 9(2 part 1):293-304 (1979); Curtin et al., Br. J. Cancer 53:361-368 (1986); Fernandes et al., Cancer Research 43:1117-1123 (1983); Ferris et al. J. Org. Chem. 44(2):173-178; Fry et al., Science 265:1093-1095 (1994); Jackman et al., Cancer Research 51:5579-5586 (1981); Jones et al. J. Med. Chem. 29(6):1114-1118; Lee and Skibo, Biochemistry 26(23):7355-7362 (1987); Lemus et al., J. Org. Chem. 54:3511-3518 (1989); Ley and Seng, Synthesis 1975:415-522 (1975); Maxwell et al., Magnetic Resonance in Medicine 17:189-196 (1991); Mini et al., Cancer Research 45:325-330 (1985); Phillips and Castle, J. Heterocyclic Chem. 17(19):1489-1596 (1980); Reece et al., Cancer Research 47(11):2996-2999 (1977); Sculier et al., Cancer Immunol. and Immunother. 23:A65 (1986); Sikora et al., Cancer Letters 23:289-295 (1984); and Sikora et al., Analytical Biochem. 172:344-355 (1988), all of which are incorporated herein by reference in their entirety, including any drawings.

Quinoxaline is described in Kaul and Vougioukas, U.S. Patent No. 5,316,553, incorporated herein by reference in its entirety, including any drawings.

Quinolines are described in Dolle et al., J. Med. Chem. 37:2627-2629 (1994); MaGuire, J. Med. Chem. 37:2129-2131 (1994); Burke et al., J. Med. Chem. 36:425-432 (1993); and Burke et al. BioOrganic Med. Chem. Letters 2:1771-1774 (1992), all of which are incorporated by reference in their entirety, including any drawings.

Typhostins are described in Allen et al., Clin. Exp. Immunol. 91:141-156 (1993); Anafi et al., Blood 82:12:3524-3529 (1993); Baker et al., J. Cell Sci. 102:543-555 (1992); Bilder et al., Amer. Physiol. Soc. pp. 6363-6143:C721-C730 (1991); Brunton et al., Proceedings of Amer. Assoc. Cancer Rsch. 33:558 (1992); Bryckaert et al., Experimental Cell Research 199:255-261 (1992); Dong et al., J. Leukocyte Biology 53:53-60 (1993); Dong et al., J. Immunol. 151(5):2717-2724 (1993); Gazit et al., J. Med. Chem. 32:2344-2352 (1989); Gazit et al., " J. Med. Chem. 36:3556-3564 (1993); Kaur et al., Anti-Cancer Drugs 5:213-222 (1994); Kaur et al., King et al., Biochem. J. 275:413-418 (1991); Kuo et al., Cancer Letters 74:197-202 (1993); Levitzki, A., The FASEB J. 6:3275-3282 (1992); Lyall et al., J. Biol. Chem. 264:14503-14509 (1989); Peterson et al., The Prostate 22:335-345 (1993); Pillemer et al., Int. J. Cancer 50:80-85 (1992); Posner et al., Molecular Pharmacology 45:673-683 (1993); Rendu et al., Biol. Pharmacology 44(5):881-888 (1992); Sauro and Thomas, Life Sciences 53:371-376 (1993); Sauro and Thomas, J. Pharm. and Experimental Therapeutics 267(3):119-1125 (1993); Wolbring et al., J. Biol. Chem. 269(36):22470-22472 (1994); and Yoneda et al., Cancer Research 51:4430-4435 (1991); all of which are incorporated herein by reference in their entirety, including any drawings.

Other compounds that could be used as modulators include oxindolinones such as those described in U.S. patent application Serial No. 08/702,232 filed August 23, 1996, incorporated herein by reference in its entirety, including any drawings.

Methods of Treating a Disease (Enablement - i.e., Dosing)

Methods of determining the dosages of compounds to be administered to a patient and modes of administering compounds to an organism are disclosed in U.S. Application Serial No. 08/702,282, filed August 23, 1996 and International patent publication number WO 96/22976, published August 1 1996, both of which are incorporated herein by reference in their entirety, including any drawings, figures or tables. Those skilled in the art will appreciate that such descriptions are applicable to the present invention and can be easily adapted to it.

The proper dosage depends on various factors such as the type of disease being treated, the particular composition being used and the size and physiological condition of the patient. Therapeutically effective doses for the compounds described herein can be estimated initially from cell culture and animal models. For example, a dose can be

formulated in animal models to achieve a circulating concentration range that initially takes into account the IC_{50} as determined in cell culture assays. The animal model data can be used to more accurately determine useful doses in humans.

Plasma half-life and biodistribution of the drug and metabolites in the plasma, tumors and major organs can also be determined to facilitate the selection of drugs most appropriate to inhibit a disorder. Such measurements can be carried out. For example, HPLC analysis can be performed on the plasma of animals treated with the drug and the location of radiolabeled compounds can be deter-mined using detection methods such as X-ray, CAT scan and MRI. Compounds that show potent inhibitory activity in the screening assays, but have poor pharmacokinetic characteristics, can be optimized by altering the chemical structure and retesting. In this regard, compounds displaying good pharmacokinetic characteristics can be used as a model.

Toxicity studies can also be carried out by measuring the blood cell composition. For example, toxicity studies can be carried out in a suitable animal model as follows: 1) the compound is administered to mice (an untreated control mouse should also be used); 2) blood samples are periodically obtained via the tail vein from one mouse in each treatment group; and 3) the samples are analyzed for red and white blood cell counts, blood cell composition and the percent of lymphocytes versus polymorphonuclear cells. A comparison of results for each dosing regime with the controls indicates if toxicity is present.

At the termination of each toxicity study, further studies can be carried out by sacrificing the animals (preferably, in accordance with the American Veterinary Medical Association guidelines Report of the American Veterinary Medical Assoc. Panel on Euthanasia, <u>Journal of American Veterinary Medical Assoc.</u>, 202:229-249, 1993). Representative animals from each treatment group can then be examined by gross necropsy for immediate evidence of metastasis, unusual illness or toxicity. Gross abnormalities in tissue are noted and tissues are examined histologically. Compounds causing a reduction in body weight or blood components are less preferred, as are compounds having an adverse effect on major organs. In general, the greater the adverse effect the less preferred the compound.

For the treatment of cancers the expected daily dose of a hydrophobic pharmaceutical agent is between 1 to 500 mg/day, preferably 1 to 250 mg/day, and most preferably 1 to 50 mg/day. Drugs can be delivered less frequently provided plasma levels of the active moiety are sufficient to maintain therapeutic effectiveness.

Plasma levels should reflect the potency of the drug. Generally, the more potent the compound the lower the plasma levels necessary to achieve efficacy.

In a final aspect, the invention features a method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein the method comprises: (a) comparing a nucleic acid target region encoding the kinase polypeptide in a sample, where the kinase polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID

NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or one or more fragments thereof, with a control nucleic acid target region encoding the kinase polypeptide, or one or more fragments thereof; and (b) detecting differences in sequence or amount between the target region and the control target region, as an indication of the disease or disorder. Preferably, the disease or disorder is selected from the group consisting of immune-related diseases and disorders, organ transplantation, myocardial infarction, cardiovascular disease, stroke, renal failure, oxidative stress-related neurodegenerative disorders, and cancer. Immune-related diseases and disorders include, but are not limited to, those discussed previously.

The term "comparing" as used herein refers to identifying discrepancies between the nucleic acid target region isolated from a sample, and the control nucleic acid target region. The discrepancies can be in the nucleotide sequences, *e.g.* insertions, deletions, or point mutations, or in the amount of a given nucleotide sequence. Methods to determine these discrepancies in sequences are well-known to one of ordinary skill in the art. The "control" nucleic acid target region refers to the sequence or amount of the sequence found in normal cells, *e.g.* cells that are not diseased as discussed previously.

The term also includes anti-sense molecules drawn thereto.

The invention has been described broadly and generically herein. Each of the narrower species and subgeneric groupings falling within the generic disclosure also form part of the invention. This includes the generic description of the invention with a proviso or negative limitation removing any subject matter from the genus, regardless of whether or not the excised material is specifically recited herein. For example, in some instances the nucleotide sequence of particular kinase polypeptides may not be part of a preferred embodiment.

The summary of the invention described above is not limiting and other features and advantages of the invention will be apparent from the following detailed description of the invention, and from the claims.

BRIEF DESCRIPTION OF THE FIGURES

Figures 1A to 1BB shows the amino acid sequences of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

Figures 2A to 2MMMM shows the nucleic acid sequences of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID

NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121.

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates in part to kinase polypeptides, nucleic acids encoding such polypeptides, cells containing such nucleic acids, antibodies to such polypeptides, assays utilizing such polypeptides, and methods relating to all of the foregoing. The present invention is based upon the isolation and characterization of new kinase polypeptides. The polypeptides and nucleic acids may be produced using well-known and standard synthesis techniques when given the sequences presented herein.

I. The Nucleic Acids of the Invention

Included within the scope of this invention are the functional equivalents of the herein-described isolated nucleic acid molecules. The degeneracy of the genetic code permits substitution of certain codons by other codons that specify the same amino acid and hence would give rise to the same protein. The nucleic acid sequence can vary

substantially since, with the exception of methionine and tryptophan, the known amino acids can be coded for by more than one codon. Thus, portions or all of the kinase genes of the invention could be synthesized to give a nucleic acid sequence significantly different from one selected from the group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121. The encoded amino acid sequence thereof would, however, be preserved.

In addition, the nucleic acid sequence may comprise a nucleotide sequence which results from the addition, deletion or substitution of at least one nucleotide to the 5'-end and/or the 3'-end of the nucleic acid sequence shown in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID

NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or a derivative thereof. Any nucleotide or polynucleotide may be used in this regard, provided that its addition, deletion or substitution does not alter the amino acid sequence of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163,

SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, that is encoded by the nucleotide sequence. For example, the present invention is intended to include any nucleic acid sequence resulting from the addition of ATG as an initiation codon at the 5'-end of the inventive nucleic acid sequence or its derivative, or from the addition of TTA, TAG or TGA as a termination codon at the 3'-end of the inventive nucleotide sequence or its derivative. Moreover, the nucleic acid molecule of the present invention may, as necessary, have restriction endonuclease recognition sites added to its 5'-end and/or 3'-end.

Such functional alterations of a given nucleic acid sequence afford an opportunity to promote secretion and/or processing of heterologous proteins encoded by foreign nucleic acid sequences fused thereto, for example. All variations of the nucleotide sequence of the kinase genes of the invention and fragments thereof permitted by the genetic code are, therefore, included in this invention.

Further, it is possible to delete codons or to substitute one or more codons with codons other than degenerate codons to produce a structurally modified polypeptide, but one which has substantially the same utility or activity as the polypeptide produced by the unmodified nucleic acid molecule. As recognized in the art, the two polypeptides are

functionally equivalent, as are the two nucleic acid molecules that give rise to their production, even though the differences between the nucleic acid molecules are not related to the degeneracy of the genetic code. This is discussed further in the "Functional Derivatives" section, herein.

Finally, many of the nucleic acid molecules of the invention are provided as a partial sequence only (Fig. 2A through 2QQ). However, it is standard for one of ordinary skill in the art to obtain a full-length sequence when provided with a partial sequence. Similarly, when provided with a partial or full-length sequence it is standard for one of ordinary skill in the art to obtain nucleic acid sequence coding for homologous proteins. Therefore, these nucleic acid molecules are also part of the invention.

The characteristics of the protein kinase nucleic acid sequences of the invention are provided in Table 1. The protein kinases fall into 10 known groups: AGC, CAMK, CKI, CMGC, dsPK, EIFK, LIMK, MLK, STE and TK. In addition, there are a significant number of protein kinases that do not belong to any of the known groups, and therefore presumably define new protein kinase groups.

Additional characteristics may be found, *inter alia*, in the tables, namely Table 1, Table 2, Table 3 and Table 4, shown below.

II. Nucleic Acid Probes, Methods, and Kits for Detection of Protein Kinases.

A nucleic acid probe of the present invention may be used to probe an appropriate chromosomal or cDNA library by usual hybridization methods to obtain other nucleic acid molecules of the present invention. A chromosomal DNA or cDNA library may be prepared from appropriate cells according to recognized methods in the art (cf. "Molecular Cloning: A Laboratory Manual", second edition, Cold Spring Harbor Laboratory, Sambrook, Fritsch, & Maniatis, eds., 1989).

In the alternative, chemical synthesis can be carried out in order to obtain nucleic acid probes having nucleotide sequences that correspond to N-terminal, kinase or C-terminal portions, for example, of the amino acid sequence of the polypeptide of interest. The synthesized nucleic acid probes may be used as primers in a polymerase chain reaction (PCR) carried out in accordance with recognized PCR techniques, essentially according to PCR Protocols, "A Guide to Methods and Applications", Academic Press,

Michael, *et al.*, eds., 1990, utilizing the appropriate chromosomal or cDNA library to obtain the fragment of the present invention.

One skilled in the art can readily design such probes based on the sequence disclosed herein using methods of computer alignment and sequence analysis known in the art ("Molecular Cloning: A Laboratory Manual", 1989, *supra*). The hybridization probes of the present invention can be labeled by standard labeling techniques such as with a radiolabel, enzyme label, fluorescent label, biotin-avidin label, chemiluminescence, and the like. After hybridization, the probes may be visualized using known methods.

The nucleic acid probes of the present invention include RNA, as well as DNA probes, such probes being generated using techniques known in the art. The nucleic acid probe may be immobilized on a solid support. Examples of such solid supports include, but are not limited to, plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, and acrylic resins, such as polyacrylamide and latex beads. Techniques for coupling nucleic acid probes to such solid supports are well known in the art.

The test samples suitable for nucleic acid probing methods of the present invention include, for example, cells or nucleic acid extracts of cells, or biological fluids. The samples used in the above-described methods will vary based on the assay format, the detection method and the nature of the tissues, cells or extracts to be assayed. Methods for preparing nucleic acid extracts of cells are well known in the art and can be readily adapted in order to obtain a sample that is compatible with the method utilized.

One method of detecting the presence of nucleic acids of the invention in a sample comprises (a) contacting said sample with the above-described nucleic acid probe under conditions such that hybridization occurs, and (b) detecting the presence of said probe bound to said nucleic acid molecule. One skilled in the art would select the nucleic acid probe according to techniques known in the art as described above. Samples to be tested include but should not be limited to RNA samples of human tissue.

A kit for detecting the presence of nucleic acids of the invention in a sample comprises at least one container means having disposed therein the above-described nucleic acid probe. The kit may further comprise other containers comprising one or more of the following: wash reagents and reagents capable of detecting the presence of bound nucleic acid probe. Examples of detection reagents include, but are not limited to

radiolabelled probes, enzymatic labeled probes (horseradish peroxidase, alkaline phosphatase), and affinity labeled probes (biotin, avidin, or steptavidin).

In detail, a compartmentalized kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allow the efficient transfer of reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the probe or primers used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, and the like), and containers which contain the reagents used to detect the hybridized probe, bound antibody, amplified product, or the like. One skilled in the art will readily recognize that the nucleic acid probes described in the present invention can readily be incorporated into one of the established kit formats that are well known in the art.

III. DNA Constructs Comprising a Protein Kinase Nucleic Acid Molecule and Cells Containing These Constructs.

The present invention also relates to a recombinant DNA molecule comprising, 5' to 3', a promoter effective to initiate transcription in a host cell and the above-described nucleic acid molecules. In addition, the present invention relates to a recombinant DNA molecule comprising a vector and an above-described nucleic acid molecule. The present invention also relates to a nucleic acid molecule comprising a transcriptional region functional in a cell, a sequence complementary to an RNA sequence encoding an amino acid sequence corresponding to the above-described polypeptide, and a transcriptional termination region functional in said cell. The above-described molecules may be isolated and/or purified DNA molecules.

The present invention also relates to a cell or organism that contains an above-described nucleic acid molecule and thereby is capable of expressing a polypeptide. The polypeptide may be purified from cells that have been altered to express the polypeptide. A cell is said to be "altered to express a desired polypeptide" when the cell, through genetic manipulation, is made to produce a protein which it normally does not produce or

which the cell normally produces at lower levels. One skilled in the art can readily adapt procedures for introducing and expressing either genomic, cDNA, or synthetic sequences into either eukaryotic or prokaryotic cells.

A nucleic acid molecule, such as DNA, is said to be "capable of expressing" a polypeptide if it contains nucleotide sequences which contain transcriptional and translational regulatory information and such sequences are "operably linked" to nucleotide sequences which encode the polypeptide. An operable linkage is a linkage in which the regulatory DNA sequences and the DNA sequence sought to be expressed are connected in such a way as to permit gene sequence expression. The precise nature of the regulatory regions needed for gene sequence expression may vary from organism to organism, but shall in general include a promoter region which, in prokaryotes, contains both the promoter (which directs the initiation of RNA transcription) as well as the DNA sequences which, when transcribed into RNA, will signal synthesis initiation. Such regions will normally include those 5'-non-coding sequences involved with initiation of transcription and translation, such as the TATA box, capping sequence, CAAT sequence, and the like.

If desired, the non-coding region 3' to the sequence encoding a kinase of the invention may be obtained by the above-described methods. This region may be retained for its transcriptional termination regulatory sequences, such as termination and polyadenylation. Thus, by retaining the 3'-region naturally contiguous to the DNA sequence encoding a kinase of the invention, the transcriptional termination signals may be provided. Where the transcriptional termination signals are not satisfactorily functional in the expression host cell, then a 3' region functional in the host cell may be substituted.

Two DNA sequences (such as a promoter region sequence and a sequence encoding a kinase of the invention) are said to be operably linked if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region sequence to direct the transcription of a gene sequence encoding a kinase of the invention, or (3) interfere with the ability of the gene sequence of a kinase of the invention to be transcribed by the promoter region sequence. Thus, a promoter region would be operably linked to a DNA sequence if the promoter were capable of effecting transcription of that DNA sequence.

Thus, to express a gene encoding a kinase of the invention, transcriptional and translational signals recognized by an appropriate host are necessary.

The present invention encompasses the expression of a gene encoding a kinase of the invention (or a functional derivative thereof) in either prokaryotic or eukaryotic cells. Prokaryotic hosts are, generally, very efficient and convenient for the production of recombinant proteins and are, therefore, one type of preferred expression system for kinases of the invention. Prokaryotes most frequently are represented by various strains of *E. coli*. However, other microbial strains may also be used, including other bacterial strains.

In prokaryotic systems, plasmid vectors that contain replication sites and control sequences derived from a species compatible with the host may be used. Examples of suitable plasmid vectors may include pBR322, pUC118, pUC119 and the like; suitable phage or bacteriophage vectors may include γgt10, γgt11 and the like; and suitable virus vectors may include pMAM-neo, pKRC and the like. Preferably, the selected vector of the present invention has the capacity to replicate in the selected host cell.

Recognized prokaryotic hosts include bacteria such as *E. coli*, *Bacillus*, *Streptomyces*, *Pseudomonas*, *Salmonella*, *Serratia*, and the like. However, under such conditions, the polypeptide will not be glycosylated. The prokaryotic host must be compatible with the replicon and control sequences in the expression plasmid.

To express a kinase of the invention (or a functional derivative thereof) in a prokaryotic cell, it is necessary to operably link the sequence encoding the kinase of the invention to a functional prokaryotic promoter. Such promoters may be either constitutive or, more preferably, regulatable (*i.e.*, inducible or derepressible). Examples of constitutive promoters include the *int* promoter of bacteriophage λ, the *bla* promoter of the β-lactamase gene sequence of pBR322, and the *cat* promoter of the chloramphenicol acetyl transferase gene sequence of pPR325, and the like. Examples of inducible prokaryotic promoters include the major right and left promoters of bacteriophage λ (P_L and P_R), the *trp, recA, λacZ, λacI*, and *gal* promoters of *E. coli*, the α-amylase (Ulmanen *et al.*, J. Bacteriol. 162:176-182, 1985) and the ς-28-specific promoters of *B. subtilis* (Gilman *et al.*, Gene Sequence 32:11-20, 1984), the promoters of the bacteriophages of *Bacillus* (Gryczan, In: The Molecular Biology of the Bacilli, Academic Press, Inc., NY, 1982), and *Streptomyces* promoters (Ward *et al.*, Mol. Gen. Genet. 203:468-478, 1986). Prokaryotic

promoters are reviewed by Glick (Ind. Microbiot. 1:277-282, 1987), Cenatiempo (Biochimie 68:505-516, 1986), and Gottesman (Ann. Rev. Genet. 18:415-442, 1984).

Proper expression in a prokaryotic cell also requires the presence of a ribosome-binding site upstream of the gene sequence-encoding sequence. Such ribosome-binding sites are disclosed, for example, by Gold *et al.* (Ann. Rev. Microbiol. 35:365-404, 1981). The selection of control sequences, expression vectors, transformation methods, and the like, are dependent on the type of host cell used to express the gene. As used herein, "cell", "cell line", and "cell culture" may be used interchangeably and all such designations include progeny. Thus, the words "transformants" or "transformed cells" include the primary subject cell and cultures derived therefrom, without regard to the number of transfers. It is also understood that all progeny may not be precisely identical in DNA content, due to deliberate or inadvertent mutations. However, as defined, mutant progeny have the same functionality as that of the originally transformed cell.

Host cells which may be used in the expression systems of the present invention are not strictly limited, provided that they are suitable for use in the expression of the kinase polypeptide of interest. Suitable hosts may often include eukaryotic cells. Preferred eukaryotic hosts include, for example, yeast, fungi, insect cells, mammalian cells either *in vivo*, or in tissue culture. Mammalian cells which may be useful as hosts include HeLa cells, cells of fibroblast origin such as VERO or CHO-K1, or cells of lymphoid origin and their derivatives. Preferred mammalian host cells include SP2/0 and J558L, as well as neuroblastoma cell lines such as IMR 332, which may provide better capacities for correct post-translational processing.

In addition, plant cells are also available as hosts, and control sequences compatible with plant cells are available, such as the cauliflower mosaic virus 35S and 19S, and nopaline synthase promoter and polyadenylation signal sequences. Another preferred host is an insect cell, for example the *Drosophila* larvae. Using insect cells as hosts, the *Drosophila* alcohol dehydrogenase promoter can be used (Rubin, Science 240:1453-1459, 1988). Alternatively, baculovirus vectors can be engineered to express large amounts of kinases of the invention in insect cells (Jasny, Science 238:1653, 1987; Miller *et al.*, In: Genetic Engineering, Vol. 8, Plenum, Setlow *et al.*, eds., pp. 277-297, 1986).

Any of a series of yeast expression systems can be utilized which incorporate promoter and termination elements from the actively expressed sequences coding for glycolytic enzymes that are produced in large quantities when yeast are grown in mediums rich in glucose. Known glycolytic gene sequences can also provide very efficient transcriptional control signals. Yeast provides substantial advantages in that it can also carry out post-translational modifications. A number of recombinant DNA strategies exist utilizing strong promoter sequences and high copy number plasmids which can be utilized for production of the desired proteins in yeast. Yeast recognizes leader sequences on cloned mammalian genes and secretes peptides bearing leader sequences (*i.e.*, pre-peptides). Several possible vector systems are available for the expression of kinases of the invention in a mammalian host.

A wide variety of transcriptional and translational regulatory sequences may be employed, depending upon the nature of the host. The transcriptional and translational regulatory signals may be derived from viral sources, such as adenovirus, bovine papilloma virus, cytomegalovirus, simian virus, or the like, where the regulatory signals are associated with a particular gene sequence which has a high level of expression. Alternatively, promoters from mammalian expression products, such as actin, collagen, myosin, and the like, may be employed. Transcriptional initiation regulatory signals may be selected which allow for repression or activation, so that expression of the gene sequences can be modulated. Of interest are regulatory signals which are temperature-sensitive so that by varying the temperature, expression can be repressed or initiated, or are subject to chemical (such as metabolite) regulation.

Expression of kinases of the invention in eukaryotic hosts requires the use of eukaryotic regulatory regions. Such regions will, in general, include a promoter region sufficient to direct the initiation of RNA synthesis. Preferred eukaryotic promoters include, for example, the promoter of the mouse metallothionein I gene sequence (Hamer *et al.*, J. Mol. Appl. Gen. 1:273-288, 1982); the TK promoter of Herpes virus (McKnight, Cell 31:355-365, 1982); the SV40 early promoter (Benoist *et al.*, Nature (London) 290:304-31, 1981); and the yeast gal4 gene sequence promoter (Johnston *et al.*, Proc. Natl. Acad. Sci. (USA) 79:6971-6975, 1982; Silver *et al.*, Proc. Natl. Acad. Sci. (USA) 81:5951-5955, 1984).

Translation of eukaryotic mRNA is initiated at the codon that encodes the first methionine. For this reason, it is preferable to ensure that the linkage between a eukaryotic promoter and a DNA sequence which encodes a kinase of the invention (or a functional derivative thereof) does not contain any intervening codons which are capable of encoding a methionine (*i.e.*, AUG). The presence of such codons results either in the formation of a fusion protein (if the AUG codon is in the same reading frame as the kinase of the invention coding sequence) or a frame-shift mutation (if the AUG codon is not in the same reading frame as the kinase of the invention coding sequence).

A nucleic acid molecule encoding a kinase of the invention and an operably linked promoter may be introduced into a recipient prokaryotic or eukaryotic cell either as a nonreplicating DNA or RNA molecule, which may either be a linear molecule or, more preferably, a closed covalent circular molecule. Since such molecules are incapable of autonomous replication, the expression of the gene may occur through the transient expression of the introduced sequence. Alternatively, permanent expression may occur through the integration of the introduced DNA sequence into the host chromosome.

A vector may be employed which is capable of integrating the desired gene sequences into the host cell chromosome. Cells which have stably integrated the introduced DNA into their chromosomes can be selected by also introducing one or more markers which allow for selection of host cells which contain the expression vector. The marker may provide for prototrophy to an auxotrophic host, biocide resistance, *e.g.*, antibiotics, or heavy metals, such as copper, or the like. The selectable marker gene sequence can either be directly linked to the DNA gene sequences to be expressed, or introduced into the same cell by co-transfection. Additional elements may also be needed for optimal synthesis of mRNA. These elements may include splice signals, as well as transcription promoters, enhancers, and termination signals. cDNA expression vectors incorporating such elements include those described by Okayama (Mol. Cell. Biol. 3:280-, 1983).

The introduced nucleic acid molecule can be incorporated into a plasmid or viral vector capable of autonomous replication in the recipient host. Any of a wide variety of vectors may be employed for this purpose. Factors of importance in selecting a particular plasmid or viral vector include: the ease with which recipient cells that contain the vector may be recognized and selected from those recipient cells which do not contain the vector;

the number of copies of the vector which are desired in a particular host; and whether it is desirable to be able to "shuttle" the vector between host cells of different species.

Preferred prokaryotic vectors include plasmids such as those capable of replication in *E. coli* (such as, for example, pBR322, ColEl, pSC101, pACYC 184, πVX; "Molecular Cloning: A Laboratory Manual", 1989, *supra*). Bacillus plasmids include pC194, pC221, pT127, and the like (Gryczan, In: The Molecular Biology of the Bacilli, Academic Press, NY, pp. 307-329, 1982). Suitable *Streptomyces* plasmids include p1J101 (Kendall *et al.*, J. Bacteriol. 169:4177-4183, 1987), and streptomyces bacteriophages such as φC31 (Chater *et al.*, In: Sixth International Symposium on Actinomycetales Biology, Akademiai Kaido, Budapest, Hungary, pp. 45-54, 1986). *Pseudomonas* plasmids are reviewed by John *et al.* (Rev. Infect. Dis. 8:693-704, 1986), and Izaki (Jpn. J. Bacteriol. 33:729-742, 1978).

Preferred eukaryotic plasmids include, for example, BPV, vaccinia, SV40, 2-micron circle, and the like, or their derivatives. Such plasmids are well known in the art (Botstein *et al.*, Miami Wntr. Symp. 19:265-274, 1982; Broach, In: "The Molecular Biology of the Yeast Saccharomyces: Life Cycle and Inheritance", Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, p. 445-470, 1981; Broach, Cell 28:203-204, 1982; Bollon *et al.*, J. Clin. Hematol. Oncol. 10:39-48, 1980; Maniatis, In: Cell Biology: A Comprehensive Treatise, Vol. 3, Gene Sequence Expression, Academic Press, NY, pp. 563-608, 1980).

Once the vector or nucleic acid molecule containing the construct(s) has been prepared for expression, the DNA construct(s) may be introduced into an appropriate host cell by any of a variety of suitable means, *i.e.*, transformation, transfection, conjugation, protoplast fusion, electroporation, particle gun technology, calcium phosphate-precipitation, direct microinjection, and the like. After the introduction of the vector, recipient cells are grown in a selective medium, which selects for the growth of vector-containing cells. Expression of the cloned gene(s) results in the production of a kinase of the invention, or fragments thereof. This can take place in the transformed cells as such, or following the induction of these cells to differentiate (for example, by administration of bromodeoxyuracil to neuroblastoma cells or the like). A variety of incubation conditions can be used to form the peptide of the present invention. The most preferred conditions are those which mimic physiological conditions.

IV. The Proteins of the Invention

A variety of methodologies known in the art can be utilized to obtain the polypeptides of the present invention. The polypeptides may be purified from tissues or cells that naturally produce the polypeptides. Alternatively, the above-described isolated nucleic acid fragments could be used to express the kinases of the invention in any organism. The samples of the present invention include cells, protein extracts or membrane extracts of cells, or biological fluids. The samples will vary based on the assay format, the detection method, and the nature of the tissues, cells or extracts used as the sample.

Any eukaryotic organism can be used as a source for the polypeptides of the invention, as long as the source organism naturally contains such polypeptides. As used herein, "source organism" refers to the original organism from which the amino acid sequence of the subunit is derived, regardless of the organism the subunit is expressed in and ultimately isolated from.

One skilled in the art can readily follow known methods for isolating proteins in order to obtain the polypeptides free of natural contaminants. These include, but are not limited to: size-exclusion chromatography, HPLC, ion-exchange chromatography, and immuno-affinity chromatography.

Further, the polypeptides of the invention include the full-length polypeptides that can be identified from the full-length or partial sequences encoded by SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182,

SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 (Figure 1). In addition, the polypeptides of the invention include the domains of these polypeptides, including, but not limited to, the N-terminal, kinase/catalytic, and C-terminal domains.

The characteristics of the protein kinase nucleic acid sequences of the invention are provided in Table 1. The protein kinases fall into 10 known groups: AGC, CAMK, CKI, CMGC, dsPK, EIFK, LIMK, MLK, STE and TK. In addition, there are a significant number of protein kinases that do not belong to any of the known groups, and therefore presumably define new protein kinase groups.

Additional characteristics are shown in, *inter alia*, the tables, namely Table 1, Table 2, Table 3 and Table 4, provided below.

V. Antibodies, Hybridomas, Methods of Use and Kits for Detection of Protein Kinases

The present invention relates to an antibody having binding affinity to a kinase of the invention. The polypeptide may have an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ

ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or a functional derivative thereof, or at least 9 contiguous amino acids thereof (preferably, at least 20, 30, 35, or 40 or more contiguous amino acids thereof). Alternatively, the antibody may bind to a part of the polypeptide not provided in the sequences above, but that is present in the full-length sequence of the polypeptide and that is easily obtained using methods standard in the art. Further, the antibody may bind specifically to particular domains of one or more of the kinases of the invention, including, but not limited to, the N-terminal, kinase/catalytic, or C-terminal domains.

The present invention also relates to an antibody having specific binding affinity to a kinase or kinase domain of the invention. Such an antibody may be isolated by comparing its binding affinity to a kinase of the invention with its binding affinity to other polypeptides. Those that bind selectively to a kinase of the invention would be chosen for use in methods requiring a distinction between a kinase of the invention and other

polypeptides. Such methods could include, but should not be limited to, the analysis of altered kinase expression in tissue containing other polypeptides.

The kinases of the present invention can be used in a variety of procedures and methods, such as for the generation of antibodies, for use in identifying pharmaceutical compositions, and for studying DNA/protein interaction.

The kinases of the present invention can be used to produce antibodies or hybridomas. One skilled in the art will recognize that if an antibody is desired, such a peptide could be generated as described herein and used as an immunogen. The antibodies of the present invention include monoclonal and polyclonal antibodies, as well fragments of these antibodies, and humanized forms. Humanized forms of the antibodies of the present invention may be generated using one of the procedures known in the art such as chimerization or CDR grafting.

The present invention also relates to a hybridoma that produces the above-described monoclonal antibody, or binding fragment thereof. A hybridoma is an immortalized cell line that is capable of secreting a specific monoclonal antibody.

In general, techniques for preparing monoclonal antibodies and hybridomas are well known in the art (Campbell, "Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology," Elsevier Science Publishers, Amsterdam, The Netherlands, 1984; St. Groth *et al.*, J. Immunol. Methods 35:1-21, 1980). Any animal (mouse, rabbit, and the like) which is known to produce antibodies can be immunized with the selected polypeptide. Methods for immunization are well known in the art. Such methods include subcutaneous or intraperitoneal injection of the polypeptide. One skilled in the art will recognize that the amount of polypeptide used for immunization will vary based on the animal that is immunized, the antigenicity of the polypeptide and the site of injection.

The polypeptide may be modified or administered in an adjuvant in order to increase the peptide antigenicity. Methods of increasing the antigenicity of a polypeptide are well known in the art. Such procedures include coupling the antigen with a heterologous protein (such as globulin or β-galactosidase) or through the inclusion of an adjuvant during immunization.

For monoclonal antibodies, spleen cells from the immunized animals are removed, fused with myeloma cells, such as SP2/0-Agl4 myeloma cells, and allowed to become monoclonal antibody producing hybridoma cells. Any one of a number of methods well known in the art can be used to identify the hybridoma cell that produces an antibody with the desired characteristics. These include screening the hybridomas with an ELISA assay, western blot analysis, or radioimmunoassay (Lutz *et al.*, Exp. Cell Res. 175:109-124, 1988). Hybridomas secreting the desired antibodies are cloned and the class and subclass are determined using procedures known in the art (Campbell, "Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology", *supra*, 1984).

For polyclonal antibodies, antibody-containing antisera is isolated from the immunized animal and is screened for the presence of antibodies with the desired specificity using one of the above-described procedures. The above-described antibodies may be detectably labeled. Antibodies can be detectably labeled through the use of radioisotopes, affinity labels (such as biotin, avidin, and the like), enzymatic labels (such as horse radish peroxidase, alkaline phosphatase, and the like) fluorescent labels (such as FITC or rhodamine, and the like), paramagnetic atoms, and the like. Procedures for accomplishing such labeling are well-known in the art, for example, *see* Stemberger *et al.*, J. Histochem. Cytochem. 18:315, 1970; Bayer *et al.*, Meth. Enzym. 62:308-, 1979; Engvall *et al.*, Immunol. 109:129-, 1972; Goding, J. Immunol. Meth. 13:215-, 1976. The labeled antibodies of the present invention can be used for *in vitro, in vivo*, and *in situ* assays to identify cells or tissues that express a specific peptide.

The above-described antibodies may also be immobilized on a solid support. Examples of such solid supports include plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, acrylic resins and such as polyacrylamide and latex beads. Techniques for coupling antibodies to such solid supports are well known in the art (Weir *et al.*, "Handbook of Experimental Immunology" 4th Ed., Blackwell Scientific Publications, Oxford, England, Chapter 10, 1986; Jacoby *et al.*, Meth. Enzym. 34, Academic Press, N.Y., 1974). The immobilized antibodies of the present invention can be used for *in vitro, in vivo*, and *in situ* assays as well as in immunochromotography.

Furthermore, one skilled in the art can readily adapt currently available procedures, as well as the techniques, methods and kits disclosed herein with regard to antibodies, to generate peptides capable of binding to a specific peptide sequence in order to generate rationally designed antipeptide peptides (Hurby *et al.*, "Application of Synthetic Peptides: Antisense Peptides", In Synthetic Peptides, A User's Guide, W.H. Freeman, NY, pp. 289-307, 1992; Kaspczak *et al.*, Biochemistry 28:9230-9238, 1989).

Anti-peptide peptides can be generated by replacing the basic amino acid residues found in the peptide sequences of the kinases of the invention with acidic residues, while maintaining hydrophobic and uncharged polar groups. For example, lysine, arginine, and/or histidine residues are replaced with aspartic acid or glutamic acid and glutamic acid residues are replaced by lysine, arginine or histidine.

The present invention also encompasses a method of detecting a kinase polypeptide in a sample, comprising: (a) contacting the sample with an above-described antibody, under conditions such that immunocomplexes form, and (b) detecting the presence of said antibody bound to the polypeptide. In detail, the methods comprise incubating a test sample with one or more of the antibodies of the present invention and assaying whether the antibody binds to the test sample. Altered levels of a kinase of the invention in a sample as compared to normal levels may indicate disease.

Conditions for incubating an antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the antibody used in the assay. One skilled in the art will recognize that any one of the commonly available immunological assay formats (such as radioimmunoassays, enzyme-linked immunosorbent assays, diffusion based Ouchterlony, or rocket immunofluorescent assays) can readily be adapted to employ the antibodies of the present invention. Examples of such assays can be found in Chard ("An Introduction to Radioimmunoassay and Related Techniques" Elsevier Science Publishers, Amsterdam, The Netherlands, 1986), Bullock *et al.* ("Techniques in Immunocytochemistry," Academic Press, Orlando, FL Vol. 1, 1982; Vol. 2, 1983; Vol. 3, 1985), Tijssen ("Practice and Theory of Enzyme Immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology," Elsevier Science Publishers, Amsterdam, The Netherlands, 1985).

The immunological assay test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as blood, serum, plasma, or urine. The test samples used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is testable with the system utilized.

A kit contains all the necessary reagents to carry out the previously described methods of detection. The kit may comprise: (i) a first container means containing an above-described antibody, and (ii) second container means containing a conjugate comprising a binding partner of the antibody and a label. In another preferred embodiment, the kit further comprises one or more other containers comprising one or more of the following: wash reagents and reagents capable of detecting the presence of bound antibodies.

Examples of detection reagents include, but are not limited to, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the chromophoric, enzymatic, or antibody binding reagents that are capable of reacting with the labeled antibody. The compartmentalized kit may be as described above for nucleic acid probe kits. One skilled in the art will readily recognize that the antibodies described in the present invention can readily be incorporated into one of the established kit formats that are well known in the art.

VI. Isolation of Compounds That Interact With Protein Kinases

The present invention also relates to a method of detecting a compound capable of binding to a protein kinase of the invention, comprising incubating the compound with a kinase of the invention and detecting the presence of the compound bound to the kinase. The compound may be present within a complex mixture, for example, serum, body fluid, or cell extracts.

The present invention also relates to a method of detecting an agonist or antagonist of kinase activity or kinase binding partner activity comprising incubating cells that produce a kinase of the invention in the presence of a compound and detecting changes in the level of kinase activity or kinase binding partner activity. The compounds thus identified would produce a change in activity indicative of the presence of the compound.

The compound may be present within a complex mixture, for example, serum, body fluid, or cell extracts. Once the compound is identified it can be isolated using techniques well known in the art.

The present invention also encompasses a method of agonizing (stimulating) or antagonizing kinase associated activity in a mammal comprising administering to said mammal an agonist or antagonist to a kinase of the invention in an amount sufficient to effect said agonism or antagonism. A method of treating diseases in a mammal with an agonist or antagonist of kinase activity comprising administering the agonist or antagonist to a mammal in an amount sufficient to agonize or antagonize kinase associated functions is also encompassed in the present application.

In an effort to discover novel treatments for diseases, biomedical researchers and chemists have designed, synthesized, and tested molecules that inhibit the function of protein kinases. Some small organic molecules form a class of compounds that modulate the function of protein kinases. Examples of molecules that have been reported to inhibit the function of protein kinases include, but are not limited to, bis monocyclic, bicyclic or heterocyclic aryl compounds (PCT WO 92/20642, published November 26, 1992 by Maguire *et al.*), vinylene-azaindole derivatives (PCT WO 94/14808, published July 7, 1994 by Ballinari *et al.*), 1-cyclopropyl-4-pyridyl-quinolones (U.S. Patent No. 5,330,992), styryl compounds (U.S. Patent No. 5,217,999), styryl-substituted pyridyl compounds (U.S. Patent No. 5,302,606), certain quinazoline derivatives (EP Application No. 0 566 266 A1), seleoindoles and selenides (PCT WO 94/03427, published February 17, 1994 by Denny *et al.*), tricyclic polyhydroxylic compounds (PCT WO 92/21660, published December 10, 1992 by Dow), and benzylphosphonic acid compounds (PCT WO 91/15495, published October 17, 1991 by Dow *et al*).

Compounds that can traverse cell membranes and are resistant to acid hydrolysis are potentially advantageous as therapeutics as they can become highly bioavailable after being administered orally to patients. However, many of these protein kinase inhibitors only weakly inhibit the function of protein kinases. In addition, many inhibit a variety of protein kinases and will cause multiple side-effects as therapeutics for diseases.

Some indolinone compounds, however, form classes of acid resistant and membrane permeable organic molecules. WO 96/22976 (published August 1, 1996 by Ballinari *et al.*) describes hydrosoluble indolinone compounds that harbor tetralin,

naphthalene, quinoline, and indole substituents fused to the oxindole ring. These bicyclic substituents are in turn substituted with polar moieties including hydroxylated alkyl, phosphate, and ether moieties. U.S. Patent Application Serial Nos. 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187) and 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298) and International Patent Publication WO 96/22976, published August 1, 1996 by Ballinari *et al.*, all of which are incorporated herein by reference in their entirety, including any drawings, describe indolinone chemical libraries of indolinone compounds harboring other bicyclic moieties as well as monocyclic moieties fused to the oxindole ring. Applications 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187), 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298), and WO 96/22976, published August 1, 1996 by Ballinari *et al.* teach methods of indolinone synthesis, methods of testing the biological activity of indolinone compounds in cells, and inhibition patterns of indolinone derivatives.

Other examples of substances capable of modulating kinase activity include, but are not limited to, tyrphostins, quinazolines, quinoxolines, and quinolines. The quinazolines, tyrphostins, quinolines, and quinoxolines referred to above include well known compounds such as those described in the literature. For example, representative publications describing quinazolines include Barker *et al.*, EPO Publication No. 0 520 722 A1; Jones *et al.*, U.S. Patent No.4,447,608; Kabbe *et al.*, U.S. Patent No. 4,757,072; Kaul and Vougioukas, U.S. Patent No. 5, 316,553; Kreighbaum and Comer, U.S. Patent No. 4,343,940; Pegg and Wardleworth, EPO Publication No. 0 562 734 A1; Barker *et al.*, Proc. of Am. Assoc. for Cancer Research 32:327 (1991); Bertino, J.R., Cancer Research 3:293-304 (1979); Bertino, J.R., Cancer Research 9(2 part 1):293-304 (1979); Curtin *et al.*, Br. J. Cancer 53:361-368 (1986); Fernandes *et al.*, Cancer Research 43:1117-1123 (1983); Ferris *et al.* J. Org. Chem. 44(2):173-178; Fry *et al.*, Science 265:1093-1095 (1994); Jackman *et al.*, Cancer Research 51:5579-5586 (1981); Jones *et al.* J. Med. Chem. 29(6):1114-1118; Lee and Skibo, Biochemistry 26(23):7355-7362 (1987); Lemus *et al.*, J.

Org. Chem. 54:3511-3518 (1989); Ley and Seng, Synthesis 1975:415-522 (1975); Maxwell *et al.*, Magnetic Resonance in Medicine 17:189-196 (1991); Mini *et al.*, Cancer Research 45:325-330 (1985); Phillips and Castle, J. Heterocyclic Chem. 17(19):1489-1596 (1980); Reece *et al.*, Cancer Research 47(11):2996-2999 (1977); Sculier *et al.*, Cancer Immunol. and Immunother. 23:A65 (1986); Sikora *et al.*, Cancer Letters 23:289-295 (1984); Sikora *et al.*, Analytical Biochem. 172:344-355 (1988); all of which are incorporated herein by reference in their entirety, including any drawings.

Quinoxaline is described in Kaul and Vougioukas, U.S. Patent No. 5,316,553, incorporated herein by reference in its entirety, including any drawings.

Quinolines are described in Dolle *et al.*, J. Med. Chem. 37:2627-2629 (1994); MaGuire, J. Med. Chem. 37:2129-2131 (1994); Burke *et al.*, J. Med. Chem. 36:425-432 (1993); and Burke *et al.* BioOrganic Med. Chem. Letters 2:1771-1774 (1992), all of which are incorporated by reference in their entirety, including any drawings.

Tyrphostins are described in Allen *et al.*, Clin. Exp. Immunol. 91:141-156 (1993); Anafi *et al.*, Blood 82:12:3524-3529 (1993); Baker *et al.*, J. Cell Sci. 102:543-555 (1992); Bilder *et al.*, Amer. Physiol. Soc. pp. 6363-6143:C721-C730 (1991); Brunton *et al.*, Proceedings of Amer. Assoc. Cancer Rsch. 33:558 (1992); Bryckaert *et al.*, Experimental Cell Research 199:255-261 (1992); Dong *et al.*, J. Leukocyte Biology 53:53-60 (1993); Dong *et al.*, J. Immunol. 151(5):2717-2724 (1993); Gazit *et al.*, J. Med. Chem. 32:2344-2352 (1989); Gazit *et al.*, " J. Med. Chem. 36:3556-3564 (1993); Kaur *et al.*, Anti-Cancer Drugs 5:213-222 (1994); Kaur *et al.*, King *et al.*, Biochem. J. 275:413-418 (1991); Kuo *et al.*, Cancer Letters 74:197-202 (1993); Levitzki, A., The FASEB J. 6:3275-3282 (1992); Lyall *et al.*, J. Biol. Chem. 264:14503-14509 (1989); Peterson *et al.*, The Prostate 22:335-345 (1993); Pillemer *et al.*, Int. J. Cancer 50:80-85 (1992); Posner *et al.*, Molecular Pharmacology 45:673-683 (1993); Rendu *et al.*, Biol. Pharmacology 44(5):881-888 (1992); Sauro and Thomas, Life Sciences 53:371-376 (1993); Sauro and Thomas, J. Pharm. and Experimental Therapeutics 267(3):119-1125 (1993); Wolbring *et al.*, J. Biol. Chem. 269(36):22470-22472 (1994); and Yoneda *et al.*, Cancer Research 51:4430-4435 (1991); all of which are incorporated herein by reference in their entirety, including any drawings.

Other compounds that could be used as modulators include oxindolinones such as those described in U.S. patent application Serial No. 08/702,232 filed August 23, 1996, incorporated herein by reference in its entirety, including any drawings.

VII. Biological Significance, Applications and Clinical Relevance of Novel Protein Kinases

For each protein kinase in this application, we provide a classification of the protein class and family to which it belongs, a summary of non-cataltyic protein motifs, a profile of its expression in several hundred tissue and cell sources, and a chromosomal location. This information can be used to suggest potential function, regulation or therapeutic utility for each of the proteins.

The kinase classification and protein domains often reflect pathways, cellular roles, or mechanisms of up- or down-stream regulation. Also disease-relevant genes often occur in families of related genes. For example if one member of a kinase family functions as an oncogene, a tumor suppressor, or has been found to be disrupted in an immune, neurologic, cardiovascular, or metabolic disorder, frequently other family members may play a related role.

The expression analysis organizes kinases into groups that are transcriptionally upregulated in tumors and those that are more restricted to specific tumor types such as melanoma or prostate. This analysis also identifies genes that are regulated in a cell cycle dependent manner, and are therefore likely to be involved in maintaining cell cycle checkpoints, entry, progression, or exit from mitosis, oversee DNA repair, or are involved in cell proliferation and genome stability. Expression data also can identify genes expressed in endothelial sources or other tissues that suggest a role in angiogenesis, thereby implicating them as targets for control of diseases that have an angiogenic component, such as cancer, endometriosis, retinopathy and macular degeneration, and various ischemic or vascular pathologies. A proteins' role in cell survival can also be suggested based on restricted expression in cells subjected to external stress such as oxidative damage, hypoxia, drugs such as cisplatinum, or irradiation. Metastases-associated genes can be implicated when expression is restricted to invading regions of a tumor, or is only seen in local or distant metastases compared to the primary tumor, or when a gene is upregulated during cell culture models of invasion, migration, or motility.

Chromosomal location can identify candidate targets for a tumor amplicon or a tumor-suppressor locus. Summaries of prevelant tumor amplicons are available in the literature, and can identify tumor types to experimentally be confirmed to contain amplified copies of a kinase gene which localizes to an adjacent region.

Based on these criteria several kinases immediately stand out as being of potential therapeutic relevance. The protein kinases can be divided into the following disease-relevant categories (nucleotide Seq ID #s in parentheses):

Tumor associated: Mok (SEQ ID NO:NO:57), EFK2, AA216804 (SEQ ID NO:11), AA435956 (SEQ ID NO:NO:48), AA278842 (SEQ ID NO:88), AA599286 (SEQ ID NO:89), AA826850 (SEQ ID NO:3), HRI (SEQ ID NO:73), MLK4 AA232253 (SEQ ID NO:82), AA883975 SGK 235 (SEQ ID NO:95), AA311714 (SEQ ID NO:101), MPSK1 (SEQ ID NO:110), R19609 (Seq ID111), AA383293 (SEQ ID NO:26).

Prostate-specific: AA234451 (SEQ ID NO:47), TSK4 (SEQ ID NO:93), RIP4 (SEQ ID NO:84), KIAA0965 (SEQ ID NO:8).

Oncogenic or proliferation associated: KIAA0781 (SEQ ID NO:38), AA789239 (SEQ ID NO:52), CCRK (SEQ ID NO:54), CLK4 (SEQ ID NO:55), H85389 (SEQ ID NO:97).

Neuronal restricted: CAMKKB (SEQ ID NO:66)

Hematopoietic expressed: PTK9L (SEQ ID NO;22), DRAK2 (SEQ ID NO:29), AI025291 (SEQ ID NO:94)

Angiogenic or endothelial expressed: DRAK1 (SEQ ID NO:31), MAK-V (SEQ ID NO:40), TRAD (SEQ ID NO:44), MOK (SEQ ID NO:57), AA08847 (SEQ ID NO:78), HGP_66444466 (SEQ ID NO:79), RSK4 (SEQ ID NO:16).

Cell cycle regulated: AA454060 (SEQ ID NO:45), KIAA0999 (Mitotic – SEQ ID NO:32), AA579641 (Mitotic – SEQ ID NO:60), AA305176 (Mitotic – SEQ ID NO:6), AA018361 (S1 phase – SEQ ID NO:100).

VIII. Transgenic Animals.

A variety of methods are available for the production of transgenic animals associated with this invention. DNA can be injected into the pronucleus of a fertilized egg before fusion of the male and female pronuclei, or injected into the nucleus of an embryonic cell (*e.g.*, the nucleus of a two-cell embryo) following the initiation of cell division (Brinster *et al.*, Proc. Nat. Acad. Sci. USA 82: 4438-4442, 1985). Embryos can

be infected with viruses, especially retroviruses, modified to carry inorganic-ion receptor nucleotide sequences of the invention.

Pluripotent stem cells derived from the inner cell mass of the embryo and stabilized in culture can be manipulated in culture to incorporate nucleotide sequences of the invention. A transgenic animal can be produced from such cells through implantation into a blastocyst that is implanted into a foster mother and allowed to come to term. Animals suitable for transgenic experiments can be obtained from standard commercial sources such as Charles River (Wilmington, MA), Taconic (Germantown, NY), Harlan Sprague Dawley (Indianapolis, IN), etc.

The procedures for manipulation of the rodent embryo and for microinjection of DNA into the pronucleus of the zygote are well known to those of ordinary skill in the art (Hogan *et al.*, *supra*). Microinjection procedures for fish, amphibian eggs and birds are detailed in Houdebine and Chourrout (Experientia 47: 897-905, 1991). Other procedures for introduction of DNA into tissues of animals are described in U.S. Patent No., 4,945,050 (Sanford *et al.*, July 30, 1990).

By way of example only, to prepare a transgenic mouse, female mice are induced to superovulate. Females are placed with males, and the mated females are sacrificed by CO_2 asphyxiation or cervical dislocation and embryos are recovered from excised oviducts. Surrounding cumulus cells are removed. Pronuclear embryos are then washed and stored until the time of injection. Randomly cycling adult female mice are paired with vasectomized males. Recipient females are mated at the same time as donor females. Embryos then are transferred surgically. The procedure for generating transgenic rats is similar to that of mice (Hammer *et al.*, Cell 63:1099-1112, 1990).

Methods for the culturing of embryonic stem (ES) cells and the subsequent production of transgenic animals by the introduction of DNA into ES cells using methods such as electroporation, calcium phosphate/DNA precipitation and direct injection also are well known to those of ordinary skill in the art (Teratocarcinomas and Embryonic Stem Cells, A Practical Approach, E.J. Robertson, ed., IRL Press, 1987).

In cases involving random gene integration, a clone containing the sequence(s) of the invention is co-transfected with a gene encoding resistance. Alternatively, the gene encoding neomycin resistance is physically linked to the sequence(s) of the invention.

Transfection and isolation of desired clones are carried out by any one of several methods well known to those of ordinary skill in the art (E.J. Robertson, *supra*).

DNA molecules introduced into ES cells can also be integrated into the chromosome through the process of homologous recombination (Capecchi, Science 244: 1288-1292, 1989). Methods for positive selection of the recombination event (*i.e.*, neo resistance) and dual positive-negative selection (*i.e.*, neo resistance and gancyclovir resistance) and the subsequent identification of the desired clones by PCR have been described by Capecchi, *supra* and Joyner *et al.* (Nature 338: 153-156, 1989), the teachings of which are incorporated herein in their entirety including any drawings. The final phase of the procedure is to inject targeted ES cells into blastocysts and to transfer the blastocysts into pseudopregnant females. The resulting chimeric animals are bred and the offspring are analyzed by Southern blotting to identify individuals that carry the transgene. Procedures for the production of non-rodent mammals and other animals have been discussed by others (Houdebine and Chourrout, *supra*; Pursel *et al.*, Science 244:1281-1288, 1989; and Simms *et al.*, Bio/Technology 6:179-183, 1988).

Thus, the invention provides transgenic, nonhuman mammals containing a transgene encoding a kinase of the invention or a gene effecting the expression of the kinase. Such transgenic nonhuman mammals are particularly useful as an *in vivo* test system for studying the effects of introduction of a kinase, or regulating the expression of a kinase (*i.e.*, through the introduction of additional genes, antisense nucleic acids, or ribozymes).

A "transgenic animal" is an animal having cells that contain DNA which has been artificially inserted into a cell, which DNA becomes part of the genome of the animal which develops from that cell. Preferred transgenic animals are primates, mice, rats, cows, pigs, horses, goats, sheep, dogs and cats. The transgenic DNA may encode human STE20-related kinases. Native expression in an animal may be reduced by providing an amount of anti-sense RNA or DNA effective to reduce expression of the receptor.

IX. Gene Therapy

Protein kinases of the invention, or their genetic sequences will also be useful in gene therapy (reviewed in Miller, Nature 357:455-460, 1992). Miller states that advances have resulted in practical approaches to human gene therapy that have demonstrated

positive initial results. The basic science of gene therapy is described in Mulligan (Science 260:926-931, 1993).

In one preferred embodiment, an expression vector containing protein kinase coding sequence is inserted into cells, the cells are grown *in vitro,* and then are infused in large numbers into patients. In another preferred embodiment, a DNA segment containing a promoter of choice (for example a strong promoter) is transferred into cells containing an endogenous gene encoding kinases of the invention in such a manner that the promoter segment enhances expression of the endogenous kinase gene (for example, the promoter segment is transferred to the cell such that it becomes directly linked to the endogenous kinase gene).

The gene therapy may involve the use of an adenovirus containing kinase cDNA targeted to a tumor, systemic kinase increase by implantation of engineered cells, injection with kinase-encoding virus, or injection of naked kinase DNA into appropriate tissues.

Target cell populations may be modified by introducing altered forms of one or more components of the protein complexes in order to modulate the activity of such complexes. For example, by reducing or inhibiting a complex component activity within target cells, an abnormal signal transduction event(s) leading to a condition may be decreased, inhibited, or reversed. Deletion or missense mutants of a component, that retain the ability to interact with other components of the protein complexes but cannot function in signal transduction may be used to inhibit an abnormal, deleterious signal transduction event.

Expression vectors derived from viruses such as retroviruses, vaccinia virus, adenovirus, adeno-associated virus, herpes viruses, several RNA viruses, or bovine papilloma virus, may be used for delivery of nucleotide sequences (*e.g.*, cDNA) encoding recombinant kinase of the invention protein into the targeted cell population (*e.g.*, tumor cells). Methods which are well known to those skilled in the art can be used to construct recombinant viral vectors containing coding sequences (Maniatis *et al.*, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, N.Y., 1989; Ausubel *et al.*, Current Protocols in Molecular Biology, Greene Publishing Associates and Wiley Interscience, N.Y., 1989). Alternatively, recombinant nucleic acid molecules encoding protein sequences can be used as naked DNA or in a reconstituted system *e.g.*, liposomes or other lipid systems for delivery to target cells (*e.g.*, Felgner *et al.*, Nature 337:387-8,

1989). Several other methods for the direct transfer of plasmid DNA into cells exist for use in human gene therapy and involve targeting the DNA to receptors on cells by complexing the plasmid DNA to proteins (Miller, *supra*).

In its simplest form, gene transfer can be performed by simply injecting minute amounts of DNA into the nucleus of a cell, through a process of microinjection (Capecchi, Cell 22:479-88, 1980). Once recombinant genes are introduced into a cell, they can be recognized by the cell's normal mechanisms for transcription and translation, and a gene product will be expressed. Other methods have also been attempted for introducing DNA into larger numbers of cells. These methods include: transfection, wherein DNA is precipitated with $CaPO_4$ and taken into cells by pinocytosis (Chen *et al.*, Mol. Cell Biol. 7:2745-52, 1987); electroporation, wherein cells are exposed to large voltage pulses to introduce holes into the membrane (Chu *et al.*, Nucleic Acids Res. 15:1311-26, 1987); lipofection/liposome fusion, wherein DNA is packaged into lipophilic vesicles which fuse with a target cell (Felgner *et al.*, Proc. Natl. Acad. Sci. USA. 84:7413-7417, 1987); and particle bombardment using DNA bound to small projectiles (Yang *et al.*, Proc. Natl. Acad. Sci. 87:9568-9572, 1990). Another method for introducing DNA into cells is to couple the DNA to chemically modified proteins.

It has also been shown that adenovirus proteins are capable of destabilizing endosomes and enhancing the uptake of DNA into cells. The admixture of adenovirus to solutions containing DNA complexes, or the binding of DNA to polylysine covalently attached to adenovirus using protein crosslinking agents substantially improves the uptake and expression of the recombinant gene (Curiel *et al.*, Am. J. Respir. Cell. Mol. Biol., 6:247-52, 1992).

As used herein "gene transfer" means the process of introducing a foreign nucleic acid molecule into a cell. Gene transfer is commonly performed to enable the expression of a particular product encoded by the gene. The product may include a protein, polypeptide, anti-sense DNA or RNA, or enzymatically active RNA. Gene transfer can be performed in cultured cells or by direct administration into animals. Generally gene transfer involves the process of nucleic acid contact with a target cell by non-specific or receptor mediated interactions, uptake of nucleic acid into the cell through the membrane or by endocytosis, and release of nucleic acid into the cytoplasm from the plasma membrane or endosome. Expression may require, in addition, movement of the nucleic

acid into the nucleus of the cell and binding to appropriate nuclear factors for transcription.

As used herein "gene therapy" is a form of gene transfer and is included within the definition of gene transfer as used herein and specifically refers to gene transfer to express a therapeutic product from a cell *in vivo* or *in vitro*. Gene transfer can be performed *ex vivo* on cells which are then transplanted into a patient, or can be performed by direct administration of the nucleic acid or nucleic acid-protein complex into the patient.

In another preferred embodiment, a vector having nucleic acid sequences encoding a protein kinase polypeptide of the invention is provided in which the nucleic acid sequence is expressed only in specific tissue. Methods of achieving tissue-specific gene expression are set forth in International Publication No. WO 93/09236, filed November 3, 1992 and published May 13, 1993.

In all of the preceding vectors set forth above, a further aspect of the invention is that the nucleic acid sequence contained in the vector may include additions, deletions or modifications to some or all of the sequence of the nucleic acid, as defined above.

In another preferred embodiment, a method of gene replacement is set forth. "Gene replacement" as used herein means supplying a nucleic acid sequence which is capable of being expressed *in vivo* in an animal and thereby providing or augmenting the function of an endogenous gene that is missing or defective in the animal.

X. Administration of Substances

Methods of determining the dosages of compounds to be administered to a patient and modes of administering compounds to an organism are disclosed in U.S. Application Serial No. 08/702,282, filed August 23, 1996 and International patent publication number WO 96/22976, published August 1 1996, both of which are incorporated herein by reference in their entirety, including any drawings, figures, or tables. Those skilled in the art will appreciate that such descriptions are applicable to the present invention and can be easily adapted to it.

The proper dosage depends on various factors such as the type of disease being treated, the particular composition being used, and the size and physiological condition of the patient. Therapeutically effective doses for the compounds described herein can be estimated initially from cell culture and animal models. For example, a dose can be formulated in animal models to achieve a circulating concentration range that initially

takes into account the IC_{50} as determined in cell culture assays. The animal model data can be used to more accurately determine useful doses in humans.

Plasma half-life and biodistribution of the drug and metabolites in the plasma, tumors, and major organs can be also be determined to facilitate the selection of drugs most appropriate to inhibit a disorder. Such measurements can be carried out. For example, HPLC analysis can be performed on the plasma of animals treated with the drug and the location of radiolabeled compounds can be determined using detection methods such as X-ray, CAT scan, and MRI. Compounds that show potent inhibitory activity in the screening assays, but have poor pharmacokinetic characteristics, can be optimized by altering the chemical structure and retesting. In this regard, compounds displaying good pharmacokinetic characteristics can be used as a model.

Toxicity studies can also be carried out by measuring the blood cell composition. For example, toxicity studies can be carried out in a suitable animal model as follows: 1) the compound is administered to mice (an untreated control mouse should also be used); 2) blood samples are periodically obtained via the tail vein from one mouse in each treatment group; and 3) the samples are analyzed for red and white blood cell counts, blood cell composition, and the percent of lymphocytes versus polymorphonuclear cells. A comparison of results for each dosing regime with the controls indicates if toxicity is present.

At the termination of each toxicity study, further studies can be carried out by sacrificing the animals (preferably, in accordance with the American Veterinary Medical Association guidelines Report of the American Veterinary Medical Assoc. Panel on Euthanasia, *Journal of American Veterinary Medical Assoc.*, *202*:229-249, 1993). Representative animals from each treatment group can then be examined by gross necropsy for immediate evidence of metastasis, unusual illness, or toxicity. Gross abnormalities in tissue are noted, and tissues are examined histologically. Compounds causing a reduction in body weight or blood components are less preferred, as are compounds having an adverse effect on major organs. In general, the greater the adverse effect the less preferred the compound.

For the treatment of cancers the expected daily dose of a hydrophobic pharmaceutical agent is between 1 to 500 mg/day, preferably 1 to 250 mg/day, and most preferably 1 to 50 mg/day. Drugs can be delivered less frequently provided plasma levels of the active moiety are sufficient to maintain therapeutic effectiveness.

Plasma levels should reflect the potency of the drug. Generally, the more potent the compound the lower the plasma levels necessary to achieve efficacy.

EXAMPLES

The examples below are not limiting and are merely representative of various aspects and features of the present invention. The examples below demonstrate the isolation and characterization of the protein kinases of the invention.

EXAMPLE 1: Isolation of cDNA clones Encoding Novel Mammalian Protein Kinases Materials and Methods Identification from cDNA databases and isolation of clones encoding novel protein kinases

Novel kinases were identified from the public EST databases using a Hidden Markov model, abbreviated HMM (Krogh, A., Brown, M., Mian, I. S., Sjolander, K., and Haussler, D. 1994. Hidden Markov models in computational biology: Applications to protein modeling. *J. Mol. Biol.*, 235:1501-1531). The model was built with 70 mammalian and yeast kinase catalytic domain sequences. These sequences were chosen from a comprehensive collection of kinases such that no two sequences had more than 50% sequence identity. ESTs were translated in six open reading frames and were searched against the model. ESTs that had a score of at least 10 against the HMM were then masked for repetitive sequences and vectors and were clustered using MSA. The resulting contigs were searched against known kinases to identify EST clones that encode novel kinases.

Approximately 40% of the ESTs encoding potentially novel kinases did not correspond to the correct EST upon sequence analysis. Most of these discrepancies were resolved by ordering additional clones, however, 14 remained unavailable. These 14 ESTs were amplified from a variety of single-stranded cDNA sources with primers derived from the corresponding EST entry as shown on Table 5. The PCR product was subcloned into a bluescript vector, digested to confirm the presence of a correct size insert and sequenced. Full sequencing of EST and PCR was carried out using a cycle sequencing Big-dye kit

with AmpliTaq DNA Polymerase, FS (ABI, Foster City, CA). Sequencing reaction products were run on an ABI Prism 377 DNA Sequencer.

Table 5: Primers used to clone PCR products corresponding to novel kinases

	ID#	ID#	Parent	5' primer	3' primer
sp	na	aa	Sequence	Sequence*	Sequence*
H	33	153	2R22-5-11	GAGATCGRNTTYAARGA RTTYGA	TGTCACNCCNAGNSWCCAN AYRTT
M	81	200	5R57_10_2_ a:TESK2_m	GCTGCTGGACAGTGACT TGTATTT	GAAAGCAAAGCCTTCACAC CTT
H	67	187	5R69_17_2_h	CTCTCACCTCAGGAACT GG	GCTTGCGGATCTTCTCA
H	46	166	SGK309_h	GACATCCTGCCGGCCAA CTACG	CGGCCCTGGAGCTGCATCA CTA
M	67	228	5R72_16_2_h	TGCGCGACACCATTGAC CAG	CTCAGGGCTTACATACAGA G
H	45	165	5R72_8_2_h	AAAGGAGAACTACATTT TGAAAAT	CTTCATCATCTCTAATACAT TGGTTGG
H	41	161	Z36720	CAAATTAAGATCATTGA CTTTGGG	GGAAACAAAGTCCTTGGCC TC
H	115	234	AL031652 - Pak6	GTGGACATCTGGTCCCT CG	GTAGGTCCTTCACTCTTGG AG

- degenerate oligonucleotide residue designation:

N= A,C,G ot T

R= A or G

Y= C or T

S = C or G

W= A or T

<u>Full-length sequence extension of protein kinases using cDNA and genomic databases</u>

Extension of partial cDNA sequences to encompass the full-length open-reading frame was carried out by iterative blastn searching of the cDNA databases listed in Table 6. All blastn searches were conducted using a blosum62 matrix, a penalty for a nucleotide mismatch of –3 and reward for a nucleotide match of 1. The gapped blast algortihm is described in: (Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and

PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402).

Table 6. Databases used for cDNA-based sequence extensions

Database	Database Date
LifeGold templates	Feb 2000
LifeGold compseqs	Feb 2000
LifeGold compseqs	Mar 2000
LifeGold compseqs	Apr 2000
LifeGold fl	Feb 2000
LifeGold flft	Apr 2000
NCBI human Ests	May 2000
NCBI murine Ests	May 2000
NCBI nonredundant	May 2000

Extension of partial cDNA sequences to encompass the full-length open-reading frame was also carried out by iterative searches of genomic databases. Three methods were used. The first method made use of the Smith-Waterman algorithm to carry out protein-protein searches of the closest homologue or orthologue to the partial kinase. The target databases consisted of Genescan and open-reading frame (ORF) predictions of all human genomic sequence derived from the human genome project (HGP) as well as from Celera. The complete set of genomic databases searched is shown in Table 7 below. Genomic sequences encoding potential extensions were further assessed by blastp analysis against the NCBI nonredundant to confirm the novelty of the hit. The extending genomic sequences were incorporated into the cDNA sequence after removal of potential introns using the Seqman program from DNAStar. The default parameters used for Smith-Waterman searches were as shown next. Matrix: blosum 62; gap-opening penalty: 12; gap extension penalty: 2. Genescan predictions were made using the Genescan program as detailed in (Chris Burge and Sam Karlin "Prediction of Complete Gene Structures in Human Genomic DNA", JMB (1997) 268(1):78-94). ORF predictions from genomic DNA were made using a standard 6-frame translation.

The second method for genomic sequence-based extensions made use of tBlastn searches of the homologue or orthologue to the partial kinase against the cDNA databases listed in Table 7. The recognition of significant hits in these databases made possible to identify bridging partial cDNA clones. The iterative application of the two methods made possible the assemblage of the virtual full-length sequence for a large number of the kinases presented in this application. All tblastn searches were conducted using a blosum62 matrix, a penalty for a nucleotide mismatch of –3 and reward for a nucleotide match of 1.

The last method for defining cDNA extensions from genomic sequence used iterative searches of genomic databases through the Genescan program to predict exon splicing and the Genewise program (http://www.sanger.ac.uk/Software/Wise2/) to predict potential ORFs based on homology to the closest orthologue/homologue.

Table 7. Databases used for genomic-based sequence extensions

Database	Number of entries	Database Date
Celera v. 1-5	5,306,158	Jan 19/00
Celera v. 6-10	4,209,980	Mar 24/00
Celera v. 11-14	7,222,425	Apr 24/00
Celera v. 15	243,044	May 14/00
HGP all Genescan	25,885	Apr 04/00
HGP; Phase 0	4,944	May 04/00
HGP; Phase 1	28,478	May 05/00
HGP; Phase 2	1,508	May 04/00
HGP; Phase 3	9,971	May 05/00

Virtual Extensions

Human AA826850 (SEQ ID NO: 3, SEQ ID NO:124)

Blastn analysis of the partial AA826850 sequence revealed an extension to encompass the complete ORF in the Incyte EST 238299.1. A frame-shift correction at position 595 of this EST (marked by X in NA sequence) generated an uninterrupted ORF.

Human AA960957 (SEQ ID NO: 4, SEQ ID NO:125)

Since the initial filing of this application, the partial AA960957 sequence appeared in the public database as the full-length gene for a protein kinase encoded by a gene that maps adjacent to the evc (AJ250839) (ellis-van creveld syndrome and weyers acrodental dysostosis) gene from 4p16.1.

Human 5R79-46-1_h (SEQ ID NO: 5, SEQ ID NO:126)

Blastn analysis of the partial 5R79-46-1 sequence revealed an extension to encompass the complete ORF in the Incyte EST 463894.6. Since the initial filing of this application, the full-length virtual 5R79-46-1 appeared in the public database as the full-[illegible] length gene for the TANK-binding kinase (TBK1) (Pomerantz,J.L. and Baltimore,D. (1999) EMBO J. 18 (23), 6694-6704). TBK1 participates in NF-kB activation through the formation of a signaling complex with TRAF2 and TANK.

Human AA305176 (SEQ ID NO: 6, SEQ ID NO:127)

Blastn analysis of the partial AA305176 sequence revealed an extension to encompass the complete ORF in the Incyte EST 220937.1.

Human AA256100 (SEQ ID NO: 8, SEQ ID NO:129)

Blastn analysis of the partial AA256100 sequence revealed an extension to encompass the complete ORF through the assembly of three partial clones: Incyte EST 480815.6, KIAA0965 (BAA76809) and AA256100.

Human AA210825 (SEQ ID NO: 9, SEQ ID NO: 130)

Blastn analysis of the partial AA210825 sequence revealed an extension to encompass the nearly complete ORF through the assembly of three partial clones: Incyte EST 014721.7, and the NCBI EST's AW01158 and AA210825. An insertion of two "N's" at positions 1915 and 1916 generated an uninterrupted ORF. Blastx analysis indicated the possibility of a start Met in the range of 400-450 nucleotides (i.e. compared to the closest homolog, human PKCmu (CAA53384.1). However, no Met was found in this region; rather ORF ends in an in-frame stop preceeded by the sequence "RGLLAPGDPPCPPPNPAPATPPSSRLPTELFSNFCDS". It is possible that part of the sequence covered by nucleotide positions 1-400 derived from AW01158 comes from an intron, explaining the absence of a start Met.

Human AA127299 (SEQ ID NO:10, SEQ ID NO:131)

No entries in the database extended this sequence. The 1684 bp insert of this EST contains a 1369 bp intron at the 3' end. Blastx and SW analysis of the 315 bp coding

region revealed homology to the extracatalytic C2 domain of PKC. This EST, may or may not encode a kinase.

Human AA316804 (SEQ ID NO:11, SEQ ID NO:132)

Since the initial filing of this application, the partial AA316804 sequence appeared in the public database as the full-length gene for the PKC family protein kinase EPK2 or PKCnu (AB015982).

Human H19102 (SEQ ID NO:14, SEQ ID NO:135)

Genewise and Genescan analyses of the partial H19102 sequence revealed an extension from the HGP phase 3 contig 3810672 to encompass the complete catalytic domain of this EST. Blastn analysis against the non-redundant database revealed that this gene is found in the cosmid AC005726 from chromosome 17. H19102 may encode a dual catalytic kinase given the homology to S6 kinase. Analysis of genomic sequence upstream of the 5' end of H19102 revealed a non-kinase gene oriented in the same polarity as H19102 suggestive of the start Met for H19102 being close to the 5' end of the H19102 sequence. From this analysis it is deduced that the second catalytic domain of H19102, if present, is most likely located within the 47334-185,215 bp region of the genomic sequence of AC005726.

Human AA476563 (SEQ ID NO:15, SEQ ID NO:136)

Since the initial filing of this application, the partial AA476563 sequence appeared in the public database as the full-length gene for the protein kinase RPS6KC1 (NM_012424) (Zhang, H. et al Genomics (1999) 61, 314-318), which is an S6 kinase mapping to 12q12-q13.1.

Human AA626690 (SEQ ID NO:16, SEQ ID NO:137)

Since the initial filing of this application, the partial AA626690 sequence appeared in the public database as the full-length gene for the protein kinase RPS6KA6 (AF184965) (Yntema,H.G et al (1999) Genomics 62, 332-343), an S6 kinase commonly deleted in patients with complex X-linked (Xq21.1) mental retardation.

Human AI215680 (SEQ ID NO: 17, SEQ ID NO:138)

Since the initial filing of this application, the partial AI215680 sequence appeared in the public database as the full-length gene encoding a hypothetical protein (AAD30182) from the locus AC006530.4 from chromosome 14.

Human AA887783 (SEQ ID NO:21, SEQ ID NO:142)

Blastn analysis of the partial AA887783 sequence revealed an extension to encompass the nearly complete ORF through the assembly of three partial clones: Incyte 415390R6 and the NCBI EST's AA887783 and N94726. Since the initial filing of this application, the nearly full-length virtual AA887783 sequence appeared in the public database as the full-length gene encoding SGK3 (AF169035), a serum- and glucocorticoid-induced protein kinase (Kobayashi,T. et al (1999) Biochemical J. 344, 189-197.

Human R47805 (SEQ ID NO:22, SEQ ID NO:143)

A cDNA clone encoding the full-length ORF of R47805 was isolated using R47805 as a screening probe. A full-length form for R47805 has also appeared in the public database as

PTK9L (NM_007284), an A6-related protein kinase.

Human H60215 (SEQ ID NO:23, SEQ ID NO:144)

Blastn analysis of the partial H60215 sequence revealed an extension to encompass the complete ORF in the public EST AI275726. This was confirmed through the full insert sequencing of this EST (2,310 bp) which corresponds to the sequence under SEQ ID NO:144.

A different stop codon was predicted for AI275726 compared to H60215 due to a single nucleotide insertion at position 1586 in AI275726. Evidence for the extra nucleotide comes from EST AI191922.

SGK324_h orthologue of W30246_m (SEQ ID NO:24 , SEQ ID NO:145)

Blastn, blastx and Smith-Waterman analyses of genomic databases revealed an extension to encompass the complete ORF corresponding to the human orthologue of murine W30246. Exons predicted from the following sequences were used for contig construction: Celera 17000189645083, 17000057549105 and 11000501939981; Incyte142404.1, HGP_7249119, Incyte 7196489H1, Celera 11000501939981, 17000028165594; Incyte 7249119_3, Celera 17000035772368, 11000502081575 and 17000140274329. The latter Celera sequence provides the N-terminus.

Human AA383293 (SEQ ID NO:26, SEQ ID NO:147)

Blastn, blastx and Smith-Waterman analyses of genomic databases revealed an extension to encompass the complete ORF corresponding for AA383293. Exons predicted from the following sequences were used for contig construction: (numbers in parenthesis

refer to the aa sequence of the closest homolog (RU2S, NP_057440) used for the Smith-Waterman query): N-term from Incyte 6010175_2 (14-97), Incyte 6981981 (134-184) 7596749 (186-232) Celera 17000020789545 (243-301) CAB75619.1 (310-341)--(56-145 DCX homology) 6010175_2 , Celera 17000030058129 (241-262 DCX homology).

Human AA021445 (SEQ ID NO:32, SEQ ID NO:152)

Blastn analysis revealed an extension to encompass the nearly complete ORF corresponding for AA021445. Contig reconstruction was as follows: nucleotides1-802 from KIAA0999 (AB023216); nucleotides 803-4321 from full-insert sequence of AA021445. A pairwise alignment between the AA021445 and KIAA0999 revealed three inserts in the extracatalytic C-terminus of 48, 48 and 161 aminoacids. In addition, both AA021445 and KIAA0999 have 15 copies of a CAG repeat. Trinucleotide repeats are often found in genes that linked to neurodegenerative diseases.

Human 2R22-55-1 (SEQ ID NO:33, SEQ ID NO:153)

Blastn analysis revealed an extension in the Incyte EST clone 321074.1 to encompass the complete ORF corresponding to 2R22-55-1.

Human orthologue of AA544838_m (SEQ ID NO:36, SEQ ID NO:156)

tBlastn analysis identified the partial human KIAA0135 (U79240) clone as the human orthologue of murine AA544838. Blastn revealed an extension KIAA0135_h (U79240) to encompass the complete ORF. The full ORF was reconstructed from Incyte406786.5, KFZp430051 and KIAA0135 (U79240).

Human orthologue of AI785735_m (SEQ ID NO:38, SEQ ID NO:158)

tBlastn analysis identified the partial human KIAA0781 (AB018324) clone as the human orthologue of murine AI785735. Blastn revealed an extension KIAA0135_h (U79240) to encompass the complete ORF. The full ORF was reconstructed from Incyte 986123.37 KIAA0781 (AB018324).

Human AA207220 (SEQ ID NO: 39, SEQ ID NO:159)

Blastn analysis revealed an extension to encompass the nearly complete ORF corresponding for AA021445. The full ORF was reconstructed from Incyte 402740.1 and AA207220. Frame corrections: deletion of 441 and 595 over Inc402740.1 seq based on blastx to keep frame open; two n insertions 940, 941 over AA207220 to keep frame open.

Human AA426580 (SEQ ID NO:40, SEQ ID NO:160)

Since the initial filing of this application, the partial AA426580 sequence appeared in the public database as the full-length gene encoding MAK-V (AJ271722) from chromosome 21q22.1.

Human 5R79-54-1 (SEQ ID NO: 41, SEQ ID NO:161)

Genewise and Genescan analyses of the partial 5R79-54-1 sequence revealed an extension from genomic sequence to encode the full ORF for 5R79-54-1.

Human orthologue of AA542015_m (SEQ ID NO: 42, SEQ ID NO:162)

tBlastn analysis identified KIAA1297 ([illegible]). Blastn extended the KIAA1297 sequence to provide the C-terminus through the Incyte 224074.1 EST. The partial ORF consists of a dual catalytic domain flanked by 6 Ig domains and 2 fibronectin repeats. Based on homology to the bt drosophila protein (AAF59316.1), the human form of AA542015 is expected to be missing 16 Ig domains.

Human R19772 (SEQ ID NO:44, SEQ ID NO:164)

The full-length ORF for R19772 was isolated by screening a cDNA library using a probe derived from R19772. Since the initial filing of this application, the R19772 sequence appeared in the public database as the full-length gene encoding Trio (Duet) (AB011422). CDNA library screening revealed multiple isoforms for this gene which are summarized in the Table below.

Table 8. Isoforms for R19772

Kestrl Name	Kestrl AA Acc #	Isoform type	Source	Description*
Trad (Duet)	R19772	B	Skeletal muscle	Deletion of K at 124
				Deletion of Q at 616
				Substitution of E for G at 762
		C	Skeletal muscle	Deletion of K at 124
				Deletion of Q at 616
				Substitution of E for G at 762

				Deletion of 32 aa (160-191)
		D	Lung tumor	Deletion of Q at 616
				Deletion of 32 aa (160-191)
		E	Lung tumor	Deletion of Q at 616
				Deletion of 32 aa (160-191)

* reference amino acid position are with respect to sequence of Trad (AB011422)

Human AA435956 (SEQ ID NO:48, SEQ ID NO:168)

Blastn analysis revealed an extension to encompass the nearly complete catalytic region of AA435956. 5' end sequence extension was provided by genomic locus AC007242.3_h (range 44880-43801). Based on blastx analysis, the extended sequence encodes is full-length at the C-terminus.

Human AA397553 (SEQ ID NO: 51, SEQ ID NO:171)

Since the initial filing of this application, the partial AA397553 sequence appeared in the public database as the full-length gene encoding CRK7 (AF227198), a novel CDC2-related protein kinase that colocalizes with interchromatin granule clusters.

Human AA789239 (SEQ ID NO: 52, SEQ ID NO:172)

Since the initial filing of this application, the partial AA789239 sequence appeared in the public database as the full-length gene encoding NKIAMRE (AF130372), a novel kinase deleted in human leukemia.

Human AA631990 (SEQ ID NO:55, SEQ ID NO:175)

Blastn analysis revealed an extension to encompass the full-length ORF for AA631990. The full ORF was reconstructed from 253847.5 and AA631990 and AA207220. Frame corrections: delete 1 C at 1380, delete 2N's at 2033/2034.

Human AA557536 (SEQ ID NO:56, SEQ ID NO:176)

Blastn analysis revealed an extension to encompass full-length ORF for AA557536. The full ORF was reconstructed from AA557536, celera 11000504061899 and the Incyte 097089.1 EST. An 85bp intron was removed from AA557536.

Human N34132 (SEQ ID NO: 63, SEQ ID NO:183)

Full sequencing of EST N34132 (1.3 kb) confirmed that this cDNA encodes a novel NEK-subfamily kinase. Blast analysis against the EST database showed that four

EST sequences (AA283140, AA283140, AA282911 and N53011) extended the sequence of N34132 at the 3' end to form a 2.31 kb contig. Blast analysis of the new contig against the nonredunat public database showed that the N34132 extended contig overlapped (100% identity) over 228 bp at its 3' end with human KIAA0344 (AB002342), a 5, 787 bp cDNA encoding a 1246 aa polypeptide. The 5' 790 bp of the KIAA0344 cDNA (encoding the 58 N-terminal protein sequence) were found to be divergent with respect to the extended 2.32 kb N34132 contig. Evidence that the extended N34132 contig (2.31kb) and KIAA0344 (AB002342) belong to the same gene is the following. First, blast analysis of the nucleotide sequences for N34132 and KIAA0344 against the NRN database confirmed that these cDNA's are transcribed from the same genomic locus defined by two overlapping BACs (AC004765 and AC004803) from chromosome 12p13.3. Second, full sequence determination of a PCR fragment amplified from single-stranded cDNA confirmed the junction between the extended N34132 contig and KIAA0344_h (AB002342). The 462 PCR product was amplified with primers CTCCTCAACAGACAGTGCAG (5' primer) and GACATTCTACTACTCGGTCTC (3' primer) designed from the N34132 extended contig and KIAA0344 sequences, respectively. The region of N34132 containing the start Met was isolated by PCR from a testis cDNA library (Clontech).

Human 5R69-17-2 (SEQ ID NO:67, SEQ ID NO:187)

The full-length ORF for 5R69-17-2 was isolated by screening a cDNA library using a probe derived from 5R69-17-2.

Human H85811 (SEQ ID NO:68, SEQ ID NO:188)

Tblastn, Smith-Waterman and blastn analyses using cDNA databases revealed an extension to encompass full-length ORF for H85811. The full ORF was reconstructed from Incyte ESTs 202971.8, 034583.3 and 034583.1 and public ESTs H85811 and AI570599.

Human R43524 (SEQ ID NO:73, SEQ ID NO:192)

Blastn analysis revealed an extension to encompass the complete catalytic region and the C-terminus of R43524. Since the initial filing of this application, the partial R43524 sequence appeared in the public database as the full-length gene encoding the heme-regulated initiation factor 2-alpha kinase (HRI) (AF181071).

Human AA088547 (SEQ ID NO:78, SEQ ID NO:197)

Genewise and Genescan analyses of genomic databases revealed an extension to encompass the complete ORF for AA088547.

Human orthologue of AA139478_m (SEQ ID NO:80, SEQ ID NO:199)

Tblastn identified the Incyte 211475.1 as the potential full-length human orthologue of murine AA139478

Human AA232253 (SEQ ID NO:82, SEQ ID NO:201)

The full-length ORF for AA232253 was isolated by screening a cDNA library using a probe derived from AA232253. Since the initial filing of this application, the AA232253 sequence appeared in the public database as the full-length gene encoding SLK (AB011422). SLK is a stress-regulated mixed lineage kinase-like protein that activation of Rac and induction of apoptosis. cDNA library screening revealed multiple isoforms for this gene which are summarized in the Table below.

Table 9. Isoforms for AA232253

Kestrl Name	Kestrl AA Acc #	Isoform type	Description*
MLK4	AA232253	MLK4	Substitution of C for W at 346
		MLK4B	Different Cterm (332-800); seq in MLK4B is as shown in *

* C-terminus specific to MLK4B

LPLAARMSEESYFESKTEESNSAEMSCQITATSNGEGHGMNPSLQAMMLMGFGDI
FSMNKAGAVMHSGMQINMQAKQNSS
KTTSKRRGKKVNMALGFSDFDLSEGDDDDDDDGEEEDNDMDNSE

Human H97685 (SEQ ID NO:84, SEQ ID NO:203)

Blastn analysis revealed an extension to encompass the full-length ORF for H97685. The full ORF was reconstructed from Incyte 474824.1 and the public ESTs H97685 and M62021.

Human AI052250 (SEQ ID NO:87, SEQ ID NO:206)

Blastn analysis revealed an extension to encompass the full-length ORF for AI052250. The full ORF was reconstructed from Incyte 396868.1, the public partial cDNA FLJ10074 (minus intron) and the public ESTs and the public ESTs AI052250 and H97685, AI499220 and M62021.

Human AA278842 (SEQ ID NO:88, SEQ ID NO:206)

A nearly full-length cDNA (FL4F12) for AA278842 was isolated by screening a cDNA library using a probe derived from AA278842. A full-length virtual ORF was generated using FL4F12 and AA278842.

Human AA599286 (SEQ ID NO:89, SEQ ID NO:208)

Since the initial filing of this application, the partial AA599286 sequence appeared in the public database as a full-length ORF (AK000342).

Human AA425725 (SEQ ID NO:90, SEQ ID NO:209)

Since the initial filing of this application, the partial AA425725 sequence appeared in the public database as MSSK1, a serine kinase gene located from human chromosome Xq28.

Human SGK022 orthologue of AA060026_m (SEQ ID NO:91, SEQ ID NO:210)

Tblastn, Smith-Waterman and blastn analyses of cDNA and genomic databases databases revealed a potential human orthologue for murine AA060026. The full-length ORF for SGK022 was reconstructed from genomic locus AC022307.

Human AA399669 (SEQ ID NO:93, SEQ ID NO:212)

Blastn analysis revealed an extension to encompass the full-length ORF for AA399669. The full ORF was reconstructed as follows: sequence 1-1007 from AL136295.2; sequence1008-2319 from AA399669 and Incyte 428177.1.

Human AA883975 (SEQ ID NO:95, SEQ ID NO:214)

Genescan and Genewise analyses of the genomic databases revealed an extension for AA883975 to encompass the full-length ORF

Human AA905446 (SEQ ID NO:96, SEQ ID NO:215)

Tblastn, Smith-Waterman and blastn analyses of cDNA and genomic databases databases revealed an extension for AA905446 to encompass the full-length ORF. For the Smith-Waterman analysis murine STK22 (NP_033462) was used as the closest orthologue. Contig formation: range 162133-163687 from HGP_h 6921333_9; removed intron (146-893) predicted from blastx analysis.

Human H29974 (SEQ ID NO: 97 SEQ ID NO:216)

Blastn analysis revealed an extension to encompass a complete catalytic ORF for AA399669. The nearly full-length ORF was reconstructed using Incyte 213829.1 and H29974.

Human AA215311 (SEQ ID NO:99, SEQ ID NO:218)

Blastn analysis revealed an extension to encompass the full-length ORF for AA21531. The full ORF was reconstructed from Incyte 067584.1, 022456.1, AA215311 and the reverse complement of CPG_043208.

Human AA018361 (SEQ ID NO:100, SEQ ID NO:219)

The full-length ORF for AA018361 was isolated by screening a cDNA library using a probe derived from AA018361. This yielded clone Sug4-30. Clone Sug4-30, like multiple, independent cDNA clones contained a 181bp intron. The existence of intron-less RNA's was confirmed by a PCR reaction that generated a product that upon sequence analysis skipped the intron region. The full-length virtual ORF for AA018361 was generated through a contig between AL117482 (seq 1-367) and the sequence for clone Sug4-30.

Human orthologue of AA396601_m (SEQ ID NO:106, SEQ ID NO:225)

tBlastn and Smith-Waterman analyses of genomic sequence revealed an extension to encompass the full catalytic region for the human orthologue of AA396601. The ORF was reconstructed from Incyte 018653.9 (7261449H1, 6891740J1) and genomic sequence CPG_040010.

Human orthologue of AA671275_m (SEQ ID NO:108, SEQ ID NO:227)

Since the initial filing of this application, a potential human orthologue for murine AA671275 appeared in the public database as the full-length ORF for vaccinia related kinase 3 (BAA90769).

Human H05721 (SEQ ID NO:111, SEQ ID NO:230)

Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for H05721.

Human AI086865 (SEQ ID NO:112, SEQ ID NO:231)

Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for AI086865. The full-length ORF was reconstructed from Celera 17000102901516, Incyte 243269.1 and public AL1377531.

Human AA836348 (SEQ ID NO:113, SEQ ID NO:232)

Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for AA836348.

Human R86668 (SEQ ID NO:14, SEQ ID NO:233)

The full-length ORF for R86668 was isolated by screening a cDNA library using a probe derived from R86668. Since the initial filing of this application, the R8668 sequence appeared in the public database as the full-length gene mitogen-activated protein kinase kinase kinase 6 (MAP3K6) (NM_00467).

Human 2R41-9-4 (SEQ ID NO: 16, SEQ ID NO:235)

The full-length virtual ORF for 2R41-9-4 was generated using genomic sequence to provide the Nterminus for the partial ORF predicted from clone 2R41-9-4

Table 10. Sequences deleted from the provisional patent due to duplication with other genes in the patent

Prov. SEQ ID NO: (na)	Prov. SEQ ID NO: (aa)
160	196
213	214
215	216
122	126
119	123
148	184
4	20
7	23
205	206
14	30
15	31
35	56
42	63
51	72
44	65
77	91

78	92
79	93
80	94
157	193

Results

Table 1 documents the results from the analysis of the nucleic acid sequence data. From left to right the data presented is as follows. "Gene name" refers to the EST or PCR fragment that defined the novel kinase. "Species" refers to the organism the sequence was derived from. "ID#" refers to the nucleic acid and amino acid sequence ID number designation from this patent. "Kinase family "and "Kinase group" refers to the protein kinase classification defined by sequence homology and based on previously established phylogenetic analysis [Hardie, G. and Hanks S. The Protein Kinase Book, Academic Press (1995) and Hunter T. and Plowman, G. Trends in Biochemical Sciences (1977) 22:18-22 and Plowman G.D. *et al.* (1999) Proc. Natl. Acad. Sci. 96:13603-13610)]. "ORF Start", "ORF End", "ORF Length" refer to the open reading frame range and length as calculated by standard nucleic acid translation programs such as MapDraw (DNAStar). "DNA Repeats" refers to regions of low complexity sequence or repetitive elements such as Alu, LINE, SINE, and LTR sequences. The chromosomal location (CHR localization) for 37 of the 110 novel protein kinases is shown on Table 1 (NA, not available). The methods for determining chromosomal position are outlined below, in Example 2.

Table 2 documents the results from the analysis of the amino acid sequence data. From left to right the data presented is as follows. "Gene name" refers to the EST or PCR fragment that defined the novel kinase. "Species" refers to the organism the sequence was derived from. "ID#" refers to the nucleic acid and amino acid sequence ID number designation from this patent. "Kinase family "and "Kinase group" refers to the protein kinase classification defined by sequence homology and based on previously established phylogenetic analysis [Hardie, G. and Hanks S. The Protein Kinase Book, Academic Press (1995) and Hunter T. and Plowman, G. Trends in Biochemical Sciences (1977) 22:18-22 and Plowman G.D. *et al.* (1999) Proc. Natl. Acad. Sci. 96:13603-13610)]. "nraa Score", "ID match aa", "Identity", "Similar", "nraa Match Acc#", Description" refer to the data obtained using a Smith-Waterman search of the amino acid sequence against the non-

redundant protein database (Matrix: Pam100; gap open/extension penalties 14/1). "Kinase Domain Start", "Kinase Domain End", "Profile Start" and "Profile End" refer to data obtained using a Hidden-Markov Model to define catalytic range boundaries. The profile has a length of 261 amino acids, corresponding to the complete protein kinase catalytic domain. Proteins in which the profile recognizes a full length catalytic domain have a "Profile Start" of 1 and a "Profile End" of 261. The boundaries of the catalytic domain within the overall protein are noted in the "Kinase Domain Start" and "Kinase Domain End" columns.

The following abbreviations were used for kinases:

ASK	Apoptosis signal-regulating kinase
CaMK	Ca2+/calmodulin-dependent protein kinase
CCRK	Cell cycle-related kinase
CDK	Cyclin-dependent kinase
CK	Casein kinase
DAPK	Death-associated protein kinase
DM	myotonic dystrophy kinase
Dyrk	dual-specificity-tyrosine phosphorylating-regulated kinase
GAK	Cyclin G-associated kinase
GRK	G-protein coupled receptor
GuC	Guanylate cyclase
HIPK	Homeodomain-interacting protein
IRAK	Interleukin-1 receptor-associated kin
MAPK	Mitogen activated protein kinase
MAST	Micotubule-associated STK
MLCK	Myosin-light chain kinase
MLK	Mixed lineage kinase
NIMA	NimA-related protein kinase
PKA	cAMP-dependent protein kinase
RSK	Ribosomal protein S6 kinase
RTK	Receptor tyrosine kinase

SGK	Serum and glucocorticoid-regulated kinase
STK	serine threonine kinase
ULK	UNC-51-like kinase

The following abbreviations were used for species

H	Human
M	Murine
R	Rat
FV	Fowlpox virus
MT	M. thermoautotrophicum
CE	Caenorhabditis elegans
DM	Drosophila melanogaster
OS	Oryza sativa
SP	Schizosaccharomyces pombe
TP	Tetrahymena pyriformis
PI	Petunia inflata
NC	Neurospora crassa
MSV	Medicago sativa
MSV	Moloney murine sarcoma virus
SA	Squalus acanthias
CS	Cucumis sativus
GM	Glycine max
LL	Lilium longiflorum
TV	Trichomonas vaginalis
MP	Mycoplasma pneumoniae
DD	Dictyostelium discoideum
SC	Saccharomyces cerevisiae
MT	Methanobacterium thermoautotrophicum

Domain and Motif Identification

A Hidden Markov model (HMM) (Krogh, A., Brown, M., Mian, I. S., Sjolander, K., and Haussler, D. (1994). Hidden Markov models in computational biology: Applications to protein modeling. J. Mol. Biol., 235:1501-1531) was used to identify, both catalytic and extracatalytic domains. Table 4 shows extra-catalytic domains that were identified using the HMM program. Other domains such as coiled-coil and pest motifs were identified as described next.

Potential coiled-coil domains were identified using the COILS program (www.ch.embnet.org/software/COILS_form.html). The matrix used was MTIDK with windows of 14, 21, 28 amino acids. Only regions scoring 0.5 or higher were considered to have potential coiled-coil domain region.

Protein sequences containing potential pest motifs were identified using the program PESTfind (www.at.embnet.org/embnet/tools/bio/PESTfind/). PEST regions in proteins are by definition sequences that tend to be rich in proline, glutamic or aspartic acid, argininine and histidine; they have been associated with increased protein turnover rates (Rogers S. *et al.* (1986) Science 234, 364-368. The algorithm defines PEST sequences as hydrophilic stretches of amino acids greater than or equal to 12 residues in length. Such regions contain at least one P, one E or D and one S or T. They are flanked by lysine (K), arginine (R) or histidine (H) residues, but positively charged residues are disallowed within the PEST sequence. PESTfind produces a score ranging form about -50 to +50. By definition, a score above zero denotes a possible PEST region; a value greater than +5 defines a high probability that there is a PEST domain.

Identification of potential coiled-coil domains and PEST domains in N34132

Potential coiled-coil domains were identified in N34132 (SEQ ID NO:183) using the COILS program. Only regions scoring 0.5 or higher were considered to have potential coiled-coil domain region. The amino acid positions within N34231 scoring for potential coil-coil regions are shown below.

Table 11 coiled-coil domains predicted for N34132

Coiled-coil Region	Amino acid range	Length (aa)
1	124-147	24
2	437-451	15
3	495-526	32
4	1,723-1,749	27

Potential PEST domains were identified in N34132 using PESTfind, a value greater than +5 defines a high probability that there is a PEST domain. The amino acid positions within N34132 scoring for potential PEST regions are shown below.

Table 12 Potential Pest domains identified in N34132

PEST Region	Score	Amino acid range	Amino Acid Length
1	+ 4.91	54-95	42
2	+11.4	537-570	34
3	+31.08	1293-1304	12
4	+10.15	1543-1565	23
5	+6.17	1698-1732	35

EXAMPLE 2. Chromosomal Localization of Novel Mammalian Protein Kinases

Materials and Methods

Several sources were used to find information about the chromosomal localization of each of the genes described in this patent. First, the accession number for the nucleic acid sequence was used to query the Unigene database. The site containing the Unigene search engine is: http://www.ncbi.nlm.nih.gov/UniGene/Hs.Home.html. Information on map position within the Unigene database is imported from several sources, including the Online Mendelian Inheritance in Man (OMIM, http://www.ncbi.nlm.nih.gov/Omim/searchomim.html), The Genome Database (http://gdb.infobiogen.fr/gdb/simpleSearch.html), and the Whitehead Institute human physical map (http://carbon.wi.mit.edu:8000/cgi-bin/contig/sts_info?database=release). For example, searching Unigene with W56561, an EST for a MAK-like kinase, the

following information is retrieved: Chr.14, D14S65-qTEL. The location of this gene on an "ideogram" of the cytogenetic map of chromosome 14 is also provided, showing that W56561 maps to the bottom of chromosome 14, between 14q31 and 14qTel. If Unigene has not mapped the EST, then the nucleic acid for the gene of interest is used as a query against databases, such as dbsts and htgs (described at http://www.ncbi.nlm.nih.gov/BLAST/blast_databases.html) containing sequences that have been mapped already. The nucleic acid sequence is searched using BLAST-2 at NCBI (http://www.ncbi.nlm.nih.gov/cgi-bin/BLAST/nph-newblast) and is used to query against either dbsts or htgs. In addition to the Whitehead and GDB sites mentioned above, Stanford University maintains a useful site for chromosomal mapping from STS data (http://www-shgc.stanford.edu/RH/rhserverformnew.html). Matches in htgs are often resolved immediately because the genomic region hit is annotated in the htgs entry. If an exact match match is found (defined roughly as 99% identity over a region of about 100 base pairs or longer, excluding any repetitive sequence), then the mapped position of the entry in the database is assigned to the original kinase query. Once a cytogenetic region has been identified by one of these approaches, disease association is established by searching OMIM (see above for URL) with the cytogenetic location. OMIM maintains a searchable catalog of cytogenetic map locations organized by disease. A thorough search of available literature for the cytogenetic region is alo made using Medline (http://www.ncbi.nlm.nih.gov/PubMed/medline.html). References for association of the mapped sites with chromosomal abnormalities found in human cancer can be found in: Knuutila, *et al.*, Am J Pathol, 1998, 152:1107-1123.

Results

The chromosomal location for 37 of the 110 novel protein kinases is shown on Table 1. Three of the novel protein kinases were mapped to regions associated with cancer amplicons, as shown on this table. The regions were also cross-checked with the Mendelian Inheritance in Man database, which tracks genetic information for many human diseases, including cancer. References for association of the mapped sites with chromosomal abnormalities found in human cancer can be found in: Knuutila, et al., Am J Pathol, 1998, 152:1107-1123. Association of these mapped regions with other diseases is

documented in the Online Mendelian Inheritance in Man (OMIM) (http://www.ncbi.nlm.nih.gov/htbin-post/Omim).

EXAMPLE 3: Generation of Specific Immunoreagents

Materials and Methods

Peptide sequences to extra-catalytic regions of novel kinases are chosen which are not homologous to other known kinases based on a Smith Waterman homology search against the non-redundant protein database and predicted to be antigenic based on the DNAStar Protean program. These peptides are conjugated to KLH using Glutaraldehyde.

Rabbits are immunized with the KLH-peptide conjugates by four injections three weeks apart. The rabbits are bled ten and fourteen days following the third injection and bled out ten days after the fourth. The serum is checked against the peptide by ELISA.

Table 13. Peptides to be used as immunogens for raising antibodies

Clone Name	SEQ ID NO (aa)	Peptide Sequence	Amino Location
AA8256850	124	KSRDNSRDSSQSEND	339-353
		TEKLKRSQDLPREPLP	372-386
		RGWREYDIHS	223-232
5R79-46-1	126	FEGPRRNKEVMYK	224-236
		KDDYNETVHKKTE	451-463
		GTHPKDRNVEKLQ	541-553
		EVSKYQEYTNELQET	643-657
AA256100	129	IDDTSNFDDFPESDI	405-419
		TEPDYKSKDWVFL	427-439
		EEKKLRRSQHARKET	61-75
AA210825	130	SNKDTLRKRHYWRLD	507-521
		RHTTRKSSTTLRE	488-500
		FQNNTTNRYYKEIPL	528-542
		GKHRKTGRDVAVK	668-680
		FPTKQESQLRNE	687-698

AA316804	132	ESHVHQEPSKRIPS	239-252
		HTKRKSSTMVKEGW	409-422
		PSDLDVERDEEAVK	375-388
		SPGQGKDHKDLSTSI	543-557
R47805	143	EPVGRWDQDYDRAVL	44-58
		KPKGPGGKRGHKRLI	325-339
		PTDVAQLPSRVPRDA	219-233
AA234[illegible]	[illegible]	DPF[illegible]GNDGSLT	293-307
		HPRPQEKDVWEE	374-385
		RENTDEVFPDEQLSD	340-354
		RSEITQPDRDIPLVR	427-441
AA460132	180	LKSYSTSSKKARPVL	222-236
		KKLDEVRLRGRKRSM	237-251
		ETEKTAQGLSNLAKT	131-145
N34132	183	SGRRRRPTKSKGSKS	1848-1862
		PGTAPSKPPLTKAPV	1474-1488
		VDSDTQPKAPGIDD	1365-1378
		AHSLDKTSHSSTTGL	1253-1267
5R69-17-2	187	GTTREKTDRVKST	178-190
		HSEAPELHGKIRSSN	138-152
		DETVTPPQFSIV	87-98
		QYDVKSEIYS	204-213
AA278842	206	TVDPEKSVRDQAFKA	515-529
		DSSTADRWDDEDWGS	637-651
		SVSEDPTQLEEVEKD	539-553
AA836348	232	NAPTKRPRSSTVTEA	323-337
		LDSEEDYYTPQKVDV	514-528
		GDKASYRQPKHVEKL	409-423

EXAMPLE 4. Expression analysis of Novel Mammalian Protein Kinases

GENE EXPRESSION ANALYSIS

Tissue Arrays

"cDNA libraries" derived from a variety of sources were immobilized onto nylon membranes and probed with 32P-labeled cDNA fragments derived from the gene(s) of interest.

Total RNA or mRNA was used as template in a reverse transcription reaction to generate single-stranded cDNAs (ss.cDNA) that were tagged with specific sequences at each end. An oligo dT primer containing a specific sequence (CDS: AAGCAGTGGTAACAACGCAGAGTACT30VN (V=A,G,C N=A,G,C,T)) anneals at the polyA track at the 3' end of the mRNA and the reverse transcriptase (MMLV RnaseH-) transcribes the antisense strand until it reaches the end of the RNA strand when it adds additional C residues. If a primer (SMII: AAGCAGTGGTAACAACGCAGAGTACGCGGG or ML2G: AAGTGGCAACAGAGATAACGCGTACGCGGG) ending with 3 Gs is added, it anneals to the added Cs and the MMLV recognizes the rest of the primer sequence as template and continues transcription. As a result, the synthesized cDNAs contain specific sequence tags at both the 5' and the 3' end. When the 5' and the 3' ends are tagged with the same sequence (CDS and SMII) it is referred to as "symmetric." When the 5' end is tagged with a different sequence than the 3' end (CDS and ML2G) is referred to as "asymmetric" A double-stranded "cDNA library " is then generated by PCR amplification using the 3'PCR and ML2 primers (3' PCR: AAGCAGTGGTAACAACGCAGAGT and ML2: AAGTGGCAACAGAGATAACGCGT) that anneal to the added sequence tags.

The amplified "cDNA libraries" were manually arrayed onto nylon membranes with a 384 pin replicator. The DNA was denatured by alkali treatment, neutralized and cross-linked by UV light. The arrays were pre-hybridized with Express Hyb (Clontech) and hybridized with 32P labeled probes generated by random hexamer priming of cDNA fragments corresponding to the genes of interest. After washing, the blots were exposed to phosphorimaging cassettes and the intensity of the signal was quantified. The amount of the DNA on the arrays was also quantified by treating non-denatured or denatured arrays with Syber Green I or Syber Green II respectively (1:100,000 in 50mM Tris, pH8.0) for 2 minutes. After washing with 50mM Tris, pH8.0, the fluorescent emission was detected

with a phosphorimager (Molecular Dynamics) and quantified. The amount of the arrayed DNA was used to normalize the hybridization signal and the corrected values are tabulated in Table 3.

Results

The results of the microarray expression analysis of the protein kinases presented in this application is shown in Table 3. Data presentation from left to right is as follows: "Tissue": tissue type of the cDNA; "Tumor sym", indicates that the tissue is derived from a tumor, "sym" refers to the fact that the 5' and 3' primers used to make the sample are the same; "Normal Sym", indicates normal tissue was used to make the sample, with symmetric primers as described above; "Tumor 1o", indicates that primary tumor tissue was used to make the cDNA; "Tumor cells", indicates that these cDNA samples were made from cultured tumor cells; "Normal", indicates that these samples are derived from normal tissue or cell lines; "Endos", indicates that these samples are derived from endothelium-related tissue sources; "p53" refers to the status, mutant or wild-type, of the p53 gene in the source samples. Normalized expression values are presented for each gene referred to by its SEQ ID# on the subsequent columns. Genes represented in expression Table 3 are: SEQ ID NO:3 (AA826850), SEQ ID NO:5 (TBK1), SEQ ID NO:6 (AA305170), SEQ ID NO:8 (AA256100), SEQ ID NO:9 (CAB43292), SEQ ID NO:11 (EPK2), SEQ ID NO:12 (PKNbeta), SEQ ID NO:14 (H19102), SEQ ID NO:16 (RSK4), SEQ ID NO:17 (AAD30182), SEQ ID NO:20 (SGK2), SEQ ID NO:22 (PTK9L), SEQ ID NO:26 (AA383293), SEQ ID NO:29 (DRAK2), SEQ ID NO:31 (DRAK1), SEQ ID NO:032 (AA015726), SEQ ID NO:40 (MAK-V), SEQ ID NO:044 (TRAD), SEQ ID NO:044 (TRAD), SEQ ID NO:45 (AA454060), SEQ ID NO:47 (AA234451), SEQ ID NO:48 (AA436054), SEQ ID NO:49 (AA626859), SEQ ID NO:51 (KIAA0904), SEQ ID NO:52 (AA789239), SEQ ID NO:54 (CCRK), SEQ ID NO:55 (CLK4), SEQ ID NO:56 (AA557536), SEQ ID NO:57 (W56561), SEQ ID NO:60 (AA579641), SEQ ID NO:63 (NEK7), SEQ ID NO:66 (CAMKKB), SEQ ID NO:68 (HIPK2), SEQ ID NO:72 (R19609), SEQ ID NO:73 (HRI), SEQ ID NO:78 (AA088547), SEQ ID NO:79 (AA449542), SEQ ID NO:082a (MLK4), SEQ ID NO:82 (MLK4b), SEQ ID NO:84 (RIP4), SEQ ID NO:88 (AA278842), SEQ ID NO:89 (AA195964), SEQ ID NO:90 (MSSK1), SEQ ID NO:93 (TSK4), SEQ ID NO:94 (AI025291), SEQ ID NO:95

(AA948538), SEQ ID NO:96 (AA905446), SEQ ID NO:97 (H85389), SEQ ID NO:100 (AA018361), SEQ ID NO:101 (AA311714), SEQ ID NO:110 (AA452647), SEQ ID NO:111 (AA310219), SEQ ID NO:112 (AI086865), SEQ ID NO:114 (MEKK6), and SEQ ID NO:116 (SuRTK106).

EXAMPLE 5. Kinase assays for Erk, JNK1 and p38 MAP kinases

293T cells were transiently transfected with HA- p38 or co-transfected with Flag-tagged wt MLK4A, kinase-dead MLK4A, wild-type MLK4B or kinase-dead MLK4B [illegible] using Lipofectamine 2000 (Lifetech). Cells were lysed 36 hr post-transfection. Cell lysates normalized to contain equivalent amounts of HA-p38 were immunoprecipitated with anti-HA antibody (Mab HA-11, Babco). Immunoprecipitates were split in two portions, one portion was Western-blotted with anti- HA antibody and the other with a phospho-specific p38 antibody (Promega) to detect activated levels of p38. Activation of Erk1 and Jnk1 was measured similarly. (This example applies to AA232253 (SEQ ID NO:82, SEQ ID NO:201).)

Results:

In transient assays wild-type MLK4A and MLK4B (but not kinase-inactive MLK4A(K45M) or MLK4B(K45M)) activate Erk, JNK1 and p38 MAP kinases.

EXAMPLE 6. RAC1 guanine-exchange factor assay

293T cells were transiently transfected with HA-Rac1 or co-transfected with Flag-tagged Duet C, Duet E, Dbl and HA-Tiam-1. Cells were lysed 36 hour post-transfection. Cell lysates normalized to contain equivalent amounts of Rac1 were affinity precipitated with immobilized GST-PBD (p21-binding domain of Pak3). Bound proteins were Western blotted and probed with anti-HA antibody to detect levels of activated Rac1. ((This example applies to R199772 (Trad/Duet)(SEQ ID NO:44, SEQ ID NO:164).)

Results:

Duet C and Duet E both act as guanine nucleotide exchange factors on Rac1.

CONCLUSION

One skilled in the art would readily appreciate that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those inherent therein. The molecular complexes and the methods, procedures, treatments, molecules, specific compounds described herein are presently representative of preferred embodiments are exemplary and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art which are encompassed within the spirit of the invention are defined by the scope of the claims.

It will be readily apparent to one skilled in the art that varying substitutions and modifications may be made to the invention disclosed herein without departing from the scope and spirit of the invention.

All patents and publications mentioned in the specification are indicative of the levels of those skilled in the art to which the invention pertains.

The invention illustratively described herein suitably may be practiced in the absence of any element or elements, limitation or limitations which is not specifically disclosed herein. Thus, for example, in each instance herein any of the terms "comprising", "consisting essentially of" and "consisting of" may be replaced with either of the other two terms. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed.

In particular, although some formulations described herein have been identified by the excipients added to the formulations, the invention is meant to also cover the final formulation formed by the combination of these excipients. Specifically, the invention includes formulations in which one to all of the added excipients undergo a reaction during formulation and are no longer present in the final formulation, or are present in modified forms.

In addition, where features or aspects of the invention are described in terms of Markush groups, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush

group. For example, if X is described as selected from the group consisting of bromine, chlorine, and iodine, claims for X being bromine and claims for X being bromine and chlorine are fully described.

Other embodiments are within the following claims.

What is claimed is:

CLAIMS

1. An isolated, enriched, or purified nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

2. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule comprises a nucleotide sequence that:

(a) encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242;

(b) is the complement of the nucleotide sequence of (a);

(c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring kinase polypeptide;

(d) encodes a kinase polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of a domain selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail;

(e) is the complement of the nucleotide sequence of (d);

(f) encodes a domain of an amino acid sequence selected from the group set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, wherein said domain is selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail;

(g) is the complement of the nucleotide sequence of (f);

(h) encodes a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID

NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of the domains selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail; or

(i) is the complement of the nucleotide sequence of (h).

3. The nucleic acid molecule of claim 1, further comprising a vector or promoter effective to initiate transcription in a host cell.

4. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule is isolated, enriched, or purified from a mammal.

5. The nucleic acid molecule of claim 4, wherein said mammal is a human.

6. A nucleic acid probe for the detection of nucleic acid encoding a kinase polypeptide in a sample, wherein said polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

7. The probe of claim 6, wherein said polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

8. A recombinant cell comprising a nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

9. The cell of claim 8, wherein said polypeptide is a fragment of a protein encoded by an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

10. An isolated, enriched, or purified kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

11. The polypeptide of claim 10, wherein said polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

12. The polypeptide of claim 10, wherein said polypeptide comprises:

(a) an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ

ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242;

(b) an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ

ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all of the domains selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail

(c) a domain of an amino acid sequence selected from the group set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID

NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 wherein said domain is selected from the group consisting of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail.

13. The kinase polypeptide of claim 10, wherein said polypeptide is isolated, purified, or enriched from a mammal.

14. The kinase polypeptide of claim 13, wherein said mammal is a human.

15. The kinase polypeptide of claim 10, wherein said polypeptide is a AA144574, AA116841, AA236100, AA305176, AA210825, AA316804, AA98[illegible], N42050, AA476563, AA626690, AA960957, H19102, AA045601, AA107515, AA109508 or AA887783 polypeptide.

16. The kinase polypeptide of claim 10, wherein said polypeptide is a H60215, AA197883, AA297313, W30246, AA172300, AA383293, AA542015, H01248, N23936, W44160, 2R22-5-11, 5R72-18-1, AA021445, AA207220, AA426580, AA544838, W90839, 5R79-54-1, AA839940, R19772 or 5R72-8-2 polypeptide.

17. The kinase polypeptide of claim 10, wherein said polypeptide is a AA234451 polypeptide.

18. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R65-16-1, AA061797, AA065538, AA124976, AA397553, AA435956, AA575635, AA626859, AA789239, AI086865, H17727, H29974, AA557536 or N28606 polypeptide.

19. The kinase polypeptide of claim 10, wherein said polypeptide is a AA631990 or W08549 polypeptide.

20. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R72-16-2, R19927 or R43524 polypeptide.

21. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R57-10-2 polypeptide.

22. The kinase polypeptide of claim 10, wherein said polypeptide is a AA232253 polypeptide.

23. The kinase polypeptide of claim 10, wherein said polypeptide is a AA430250, AA836948, R86558 or N34132 polypeptide.

24. The kinase polypeptide of claim 10, wherein said polypeptide is a AA098024or SuRTK106 polypeptide.

25. The kinase polypeptide of claim 10, wherein said polypeptide is a R47805, AA099102, AA589241, H85811, AA013524, AA452647, AA840598, AA088547, AA139478, AA826850, R87679, W65887, H97685, W20810, AA599286, AA425725, AA103218, AA711829, AA060026, AA399669, AA758539, AA883975, AA948538, AA018361, AA215311, AA311714, AA498104, 5R69-17-2, 5R69-23-3, 5R69-26-2, AA118352, AA396601, AA671275, AA278842, AA460132 or H05721 polypeptide.

26. An antibody or antibody fragment having specific binding affinity to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

27. The antibody or antibody fragment of claim 26, wherein said polypeptide comprises:

(a) an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ

ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242;

(b) an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ

ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of the domains selected from the group consisting of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail.

(c) a domain of an amino acid sequence selected from the group set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID

NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 wherein said domain is selected from the group consisting of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail.

28. A hybridoma which produces an antibody having specific binding affinity to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150. SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202. SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

29. A method for identifying a substance that modulates kinase activity comprising:

(a) contacting a kinase polypeptide selected from the group consisting SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136,

SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 with a test substance;

(b) measuring the activity of said polypeptide; and

(c) determining whether said substance modulates the activity of said polypeptide.

30. A method for identifying a substance that modulates kinase activity in a cell comprising:

(a) expressing a kinase polypeptide in a cell, wherein said polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID

NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242;

(b) adding a test substance to said cell; and

(c) monitoring a change in cell phenotype or the interaction between said polypeptide and a natural binding partner.

31. A method for treating a disease or disorder by administering to a patient in need of such treatment a substance that modulates the activity of a kinase selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

32. The method of claim 31, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer.

33. The method of claim 31, wherein said substance modulates kinase activity *in vitro*.

34. The method of claim 33, wherein said substance is a kinase inhibitor.

35. A method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein said method comprises:

(a) contacting said sample with a nucleic acid probe which hybridizes under hybridization assay conditions to a nucleic acid target region of a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, said probe comprising the nucleic acid sequence encoding said polypeptide, fragments thereof, or the complements of said sequences and fragments; and

(b) detecting the presence or amount of the probe:target region hybrid as an indication of said disease.

36. The method of claim 35, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer.

37. A method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein said method comprises:

(a) comparing a nucleic acid target region encoding said kinase polypeptide in a sample, wherein said kinase polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ

ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or one or more fragments thereof, with a control nucleic acid target region encoding said kinase polypeptide, or one or more fragments thereof; and

(b) detecting differences in sequence or amount between said target region and said control target region, as an indication of said disease or disorder.

38. The method of claim 37, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer.

Table 1

Gene Name	SP	Prov_Seq_ID_NA	Prov_Seq_ID_AA	SEQ_ID_#_na	SEQ_ID_#_aa	Family	Group	Length_NA	Length_AA	ORF_Start	ORF_end	ORF_Length	DNA Repeats	CHR localization
X69117_h BARK2_h	H	x	x	1	122	AGC	GRK	2067	688	1	2064	2064	x	22q11
AA144574_m BARK2_m	M	1	17	2	123	AGC	GRK	1368	378	2	1135	1134	x	NA
AA826850_h	H	140	176	3	124	AGC	Mo3C11.1_ce	1768	419	8	1264	1257	285-304	NA
AA960957_h	H	11	27	4	125	AGC	Mo3C11.1_ce	3224	414	65	1306	1242	x	4p16.1
5R79-46-1_h, TBK1_h	H	207	208	5	126	AGC	Mo3C11.1_ce	3013	729	93	2279	2187	x	NA
AA305176_h	H	4,2	18,20	6	127	AGC	NDR	1421	329	53	1039	987	x	10p11.2
AA116841_m	M	4,2	18,20	7	128	AGC	NDR	582	88	3	266	264	x	NA
AA256100_h	H	3	19	8	129	AGC	NDR	4983	464	86	1477	1392	x	12q11
AA210825_h	H	5	21	9	130	AGC	PKC	3263	978	117	3050	2934	x	19q13-q13.3
AA127299_h	H	203	204	10	131	AGC	PKC	316	106	1	315	318	x	NA
AA316804_h, EPK2	H	6	22	11	132	AGC	PKC	2673	890	1	2670	2670	x	2p21
N42050_h PKNbeta	H	8	24	12	133	AGC	PKC	2670	889	1	2667	2667	2221-2280	NA
AI021023_m PKNbeta_m	M	x	x	13	134	AGC	PKC	929	206	2	616	615	x	NA
H19102_h	H	12	28	14	135	AGC	S6K	1155	384	1	1152	1152	599-638	CHR17
AA476563_h RPS6KC1	H	9	25	15	136	AGC	S6K	1410	469	1	1407	1407	x	12q12-q13.1
AA628890_h RSK4	H	10	26	16	137	AGC	S6K	2238	745	1	2235	2235	x	Xq21.1
AA215680_h	H	227	228	17	138	AGC	S6K	1650	549	1	1647	1647	767-786	14q24.3
SGK_h	H	x	x	18	139	AGC	SGK	1296	431	1	1293	1293	656-683	6q21-q22
AA107515_m	M	x	x	19	140	AGC	SGK	2432	430	75	1364	1290	1804-1830	NA
AA109508_m	M	13	29	20	144	AGC	SGK	1348	244	2	733	732	x	NA
AA887783_h SGK3, SGKL	H	16	32	21	142	AGC	SGK	2250	446	36	1373	1338	x	NA
R47805_h PTK9L	H	131	167	22	143	Atypical	A6	1050	349	1	1047	1047	x	3p14.3
H60215_h	H	33	54	23	144	CAMK	AMPK	2310	440	420	1739	1320	x	1p31.1-1p32.3
SGK324_h	H	x	x	24	145	CAMK	CAMK	3240	692	7	2082	2076	206-227	NA
W30246_m SGK324_m	M	36	57	25	146	CAMK	CAMK	1248	297	1	891	891	x	NA
AA383293_h	H	38	59	26	147	CAMK	CAMK	2424	686	1	2058	2058	439-458	NA
AA197883_m	M	34	55	28	148	CAMK	CAMK	2421	806	1	2418	2418	x	NA
AA172300_h DRAK2	H	37	58	29	149	CAMK	DAPK	1628	373	262	1380	1119	x	2q31-2q24.3
W44150_m DRAK2_m	M	x	x	30	150	CAMK	DAPK	2671	372	171	1286	1116	x	NA
H01248_h, DRAK1_h	H	40	61	31	151	CAMK	DAPK	1245	414	1	1242	1242	91-110	7p11-q11
AA021445_h	H	45	66	32	152	CAMK	EMK	4321	1311	146	4078	3933	x	11q22.1-11q22.3
2R22-5-11_h	H	43	64	33	153	CAMK	EMK	2311	436	871	2178	1308	81-2281, 1258-127	NA
R31237_1_h, AAC33487	H	x	x	34	154	CAMK	EMK	2190	729	1	2187	2187	x	NA
W90839_m	M	49	70	35	155	CAMK	EMK	1594	520	1	1560	1560	x	NA
406788.5_h	H	x	x	36	156	CAMK	EMK	4139	1330	77	4066	3990	x	2q34-q37
AA544838_m 406786_m	M	48	69	37	157	CAMK	EMK	1350	230	3	692	690	1002-1022	NA
AA785735_h	H	x	x	38	158	CAMK	EMK	5183	926	155	2932	2778	x	NA
AA207220_h	H	46	67	39	159	CAMK	EMK	2291	629	103	1969	1887	x	NA
AA426580_h, MAK_V_h	H	47	68	40	160	CAMK	EMK	2145	714	1	2142	2142	x	21q11
Z36720_h	H	50	71	41	161	CAMK	MLCK	2625	874	1	2622	2622	x	NA
SGK088_h	H	x	x	42	162	CAMK	Trio	7710	2286	1	6858	6858	x	NA
AA542015_m SGK088_m	M	39	60	43	163	CAMK	Trio	1251	127	1	381	381	x	NA
R19772_h	H	52	73	44	164	CAMK	Trio	3864	1287	1	3861	3861	x	3q13.3-q21
5R72_8_2_h	H	53	74	45	165	CAMK	Unique	2586	514	406	1947	1542	x	11p15.1-11p15.2
SGK309_h	H	159	195	46	166	CKI	CKI	1620	508	97	1620	1524	843-862	NA
AA234451_h	H	75	76	47	167	CKI	CKI	2452	478	406	1839	434	x	NA
AA435956_h	H	82	96	48	168	CMGC	CDK	1077	266	1	798	798	x	NA
AA626859_h	H	84	98	49	169	CMGC	CDK	911	247	2	742	741	84-119	NA
AA061797_m	M	x	x	50	170	CMGC	CDK	2615	296	2	889	188	x	NA
AA397553_h CRK7	H	81	95	51	171	CMGC	CDK	4473	1490	1	4470	4470	1219-1238	NA
AA789239_h	H	85	99	52	172	CMGC	CDK	1866	534	6	1607	1602	x	5q23-q23.3
AA124976_m	M	x	x	53	173	CMGC	CDK	1688	337	1	1011	1011	x	NA
AA575635_m CCRK_m	M	x	x	54	174	CMGC	CDK	1380	211	1	633	633	163-191	NA
AA631990_h CLK4	H	106	107	55	175	CMGC	CLK	2488	499	34	1530	1497	x	NA
AA557536_h	H	89	103	56	176	CMGC	RCK	1831	545	30	1664	1635	516-536	NA
N26806_h, MOK	H	90	104	57	177	CMGC	RCK	1260	419	1	1257	1257	x	14q32
AB023153_h, ICK	H	x	x	58	178	CMGC	RCK	1899	632	1	1896	1896	x	NA
AA839940_m	M	x	x	59	179	CMGC	RCK	1776	413	1	1239	1239	x	NA
AA460132_h	H	165	201	60	180	Microbial PK	YGR262_sc	1428	253	199	957	759	x	20q12 Amplicon
SGK034_h	H	x	x	61	181	Other	C26C2_ce	3304	462	1	1386	1386	x	NA
AA103218_m SGK034_m	M	147	183	62	182	Other	C26C2_ce	2326	281	2	844	843	x	NA
NEK7_h, N34132_h	H	122	126	63	183	Other	C26C2_ce	7326	1952	42	5897	5856	x	12p13.33

Table 1 (cont'd)

Gene Name	SP	Prov_Seq_ID_NA	Prov_Seq_ID_AA	SEQ_ID_#_na	SEQ_ID_#_aa	Family	Group	Length_NA	Length_AA	ORF_Start	ORF_end	ORF_Length	DNA Repeats	CHR localization
BCON3_h	H	x	x	64	184	Other	C26C2_ce	2164	536	113	1717	1605	246-267	NA
AA711829_m	M	148	184	65	185	Other	C26C2_ce	1568	378	1	1134	1134	x	NA
AA099102_h CaMKKB	H	132	168	66	186	Other	CAMKK	1767	588	1	1764	1764	65-84	12q23-q14
5R69_17_2_h	H	158	194	67	187	Other	CTR1	3387	241	1850	2572	723	499-521	NA
H85811_h	H	134	170	68	188	Other	DYRK	3993	1171	183	3695	3513	1328-1348	CHR7
AA02193_h DYRK3	H	x	x	69	189	Other	DYRK	2141	553	253	1911	1659	x	NA
AA589241_m DYRK3_m	M	133	169	70	190	Other	DYRK	741	168	3	506	504	x	NA
5R72_16_2_h, R19027_h	H	109	112	71	191	Other	EIFK	5163	1649	20	4966	4947	x	NA
R43524_h, HRI_h, R19609	H	111	114	73	192	Other	EIFK	1893	630	1	1890	1890	x	[illegible]p22-p22.3
17000057519457_h	H	x	x	74	193	Other	Endop	3055	253	219	977	759	2283-2365	NA
AA013524_m	M	135	171	75	194	Other	Endop	926	216	1	648	648	x	NA
17000139801197_h, IRAKM	H	x	x	76	195	Other	IRAK	1791	596	1	1788	1788	x	NA
AA840598_m IRAKM_m	M	137	173	77	196	Other	IRAK	2243	392	1	1176	1176	x	NA
AA088547_h	H	138	174	78	197	Other	IRE	2769	922	1	2766	2766	x	NA
HGP_6644466	H	x	x	79	198	Other	KYK2_dd	1857	322	179	1144	966	x	NA
AA449542_m	M	139	176	80	199	Other	KYK2_dd	1251	280	2	841	840	602-621	NA
5R57_10_2_m TESK2_m	M	115	116	81	200	Other	LIMK	140	41	2	124	123	x	NA
AA232253_h	H	117	118	82	201	Other	MLK	2403	800	1	2400	2400	x	NA
AI375137_h	H	209	210	83	202	Other	MLK	2506	836	1	2505	2505	2219-2238	NA
H97685_h	H	143	179	84	203	Other	RIP	2384	634	161	2062	1902	x	[illegible]q31
W20810_m	M	144	180	85	204	Other	RIP	1073	289	3	859	857	x	NA
AA744236_h	H	211	212	86	205	Other	SCY1_sc	2037	688	1	2064	2064	x	1q23
AI052250_h	H	225	226	87	206	Other	SCY1_sc	1739	505	174	1688	1515	x	NA
AA278842_h	H	164	200	88	207	Other	SCY1_sc	2688	808	105	2528	2424	1764-1783	11q12-q13 Amplicon
AA599288_h	H	145	181	89	208	Other	SLOB?	1949	649	1	1949	1949	x	NA
AA426725_h	H	146	182	90	209	Other	SRPK	1602	533	1	1599	1599	x	[illegible]q25
SGK022_h	H	x	x	91	210	Other	STK22A	1038	268	184	987	804	x	[illegible]
AA060026_m SGK022_m	M	149	185	92	211	Other	STK22A	1004	268	147	950	804	x	NA
AA399669_h	H	150	186	93	212	Other	STK22A	1537	292	372	1244	876	x	1[illegible]p11-q11
AA758539_h	H	151	187	94	213	Other	STK22A	1322	358	101	1174	1074	x	NA
AA883975_h	H	153	189	95	214	Other	TSK	922	273	1	819	819	x	NA
AA905446_h	H	223	224	96	215	Other	TSK	1066	216	365	1012	648	x	NA
H29974_h	H	66	102	97	216	Other	UNC	1636	333	2	1000	999	x	NA
AA498104_m H29974_m	M	x	x	98	217	Other	UNC	1490	412	1	1236	1236	701-729	NA
AA215311_h	H	155	191	99	218	Other	UNC	2011	341	199	1221	1023	x	NA
AA018361_h	H	154	190	100	219	Other	UNC	2759	481	113	1555	1443	x	[illegible]q23
AA311714_h	H	156	192	101	220	Other	UNC	1876	565	138	1833	1696	x	NA
SGK384_h	H	x	x	102	221	Other	Unique	117	39	1	117	117	x	[illegible]
AA210451_m SGK384_m	M	106	108	103	222	Other	Unique	2721	349	222	1268	1047	2251-2266	NA
SGK071_2_h	H	x	x	104	223	Other	Unique	2115	704	1	2112	2112	57-76, 318-337	NA
AA118352_m SGK071_m	M	161	197	105	224	Other	Unique	1729	540	3	1622	1620	x	NA
018653.9_h	H	162	198	106	225	Other	Unique	2461	540	1	1620	1620	240-259	NA
AA396601_m	M	x	x	107	226	Other	Unique	1886	365	3	1097	1095	x	NA
AA671275_h VRK3	H	163	199	108	227	Other	VRK	1425	474	1	1422	1422	x	19q13
S71575_m VRK3_m	M	x	x	109	228	Other	VRK	1009	234	3	704	702	937-957	NA
AA452647_h MPSK1	H	136	172	110	229	Other	YPL236_sc	918	305	1	915	915	x	[illegible]q21
H05721_h	H	166	202	111	230	Other	YQ09_ce	2688	581	95	1837	1743	x	1p[illegible]2-31 Amplicon
AI088865_h	H	86	100	112	231	STE	NEK	2483	698	7	2100	2094	x	NA
AA836348_h	H	120	124	113	232	STE	NEK	2511	636	1	2508	2508	x	NA
R88668_h, MKK6	H	121	125	114	233	STE	STE11	3036	1011	1	3033	3033	x	1p3[illegible]3-p31.1
PAK6_h 5R95-20-11	H	219	220	115	234	STE	STE20-02	2160	719	1	2157	2157	x	20p[illegible]
SuRTK106_h 2R41-9-4_h	H	126,127	129, 130	116	235	TK	RTK-20	2460	495	1	1485	1485	x	12p12.3
AA098024_m	M	128,127	130	117	236	TK	RTK-20	1793	183	1	549	549	1362-1382	NA
SGK2alpha_h	H	x	x	118	237	AGC	SGK	1812	367	88	1188	1101	x	NA
H08960_h CCRK	H	87	101	120	238	CMGC	CDK	1359	452	1	1356	1356	x	9q21[illegible]-q21.3
NM_007170_h TESK2	H	x	x	121	239	Other	LIMK	3016	555	396	2060	1665	x	NA

Table 2

SP	Patent Seq ID# na	Patent Seq ID# aa	Family	Group	nraa Pscore	Length aa	ID match aa	% Identity	% Similar	nraa Match ACC#	Description	Kinase Domain(s) start	Kinase Domain (s) end	Profile start	Profile end
H	1	122	AGC	GRK	2.7e-314	688	687	100	100	CAB4[illegible]57.1	BARK2 [Homo sapiens]	[illegible]	453	1	261
M	2	123	AGC	GRK	1.30E-190	378	371	98	99	NP_037029.1	Adrenergic receptor kinase, beta 2 (G-protein-linked receptor kin	[illegible]	143	121	261
H	3	124	AGC	o3C11.1_c	5.80E-106	419	262	71	86	CAB70471.1	Serine/threonine protein kinase [Homo sapiens]	[illegible]	286	1	261
H	4	125	AGC	o3C11.1_c	1.40E-137	414	414	100	100	CAB76471.1	Serine/threonine protein kinase [Homo sapiens]	[illegible]	283	1	261
H	5	126	AGC	o3C11.1_c	0	729	729	100	100	NP_03[illegible]66.1	TANK-binding kinase 1 [Homo sapiens]	9	304	1	261
H	6	127	AGC	NDR	1.20E-09	329	73	46	66	BAA76817.1	KIAA0973 protein [Homo sapiens]	[illegible]38	310	1	261
M	7	128	AGC	NDR	1.30E-19	86	42	49	71	AAF5[illegible]94.1	CG7719 gene product [Drosophila melanogaster]	24	44	242	261
H	8	129	AGC	NDR	6.10E-181	464	463	100	100	BAA76809.1	KIAA0965 protein [Homo sapiens]	90	383	1	261
H	9	130	AGC	PKC	8.60E-160	978	616	67	80	NP_00[illegible]733.1	Protein kinase C, mu [Homo sapiens]	651	907	1	261
H	10	131	AGC	PKC	1.10E-10	108	42	42	57	P05[illegible]27	Protein kinase C, BETA-II TYPE (PKC-BETA-2) [Homo sapiens]	19	24	256	261
H	11	132	AGC	PKC	0	890	890	100	100	NP_0[illegible]304.1	Protein kinase C, nu [Homo sapiens]	576	832	1	261
H	12	133	AGC	PKC	9.4e-319	889	889	100	100	NP_0[illegible]437.1	PKNbeta [Homo sapiens]	550	818	1	261
M	13	134	AGC	PKC	1.20E-106	205	204	100	100	JC7083	Protein kinase N beta [Homo sapiens]	1	134	126	261
H	14	135	AGC	S6K	3.60E-12	384	94	38	55	AAC[illegible]2495.1	Ribosomal protein S6 kinase 3 [Homo sapiens]	61	333	1	261
H	15	136	AGC	S6K	2.90E-257	469	469	100	100	NP_030[illegible]36.1	Ribosomal protein S6 kinase, 52kD, polypeptide 1 [Homo sapien	225	459	1	261
H	16	137	AGC	S6K	7.00E-176	745	745	100	100	NP_055[illegible]1.1	Ribosomal protein S6 kinase, 90kD, polypeptide 6 [Homo sapien	73 & 426	330 & 683	1	261
H	17	138	AGC	S6K	9.60E-222	549	549	100	100	AAD30182.1	Unknown [Homo sapiens]	153	539	1	261
H	18	139	AGC	SGK	9.20E-103	431	430	100	100	AAD41[illegible]1.1	SGK [Homo sapiens]	98	355	1	261
M	19	140	AGC	SGK	2.90E-157	430	426	99	99	NP_0[illegible]1.1	Serum/glucocorticoid regulated kinase [Mus musculus]	98	354	1	261
M	20	141	AGC	SGK	2.00E-76	244	244	100	100	AAF[illegible]2757.2	Protein kinase [Homo sapiens]	1	169	24	261
H	21	142	AGC	SGK	4.10E-211	446	375	88	88	AAF27051.1	SGK-like protein SGKL [Homo sapiens]	182	369	1	261
H	22	143	Atypical	A6	5.60E-216	349	349	100	100	NP_009215.1	Protein tyrosine kinase 9-like (A6-related protein) [Homo sapien	10	17	253	261
H	23	144	CAMK	AMPK	1.40E-19	440	68	39	61	CAA04119.1	Phosphoprotein [Homo sapiens]	40	333	1	261
H	24	145	CAMK	CAMK	1.50E-165	699	466	65	77	O1507[illegible]	DCAMKL1 (DOUBLECORTIN-LIKE AND CAM KINASE-LIKE 1)	368	625	1	261
M	25	146	CAMK	CAMK	1.60E-62	297	199	67	83	AAF26675.1	CPG16 [Mus musculus]	59	297	1	261
H	26	147	CAMK	CAMK	2.60E-48	708	181	44	60	O15075	DCAMKL1 (DOUBLECORTIN-LIKE AND CAM KINASE-LIKE 1)	415	673	1	261
M	28	148	CAMK	CAMK	2.60E-31	806	147	55	73	AAF26675.1	CPG16 [Mus musculus]	514	771	1	261
H	29	149	CAMK	DAPK	3.10E-121	372	372	100	100	NP_0[illegible]217.1	Death-associated protein kinase-related 2	33	293	1	261
M	30	150	CAMK	DAPK	7.90E-93	372	340	91	95	NP_0[illegible]217.1	Death-associated protein kinase-related 2	32	293	1	261
H	31	151	CAMK	DAPK	1.20E-113	414	414	100	100	NP_[illegible]4751.1	Death-associated protein kinase-related 1	61	321	1	261
H	32	152	CAMK	EMK	5.90E-185	1311	1053	80	80	BAA76843.1	KIAA0999 protein [Homo sapiens]	8	259	1	261
H	33	153	CAMK	EMK	1.20E-45	436	153	51	70	T224[illegible]	Hypothetical protein F49C5.4 - [Caenorhabditis elegans]	74	325	1	261
H	33	153	CAMK	EMK	1.40E-32	436	122	46	65	AAC15093.1	Cdc25C associated protein kinase C-TAK1 [Homo sapiens]				
H	34	154	CAMK	EMK	1.30E-184	729	729	100	100	AAC[illegible]	Cdc25C associated protein kinase C-TAK1 [Homo sapiens]	56	307	1	261
M	35	155	CAMK	EMK	3.50E-126	462	462	100	100	AAC[illegible]487.1	R31237_1, partial CDS [Homo sapiens]	59	340	1	261
H	36	156	CAMK	EMK	0	1330	1235	100	100	BAA[illegible]484.1	KIAA0135 gene is related to pim-1 oncogene. [Homo sapiens]	[illegible]99	1258	1	261
M	37	157	CAMK	EMK	5.10E-59	230	183	79	85	BAA[illegible]84.1	KIAA0135 gene, related to pim-1 oncogene. [Homo sapiens]	1	158	23	261
H	38	158	CAMK	EMK	3.00E-111	926	636	100	100	BAA[illegible]01.1	KIAA0781 protein [Homo sapiens]	[illegible]	271	1	261
H	39	159	CAMK	EMK	7.30E-80	629	367	57	69	NP_0[illegible]355.1	KIAA0537 gene product [Homo sapiens]	[illegible]	304	1	261
H	40	160	CAMK	EMK	1.40E-244	714	714	100	100	NP_065401.1	Hormonally upregulated neu tumor-associated kinase [Homo sa	[illegible]	320	1	261
H	41	161	CAMK	MLCK	8.20E-76	874	211	63	80	AA[illegible]198.1	Skeletal muscle myosin light chain kinase [Gallus gallus]	[illegible]0	825	1	261
H	42	162	CAMK	Trio	0	2288	2227	100	100	BAA[illegible]15.1	KIAA1297 protein [Homo sapiens]	62[illegible] & 1086	873 & 1356	1	261
M	43	163	CAMK	Trio	7.80E-37	127	67	99	99	BAA[illegible]35.1	KIAA1297 protein [Homo sapiens]	[illegible]	78	186	261
H	44	164	CAMK	Trio	0	1287	1284	100	100	NP_0[illegible]95.1	STK with Dbl- and pleckstrin homology domains [Homo sapiens	[illegible]	1239	1	261
H	45	165	CAMK	Unique	5.00E-20	514	114	41	63	P25[illegible]	MLCK [Dictyostelium discoideum]	[illegible]6	381	1	261
H	46	166	CKI	CKI	3.30E-69	508	181	53	65	AAF5[illegible]40.1	CG11533 gene product [Drosophila melanogaster]	34	313	1	261
H	47	167	CKI	CKI	8.60E-98	478	188	57	68	AAF5[illegible]10.1	CG11533 gene product [Drosophila melanogaster]	[illegible]1	471	1	261
H	48	168	CMGC	CDK	9.60E-39	266	138	62	79	NP_0[illegible]27.1	PFTAIRE protein kinase 1 [Homo sapiens]	1	218	23	261
H	49	169	CMGC	CDK	7.10E-48	247	146	59	75	NP_0[illegible]87.1	Cyclin-dependent kinase-like 1 (CDC2-related kinase) [Homo sa	1	191	23	261

Table 2 (cont'd)

M	50	170	CMGC	CDK	2.90E-64	298	193	65	78	NP_00[illegible]107.1	Cyclin-dependent kinase-like 1 (CDC2-related kinase) [Homo sa	1	240	24	261
H	51	171	CMGC	CDK	1.10E-264	1490	1490	100	100	AAF36[illegible]01.1	CDC2-related protein kinase 7 [Homo sapiens]	21	1020	1	261
H	52	172	CMGC	CDK	9.20E-101	534	377	82	82	AA[illegible]36509.1	NKIAMRE [Homo sapiens]	4	385	1	261
M	53	173	CMGC	CDK	1.40E-128	337	225	92	96	AAF[illegible]48[illegible]1.1	NKIATRE alpha [Rattus norvegicus]	1	28	235	261
M	54	174	CMGC	CDK	3.00E-68	211	159	79	84	NP_[illegible]38251.1	Cell cycle related kinase [Homo sapiens]	1	153	134	261
H	55	175	CMGC	CLK	1.50E-242	499	436	91	93	NP_031740.1	Cyclin-dependent kinase-like 1 (CDC2-related kinase) [Homo sa	177	493	1	261
H	56	176	CMGC	RCK	9.10E-69	544	349	57	64	AAD12719.1	Extracellular signal-regulated kinase 7; ERK7 [Rattus norvegicus	[illegible]3	305	1	261
H	57	177	CMGC	RCK	2.30E-159	419	419	100	100	NP_[illegible]53041.1	Renal tumor antigen [Homo sapiens]	[illegible]	285	1	261
H	58	178	CMGC	RCK	1.50E-180	632	632	100	100	AAF[illegible]7278.1	Intestinal cell kinase [Homo sapiens]	[illegible]	284	1	261
M	59	179	CMGC	RCK	1.60E-79	413	198	60	77	P20689	MLCK [Rattus norvegicus]	[illegible]9	384	1	261
H	60	180	Microbial PK	YGR262_sc	2.50E-45	253	102	46	67	AAF[illegible]0799.1	CG10673 gene product [Drosophila melanogaster]	101	187	65	147
H	61	181	Other	C26C2_ce	2.30E-158	509	258	100	100	CAB[illegible]0834.1	Hypothetical protein [Homo sapiens]	[illegible]2	267	1	261
M	62	182	Other	C26C2_ce	1.80E-152	281	243	94	98	CAB70834.1	Hypothetical protein [Homo sapiens]	[illegible]0	86	235	261
H	63	183	Other	C26C2_ce	6.70E-300	1952	1193	99	99	NP_0[illegible]6638.1	KIAA0344 gene product [Homo sapiens]	2[illegible]1	479	1	261
H	64	184	Other	C26C2_ce	1.10E-264	535	535	100	100	NP_0[illegible]524.1	Nuclear receptor binding protein [Homo sapiens]	[illegible]3	327	1	261
M	65	185	Other	C26C2_ce	2.50E-208	378	372	98	100	NP_03[illegible]524.1	Nuclear receptor binding protein [Homo sapiens]	1	170	85	261
H	66	186	Other	CAMKK	3.80E-148	588	588	100	100	AAD31807.1	Ca2+/calmodulin-dependent protein kinase kinase beta [Homo s	165	448	1	261
H	67	187	Other	CTR1	9.90E-24	287	87	33	52	JQ1[illegible]43	Hypothetical 33.6K protein - rabbit fibroma virus	24	285	1	261
H	68	188	Other	DYRK	0	1171	1137	97	99	AAD52566.1	Nuclear body associated kinase 1a [Mus musculus]	199	527	1	261
H	69	189	Other	DYRK	2.10E-280	553	553	100	100	NP_[illegible]03573.1	Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	174	467	1	261
M	70	190	Other	DYRK	2.30E-96	168	149	90	98	NP_[illegible]573.1	Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	78	103	235	261
H	71	191	Other	EIFK	0	1649	1493	90	96	NP_[illegible]3747.1	GCN2 eIF2alpha kinase [Mus musculus]	180 & 590	539 & 1001	1	261
H	73	192	Other	EIFK	1.50E-220	630	630	100	100	NP_[illegible]55228.1	Heme-regulated initiation factor 2-alpha kinase [Homo sapiens]	167	583	1	261
H	74	193	Other	Endop	2.50E-45	253	102	46	67	AAF50799.1	CG10673 gene product [Drosophila melanogaster]	101	187	65	147
M	75	194	Other	Endop	3.70E-45	216	100	45	64	AA[illegible]50799.1	(AE003587) CG10673 gene product [Drosophila melanogaster]	116	160	116	147
H	76	195	Other	IRAK	0	596	596	100	100	NP_00[illegible]130.1	Interleukin-1 receptor-associated kinase M [Homo sapiens]	165	443	1	261
M	77	196	Other	IRAK	1.20E-170	392	293	75	85	NP_00[illegible]30.1	Interleukin-1 receptor-associated kinase M [Homo sapiens]	1	239	19	261
H	78	197	Other	IRE	1.5e-323	922	746	82	89	NP_036146.1	Ire1, inositol-requiring 1 gene [Mus musculus]	516	777	1	261
H	79	198	Other	KYK2_dd	8.70E-40	225	102	45	62	AAF48[illegible]8.1	CG8173 gene product [Drosophila melanogaster]	32	318	1	261
M	80	199	Other	KYK2_dd	5.90E-32	280	109	32	50	AAF[illegible]3.1	CG8173 gene product [Drosophila melanogaster]	12	266	1	261
M	81	200	Other	LIMK	2.60E-17	41	37	92	95	NP_009101.1	testis-specific kinase 2 [Homo sapiens]	12	39	101	128
H	82	201	Other	MLK	2.50E-282	800	799	100	100	AAF63490.1	Mixed lineage kinase [Homo sapiens]	16	259	1	261
H	83	202	Other	MLK	8.60E-251	835	835	100	100	AAD29832.1	Putative protein-tyrosine kinase [Homo sapiens]	463	723	1	261
H	84	203	Other	RIP	2.20E-158	634	385	100	100	BAA32317.1	KIAA0472 protein [Homo sapiens]	357	620	1	261
M	85	204	Other	RIP	5.30E-158	289	288	100	100	AAF03133.1	Receptor interacting protein 3 [Mus musculus]	7	27	181	202
H	86	205	Other	SCY1_sc	0	688	688	100	100	CAB53300.1	Hypothetical protein [Homo sapiens]	57	83	50	78
H	87	206	Other	SCY1_sc	1.70E-209	505	354	98	98	BAA92598.1	KIAA1360 protein [Homo sapiens]	32	327	1	261
H	88	207	Other	SCY1_sc	2.20E-157	808	396	45	61	AAF56933.1	CG1973 gene product [Drosophila melanogaster]	65	131	47	116
H	89	208	Other	SLOB?	7.40E-198	649	649	100	100	BA[illegible]1097.1	Unnamed protein product [Homo sapiens]	230	305	81	143
H	90	209	Other	SRPK	5.80E-252	533	533	100	100	NP_[illegible]55185.1	Serine/threonine kinase 23 [Homo sapiens]	79	531	1	261
H	91	210	Other	STK22A	3.80E-53	268	122	46	70	NP_033461.1	Serine/threonine kinase 22A (spermiogenesis associated) [Mus	10	265	1	261
M	92	211	Other	STK22	2.70E-52	268	127	48	68	NP_03[illegible]432.1	serine/threonine kinase 22B (spermiogenesis associated)	[illegible]0	265	1	261
H	93	212	Other	STK22A	4.60E-16	292	112	45	64	NP_03[illegible]461.1	Serine/threonine kinase 22A (spermiogenesis associated)	[illegible]5	280	1	261
H	94	213	Other	STK22A	5.10E-123	358	322	90	96	NP_[illegible]33462.1	Serine/threonine kinase 22B (spermiogenesis associated) [Mus	[illegible]2	272	1	261
H	95	214	Other	TSK	2.10E-33	273	122	46	62	NP_[illegible]1.1	Serine/threonine kinase 22A (spermiogenesis associated)	[illegible]2	267	1	261
H	96	215	Other	TSK	2.50E-32	216	93	41	58	NP_[illegible]33462.1	Serine/threonine kinase 22B (spermiogenesis associated)	1	213	7	261
H	97	216	Other	UNC	0.000062	333	57	36	56	AAD[illegible]2787.1	Putative protein kinase [Arabidopsis thaliana]	1	329	1	261
M	98	217	Other	UNC	0.002492	412	53	37	52	BAA77341.1	UNC-51-like kinase (ULK) 2 [Mus musculus]	[illegible]0	408	1	261
H	99	218	Other	UNC	0.001096	341	50	38	56	BAA[illegible]7341.1	UNC-51-like kinase (ULK) 2 [Mus musculus]	[illegible]	340	1	261
H	100	219	Other	UNC	1.90E-68	480	247	100	100	T1[illegible]235	Hypothetical protein DKFZp434C131.1 - human (fragment)	[illegible]	313	1	261
H	101	220	Other	UNC	1.60E-208	565	468	96	96	BAA[illegible]270.1	Unnamed protein product [Homo sapiens]	[illegible]	265	1	261
H	102	221	Other	Unique	6.70E-10	39	27	69	90	AA[illegible]75.1	Serum-inducible kinase [Homo sapiens]	1	39	84	124

Table 2 (cont'd)

M	103	222	Other	Unique	0.000022	349	38	30	50	CAA18116.1	Serine/threonine protein kinase like protein [Arabidopsis thalia	60	159	1	88
H	104	223	Other	Unique	0.000126	704	54	30	46	BA[illegible]6578.1	KIAA1264 protein [Homo sapiens]	1	246	25	261
M	105	224	Other	Unique	0.007386	640	25	42	61	AAF47316.1	Tie gene product [Drosophila melanogaster]	9	104	168	261
H	106	225	Other	Unique	0.31334	540	52	30	42	P10162	SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [Homo s	1	272	18	73
M	107	226	Other	Unique	0.022948	365	25	34	57	NP_003276.1	testis-specific kinase 1 [Homo sapiens]	68	98	42	71
H	108	227	Other	VRK	3.10E-263	474	474	100	100	BAA[illegible]769.1	Vaccinia related kinase 3 [Homo sapiens]	247	318	63	136
M	109	228	Other	VRK	1.20E-111	234	191	82	90	BAA90769.1	(AB031052) vaccinia related kinase 3 [Homo sapiens]	7	78	63	136
H	110	229	Other	YPL236_sc	7.40E-144	305	304	100	100	AA[illegible]8337.1	MPSK [Homo sapiens]	20	290	1	261
H	111	230	Other	YQ09_ce	5.10E-49	581	135	43	63	AAF4[illegible]58.1	CG4523 gene product [Drosophila melanogaster]	156	507	1	261
H	112	231	STE	NEK	3.30E-30	698	122	48	67	[illegible]61654	NEK1 (NIMA-RELATED PROTEIN KINASE 1) [Mus musculus]	4	251	1	261
H	113	232	STE	NEK	2.70E-119	836	357	86	86	AAD31939.1	(AC007056) unknown [Homo sapiens]	52	308	1	261
H	114	233	STE	STE11	1.10E-291	1011	1011	100	100	NP_004663.1	mitogen-activated protein kinase kinase kinase 6 [Homo sapiens	376	629	6	261
H	115	234	STE	STE20-02	7.70E-177	719	719	100	100	BAA94194.1	(AB040812) protein kinase PAK5 [Homo sapiens]	449	700	1	261
H	116	235	TK	RTK-20	4.90E-24	495	77	38	58	AA[illegible]86465.1	(U40827) protein tyrosine kinase [Mus musculus]	187	453	1	261
M	117	236	TK	RTK-20	5.30E-18	183	63	39	57	NP_032036.1	fibroblast growth factor receptor 3 [Mus musculus]	8	143	123	261
H	118	237	AGC	SGK	8.30E-112	367	367	100	100	AAF12757.2	SGK2alpha protein kinase [Homo sapiens]	35	292	1	261
H	120	238	CMGC	CDK	2.80E-137	452	452	100	100	NP_036251.1	Cell cycle related kinase [Homo sapiens]	4	287	1	261
H	121	239	Other	LIMK	6.50E-233	555	555	100	100	NP_009101.1	Testis-specific kinase 2 [Homo sapiens]	62	293	5	261

Table 3

Tissue	Tumor-pym	Normal-pym	Tumor - tu	Tumor cells	Normal	Endos	p53	SEQ 683 A	SEQ 5 TIM	SEQ 686 A	SEQ 688 A	SEQ 8 CA	SEQ 11 EP	SEQ 12 PK	SEQ 14 H1	SEQ 16 R1
adrenal gland - h		1						7480	13881	543727	20848	34705	58893	11606	46820	13166
lymph node - h		2						8151	32265	1203404	118257	106718	95338	19897	94838	16258
bone marrow - h		3						4465	8236	1477546	36387	32237	33858	13181	82024	12108
mammary gland - h		4						884	376	109867	4031	4318	1984	1985	34739	2803
brain - h		5						6880	5023	238763	63822	21980	7881	7736	84253	7107
pancreas - h		6						8433	3674	334855	60825	32380	8821	11800	71840	12784
cerebellum - h		7						8350	19704	767223	84806	36882	16370	29280	83436	13345
pituitary gland - h		8						8542	7856	712184	80487	38580	19473	11010	87365	12186
fetal brain - h		9						18719	8046	987041	85401	30156	23343	13781	103271	8807
placenta - h		10						8783	15464	1232178	46305	45070	24271	13807	80342	10001
fetal kidney - h		11						4707	10838	837527	81080	67846	31171	19880	88094	10880
prostate - h		12						3477	1784	122058	60389	48812	11798	9464	74934	11164
fetal liver - h		13						3307	5294	1949111	28186	38129	17029	10418	58877	9440
salivary gl. - h		14						2726	3880	439781	37847	37758	11433	13888	80783	14403
fetal lung - h		15						6315	8481	1385487	79878	69494	31911	34594	92518	15836
skeletal muscle - h		16						8483	5785	167882	81863	13318	10888	11874	57831	8286
heart - h		17						3012	1915	227834	27479	20873	6367	11717	43881	7783
small intestine - h		18						3820	9581	585318	28587	28883	11720	12220	42879	11051
kidney - h		19						3588	8453	413001	41491	24102	7829	8888	48325	12082
spinal cord - h		20						9188	2788	234806	21586	12872	12298	4848	54755	8758
liver - h		21						3783	4479	238887	24080	18281	11558	8365	48332	8300
Spleen - h		22						3384	1519	208806	48111	20875	16788	8188	44888	8881
lung - h		23						4121	1821	488627	35813	25347	[illegible]	4417	[illegible]	7784
stomach - h		24						2858	419	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1109
testis - h		25						8842	[illegible]	1252031	[illegible]	[illegible]	117843	[illegible]	[illegible]	11136
thymus - h		27						7858	4898	1976482	122844	52848	48828	31139	[illegible]	33780
HPAEC		28				28		7304	0	88888	24171	28774	3019	14479	67087	8110
thyroid gland - h		29						3870	1873	194311	42836	28881	9827	8143	43870	8802
RPTEC		30				30		24571	1823	86380	21213	3357	3387	15054	42340	7144
trachea - h		31						6734	3082	687793	88848	49813	15288	18042	78886	11767
HMEC		32						7791	1366	138886	24824	15301	4715	11713	89184	3838
uterus - h		33						8388	4848	534257	24433	33931	14725	19088	88878	8840
HCAEC		34						7876	0	82241	28246	12125	1768	29455	51717	8203
Pancreas - h		35						11988	918	41843	19582	15418	8148	6513	48843	7584
lymph node - h		36						8132	731	47830	15791	20736	8420	3812	84078	7385
Skeletal muscle - h		37						5808	77	0	11080	6411	5284	2070	38348	3490
fetal liver - h		38						8888	2171	148483	18356	15886	6458	2447	98121	8104
Heart - h		39						7081	745	8019	15383	8552	2515	3830	47872	7275
thymus - h		40						8710	2472	87229	40813	17473	10184	1902	70722	18210
Duodenum - h		41						2879	0	28026	8776	14880	4049	9070	42191	6580
Fetal brain - h		42						12385	3365	21478	20505	16311	15818	3083	88880	9323
Salivary gl. - h		43						4480	0	8914	17344	12177	4150	3290	25172	8985
testis - h		44						8862	23888	33514	19883	14856	17832	4388	57084	6767
HT210-normal					305			115	367	9191	3386	2191	1738	134	12858	1834
HT213-normal					303			0	427	9712	1918	0	144	1080	8245	803
HT187-normal					301			0	15	36470	2726	735	12030	854	18328	4100
Bov-13					366	356		8533	1888	583114	48108	10800	38148	4882	82144	17804
Bov-12					364	364		11220	1285	86790	68804	9439	12012	3487	58087	13430
cerebellum - h					344			0	242	31891	2539	1746	3851	1243	27728	4340
brain - h					342			0	585	38541	2880	0	2454	2223	21402	4429
RPTEC					338	338		1977	0	29114	34733	2278	333	6057	71803	20777
lymph node - h					332			706	0	1941	7347	7055	14451	1180	30788	8836
h adult SMC 10/21/82 #17					330			606	0	6514	8887	1044	8	540	47380	8884
Fetal brain - h					328			7130	318	154277	48829	10433	8086	2972	70808	18134
HT388-normal					327			638	0	217305	8223	330	8848	632	50874	7284
thymus - h					326			6784	80	298230	84119	18538	7917	2385	70806	13384
HT148 - normal					321			197	81	801	2827	0	198	1743	41371	8588
HEPM 2d untreated					320			3252	0	88128	12132	3837	4353	3048	81910	10734
uterus - h					319			4813	4034	653304	38032	18859	31221	6216	68463	16656
trachea - h					318			4883	238	119863	34208	13580	18150	4760	40848	11180
thyroid gland - h					314			2530	845	888401	34480	13185	38383	6319	44848	13837
salivary gl. - h					311			881	447	181154	19056	8484	8878	1858	81587	11348
prostate - h					308			46	882	103824	14523	5434	8183	1052	47808	18348
pituitary gland - h					307			1226	0	118830	18053	2008	4827	819	34784	8532
pancreas - h					306			180	807	101847	8852	3838	7486	1847	44817	10318
mammary gland - h					303			1134	700	1072119	34305	8728	22383	3808	68481	12912
bladder - h					302			14712	0	38781	25867	8808	7386	3829	72421	11880
testis - h					298			4367	11127	777026	63086	20243	28778	8832	83188	23280
liver - h					297			2935	1344	481071	20812	18344	10088	[illegible]	61744	[illegible]
Colon - h					293			86	1597	218030	20781	8703	[illegible]	[illegible]	83725	[illegible]
spinal cord - h					294			2252	[illegible]	338128	28947	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
small intestine - h					292			156	[illegible]	297078	[illegible]	3217	6850	1330	41032	6795
skeletal muscle - h					280			1376	1462	417579	27541	13818	30844	8272	90372	13925
bone marrow - h					278			0	918	34547	2111	3118	3421	1687	50857	10434
adrenal gland - h					277			0	2174	88342	4718	2570	8223	882	84753	8058
HPAEC					275	275		581	123	4987	8846	1414	652	1062	37188	7713
HT380-normal					268			0	80	79106	4467	0	4488	881	28846	3881
HT383-normal					258			253	880	13358	4838	878	11888	308	44114	7870
Bov-11					238	238		1719	4286	208888	19772	1587	19433	4370	73587	13425
Bov-8					235	235		41	881	82153	8231	1848	7758	8820	80453	7386
HT372-normal					234			787	0	34038	18387	5368	8132	2350	78267	14120
Bov-7					233	233		8	1938	83384	7278	2874	8250	2888	71564	9109
Bov-6					231	231		381	3434	48140	7045	8702	6877	2380	82712	9473
Bov-2					229	229		488	1684	74812	8538	798	7032	3425	45448	8479
Bov-1					227	227		826	4804	83881	6236	1908	4847	1048	41888	8088
bladder - h					222			329	458	8047	2858	2388	3425	171	33431	5059
Heart - h					219			882	0	6143	8888	2384	7814	1837	48488	8442
stomach - h					214			486	1512	128784	14838	3782	13118	1751	58881	10281
fetal liver - h					213			884	347	8478	8418	1848	1036	476	28067	8120
placenta - h					212			622	1977	218837	5781	2184	8198	1232	43829	8805
HCAEC					211	211		143	0	5183	8867	184	568	1143	34737	8333
fetal brain - h					210			887	3137	83807	8488	7857	14801	1815	70127	13888
HMEC					209			294	102	8834	8400	8	214	886	48670	8198
Duodenum - h					205			1	0	4305	8829	630	1551	579	38259	8176
Skeletal muscle - h					203			633	0	5083	6853	674	1211	1041	34158	5114
Pancreas - h					201			418	16	88167	6467	3004	4306	881	33307	8580
testis - h					199			738	154	3162	2304	2527	3463	347	28863	4123
Salivary gl. - h					197			436	16	37817	4651	2308	5218	762	30888	4117
HEPM 3d TGFB1 detergent-Oligos					196			82	0	4577	3408	236	1291	374	21318	2320
thymus - h					193			2883	0	247405	21041	4884	10787	3456	23113	8284
WI-38 72h					178			0	0	8881	2190	0	383	0	21346	1771
lymph node - h					81			314	273	34898	18701	4088	4334	2288	27381	4206
lung - h					59			787	1251	340147	8218	10510	18888	2388	79535	9191
kidney - h					67			0	334	48381	8070	3152	7038	4	58808	7384
heart - h					55			0	1134	38702	3229	3702	4377	442	37503	3884
fetal lung - h					53			8	1323	24481	1808	232	1176	1297	12836	1580
fetal liver - h					51			235	37	43001	3182	510	4042	297	21581	2372
fetal kidney - h					49			277	441	37881	3888	2842	11886	3198	31744	4737
HELA-2h-031000				79				1379	744	108312	8863	2313	8288	1472	38880	6384
HELA-4h-031000				81				488	2343	171123	4142	2131	8136	8198	57302	7191
HELA-6h-031000				83				635	1081	88381	3757	1880	4822	1615	63322	5782
HELA-0h-031000				86				846	85	201388	5429	1801	8703	1222	28774	4729
HELA-8h-031000				88				1271	184	183436	8381	4781	8488	2346	58350	11046
HELA-9h-031000				89				380	418	78138	7198	1847	8881	1636	58168	7319
HELA-10h-031000				93				818	884	88533	6044	4308	19174	8137	62933	8060
HELA-11h-031000				94				0	8	33279	4208	312	4863	1654	43482	6081
HELA-12h-031000				96				8	367	43824	9307	1105	6847	885	34825	6862
NCI-H2224				146				1456	248	44458	3418	38703	29486	2702	18600	3128
NCI-H460				148				1834	188	13845	3671	3808	21487	695	22032	3248
NCI-H522				150				813	284	33841	2979	3237	9837	816	30184	1818
SNB-19				152				1116	0	13025	1124	8588	6003	0	18078	2527
SNB-75				154				1156	0	22080	3786	3838	9158	1642	27275	4188
SF-268				156				231	0	4801	2786	3218	8886	447	18225	3182
SF-295				158				8	342	18878	2136	882	578	848	9338	1613
CCRF-CEM				160				1001	258	18120	317	8342	2231	418	18838	1884
DU-145				162				208	405	7842	1488	2828	2384	119	14306	1886
HCT 116				164				721	0	21002	1198	8855	2880	3888	13034	1853

Table 3 (cont'd)

								SEQ 843 A	SEQ 3 TIM	SEQ 866 A	SEQ 866 A	SEQ 8 CA	SEQ 11 EF	SEQ 12 PK	SEQ 14 HY	SEQ 16 RS
Tissue	Tumor-cyto	Normal-cyto	Tumor - Ts	Tumor cells	Normal	Endo	p53	13871	0	998824	36841	16731	12712	8878	49043	5814
Hs 578T	153							13420	7292	37528	28252	9707	8784	8670	48543	5180
MCF-7/ADR-RES	152							15337	1080	938867	82916	21779	19860	10782	63848	9415
MCF7	151							8452	888	384414	17174	18734	18348	2544	63303	4830
M14	149							11458	0	158816	13867	18437	42807	4528	38008	8237
UACC-257	147							3958	123	56725	21571	11118	27884	1929	27441	4561
UACC-62	146							4479	0	350827	13751	7222	23847	2134	28861	5834
SK-MEL-28	144							5287	0	267414	15138	8047	23633	4136	66230	6343
UO-31	143							6444	808	420000	19468	4634	38782	7944	29301	6342
SK-MEL-5	142							5833	377	43470	12308	4008	4523	2794	30902	3122
KM-12	141							2848	331	351883	16808	13817	13874	7005	30577	5798
SK-MEL-2	140							1187	0	232056	14372	8258	17403	6476	34739	19341
HCT-15	139							6688	0	463468	16670	8878	21327	8334	45088	7827
Malme-3M	138							6349	0	384008	16786	8368	17491	4888	57738	10846
COLO 205	137							4209	284	1678884	23763	10725	23844	5088	28010	7615
LOX IMVI	136							11828	0	622858	16654	8852	19514	7213	38869	5702
SW-620	135							3636	1582	230633	21153	7632	8482	4081	43307	8044
TK-10	134							3482	0	184876	53888	7388	8548	4085	37409	5317
HCT 116	133							3384	0	385384	17720	4882	13844	8047	34175	4877
786-0	132							8870	2267	388088	17568	5751	16030	3971	62382	8455
HCC-2998	131							9882	177	84811	18458	16308	8438	4882	38880	6795
ACHN	130							13088	0	48824	14186	4678	8473	3308	26250	8853
PC-3	129							8833	278	488833	21816	7110	11088	[illegible]	40444	8880
[illegible]	128							18878	138	38580	[illegible]	3150	3940	[illegible]	[illegible]	[illegible]
[illegible]	127							7245	7722	77382	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
CAKI-1	126							3585	257	70331	13347	3626	10131	2543	37809	4327
SR	125							9123	0	64348	18090	41974	17229	4374	38104	6293
A498	124							2278	0	272808	14388	9418	28708	1191	50465	8058
RPMI 8226	123							6283	217	203577	17182	14356	29787	8795	32578	5287
SN12C	122							11442	0	137022	6888	5329	22423	4164	28640	4099
HL-60	121							4384	0	440040	12798	16231	15488	2886	28008	4479
MOLT-4	120							3830	380	1088525	16534	5732	41980	4117	25375	6636
OVCAR-8	119							2180	788	804733	14167	8845	34929	8340	84313	8030
K-562	118							2858	3887	4885335	18538	8040	112387	8881	42598	8203
OVCAR-4	117							4840	0	2880707	21787	8518	81843	9580	28120	4575
CCRF-CEM	116							3371	0	661958	10974	7064	21920	5119	53817	8812
OVCAR-3	115							4819	0	882876	13641	4718	10863	2804	34685	6113
SF-539	114							2174	388	345780	13736	5856	11635	2280	19576	4413
HOP-62	113							11505	218	88883	31027	8440	7184	2888	40830	7862
SF-295	112							17217	508	279860	27277	12358	18817	6359	47438	6328
A549/ATCC	111							3084	1363	233341	16800	6861	11824	2279	30246	3718
SF-268	110							4147	0	1126304	19715	10186	22852	3153	44511	6845
NCI-H522	109							8838	373	230300	18786	8509	12058	6749	84076	8280
U251	108							8777	0	462383	13088	6889	18883	4436	28806	5244
NCI-H460	107							2579	830	27882	8830	323	8218	2327	41104	4518
SNB-75	106							8471	921	888327	19448	14479	18623	3332	49837	8532
NCI-H322M	105							7360	0	219881	17548	7858	12434	3103	80664	5744
SNB-19	104							32859	310	108328	20888	18728	24187	3054	61587	8880
NCI-H226	103							8457	0	302788	18647	7470	11871	2287	33178	2884
SK-OV-3	102							9814	371	108082	13285	8342	15724	2888	39481	3518
NCI-H23	101							18803	788	313546	14157	8518	8679	2881	41888	3318
IGROV1	100							5228	1118	388818	18812	8432	21788	2010	29017	3824
EKVX	99							12781	814	18774	10381	4170	8004	3120	21129	4019
OVCAR-5	98							7888	0	317848	22815	4246	39800	3282	33300	3880
HOP-92	97							11086	0	177831	18183	8067	4047	3528	32080	4127
h fibroblasts 3/31/03 P12	48							4478	137	8872	14410	12898	3086	588	30837	5335
h adult SMC 10/21/03 P17	47							13882	248	153425	22184	6859	14419	3871	29128	5742
h keratinocytes 3/23/03 P10	46							8008	0	858464	13245	18288	18157	3439	22863	8471
TCOP	26						wt	1481	8421	44805	11798	0	0	0	0	0
A549-1							wt	139	4212	38038	6787	0	0	0	0	0
A549-2							wt	278	6323	38473	10836	0	0	0	0	0
A549-4							wt	488	2872	28688	10727	0	0	0	0	0
A549-5							wt	148	182	15730	8788	0	0	0	0	0
A549-7							mutant	848	1343	88034	18784	0	0	0	0	0
EKVX-1							mutant	1480	43880	78383	25014	0	0	0	0	0
EKVX-4							mutant	835	834	22887	12511	0	0	0	0	0
EKVX-3							mutant	0	0	28800	7740	0	0	0	0	0
EKVX-5							mutant	732	1576	[illegible]	11042	0	0	0	0	0
EKVX-7							[illegible]	806	718	[illegible]	[illegible]	0	[illegible]	[illegible]	0	0
MCF-7-1							wt	[illegible]	6245	[illegible]	7883	0	0	[illegible]	[illegible]	[illegible]
MCF-7-2							wt	[illegible]	1156	[illegible]	[illegible]	0	[illegible]	0	[illegible]	0
MCF-7-4							wt	224	1050	81146	11813	0	0	0	0	0
MCF-7-5							wt	0	1337	18567	8728	0	0	0	0	0
MCF-7-7							mutant	0	2885	91125	18486	0	0	0	0	0
ADR-RES-1							mutant	425	525	27834	8882	0	0	0	0	0
ADR-RES-3							mutant	0	861	15878	4449	0	0	0	0	0
ADR-RES-4							mutant	388	472	35888	7648	0	0	0	0	0
ADR-RES-5							mutant	880	7382	13823	13082	0	0	0	0	0
ADR-RES-7							wt	818	0	41827	24087	0	0	0	0	0
WI 38-1							wt	808	217	40870	18323	0	0	0	0	0
WI 38-3							wt	842	781	32710	9317	0	0	0	0	0
WI 38-4							wt	1181	3721	17881	11387	0	0	0	0	0
WI 38-5							wt	218	4617	84194	12288	0	0	0	0	0
WI 38-7							HPV E6	532	12821	18483	13318	0	0	0	0	0
HeLa-1							HPV E6	488	843	81837	17033	0	0	0	0	0
HeLa-3							HPV E6	882	3311	46388	7885	0	0	0	0	0
HeLa-4							HPV E6	213	1188	40254	18827	0	0	0	0	0
HeLa-5							HPV E6	0	1049	37586	8675	0	0	0	0	0
HeLa-7							mutant	844	0	88867	14723	0	0	0	0	0
H1299-1							mutant	338	0	88284	14722	0	0	0	0	0
H1299-3							mutant	338	2870	78788	28363	0	0	0	0	0
H1299-4							mutant	204	1886	33336	10427	0	0	0	0	0
H1299-5							mutant	448	0	41846	10384	0	0	0	0	0
H1299-7							wt	194	4278	37307	8382	0	0	0	0	0
A549-2							mutant	538	3083	23382	15828	0	0	0	0	0
EKVX-2							wt	408	8587	28030	8134	0	0	0	0	0
HCT-116-1							wt	1123	3786	48630	21138	0	0	0	0	0
HCT-116-2							mutant	881	1388	43251	13827	0	0	0	0	0
HT29-2							wt	0	1849	18807	13005	0	0	0	0	0
SF539-1							wt	112	2474	48381	13141	0	0	0	0	0
SF539-2							mutant	882	317	42852	13335	0	0	0	0	0
SF-268-1							mutant	819	550	74595	12538	0	0	0	0	0
SF-268-2							wt	332	88	78236	13108	0	0	0	0	0
OVCAR-4-1							wt	342	1543	101777	10427	0	0	0	0	0
OVCAR-4-2							mutant	728	581	18806	14287	0	0	0	0	0
OVCAR-5-1							mutant	10	10	9110	8475	0	0	0	0	0
OVCAR-5-2							wt	281	1433	11082	7083	0	0	0	0	0
MCF-7-2							mutant	0	731	31787	18443	0	0	0	0	0
ADR-RES-2							HPV E6	818	0	113434	14374	0	0	0	0	0
HeLa-2							mutant	336	0	68775	9762	0	0	0	0	0
SW480-1							mutant	1081	7828	68138	12357	0	0	0	0	0
SW480-2							mutant	6823	2573	57384	15081	0	0	0	0	0
H1299-2							mutant	882	18787	9647	19488	0	0	0	0	0
C33A-1							mutant	884	1185	43084	11732	0	0	0	0	0
C33A-2							mutant	888	85	194505	10872	0	0	0	0	0
U2OS-1							mutant	721	0	148871	22177	0	0	0	0	0
U2OS-2							wt	287	882	28884	18911	0	0	0	0	0
Hs68-1							wt	883	985	35777	11870	0	0	0	0	0
Hs68-2							wt	415	2478	38744	25538	0	0	0	0	0
WI 38-2								874	288	8294	118430	0	0	0	0	0
MMset-1								1123	3267	38128	18855	0	0	0	0	0
MMset-2								885	888	34711	31829	0	0	0	0	0
MMset-3								1856	0	13352	28485	0	0	0	0	0
MMset-4								750	0	8477	277572	0	0	0	0	0
MMset-5								872	8438	13002	31580	0	0	0	0	0
MMset-6								1358	1887	14384	24788	0	0	0	0	0
MMset-8								834	0	15325	11836	0	0	0	0	0
MMset-9																

Table 3 (cont'd)

Tissue	Tumor-sym	Normal-sym	Tumor - fn	Tumor cells	Normal	Endos	p53	SEQ 893 A	SEQ 8 TB	SEQ 896 A	SEQ 898 A	SEQ 9 CA	SEQ 11 EP	SEQ 12 PK	SEQ 14 HT	SEQ 16 RS
DuPong-7								4081	4153	130781	48007	0	0	0	0	0
DuPong-8								1843	0	120284	31588	0	0	0	0	0
DuPong-9								1704	352	23137	22363	0	0	0	0	0
DuPong-11								2364	2918	88638	34363	0	0	0	0	0
DuPong-12								1821	0	143619	14784	0	0	0	0	0
DuPong-10								1137	11437	58719	28813	0	0	0	0	0
DuPong-1								1808	0	178675	67121	0	0	0	0	0
DuPong-2								778	282	80117	44171	0	0	0	0	0
DuPong-3								1838	5088	89419	23252	0	0	0	0	0
DuPong-4								44	3575	48080	19488	0	0	0	0	0
DuPong-6								447	217	37705	8888	0	0	0	0	0
DuPong-5								1734	0	104257	34088	0	0	0	0	0
A549-8							wt	141	1863	30864	11749	0	0	0	0	0
EKVX-8							mutant	281	8488	74732	34175	0	0	0	0	0
HCT-116-7							wt	458	0	46374	16408	0	0	0	0	0
HCT-116-8							wt	368	848	88848	23678	0	0	0	0	0
HT29-1							mutant	230	3881	23184	18810	0	0	0	0	0
HT29-7							mutant	78	3147	6867	8481	0	0	0	0	0
HT29-8							mutant	181	467	58732	18019	0	0	0	0	0
SF539-7							wt	7388	375	15224	8477	0	0	0	0	0
SF539-8							wt	0	0	87679	8738	0	0	0	0	0
SF-268-7							mutant	807	448	30857	13175	0	0	0	0	0
SF-268-8							[illegible]	807	0	[illegible]	[illegible]	[illegible]	0	0	0	0
KM12L4-7							wt	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	0	0	0	0
KM12L4-8							wt	[illegible]	[illegible]	105??2	[illegible]	[illegible]	0	0	0	0
OVCAR5-7							mutant	0	228	52888	18798	0	0	0	0	0
OVCAR5-8							mutant	158	0	17818	10887	0	0	0	0	0
MCF-7-8							wt	555	740	24198	11183	0	0	0	0	0
ADR-RES-8							mutant	822	3813	12568	17722	0	0	0	0	0
HeLa-8							HPV E6	0	2243	23863	6188	0	0	0	0	0
SW480-7							mutant	727	1081	24521	12811	0	0	0	0	0
SW480-8							mutant	226	7328	43102	9808	0	0	0	0	0
H1299-8							mutant	102	2383	53883	18781	0	0	0	0	0
C33A-7							mutant	372	3128	11403	6774	0	0	0	0	0
C33A-8							mutant	0	1613	38317	18679	0	0	0	0	0
U2OS-7							mutant	20	2184	72882	14777	0	0	0	0	0
U2OS-8							mutant	87	0	158867	9829	0	0	0	0	0
HuH-7							wt	838	4034	28229	10888	0	0	0	0	0
HuH-8							wt	302	4497	24757	14258	0	0	0	0	0
WI 38-8							wt	232	87	9258	7618	0	0	0	0	0
488 metallo RNA								8548	0	815448	28823	15276	21829	3328	37888	7008
CRL1572 2/17/00								110	0	3070	1153	887	2881	1237	25884	2088
Bov-4						80		348	1576	68018	7421	4930	12083	23383	88810	8229
HT388								1340	686	87815	8767	4804	8347	816	32554	7686
HT378								457	645	18888	8158	4064	4910	729	37858	5788
HT384								3179	0	88246	34036	7365	18311	2528	78812	7937
HT308								0	380	88198	8834	704	7808	2308	21782	8807
Bov-3						173		48	505	8632	3882	183	2025	795	38821	2784
Bov-5						176		8	420	8084	1236	1888	983	791	18850	1888
Bov-6						177		325	0	8391	5220	858	1788	715	38076	4398
h keratinocytes 2/28/00 P10								1083	0	14485	12819	1888	1118	1842	80327	8863
Bov-10						237		881	0	83881	6288	1942	8225	2251	45182	7011
HT816								136	0	18813	8610	8886	18018	1115	88288	14731
h fibroblasts 2/21/00 P12								515	0	27283	8058	253	2038	1888	44374	8188
prostate, h								384	37	2733	5219	1566	387	34	28836	8417
MRG?-OS poly A+								488	0	288879	11883	2188	10484	1829	24878	4588
SA-OS [illegible] poly A+								1281	0	28774	11088	2832	1808	1585	27087	4279
MX poly A+								1883	384	75322	17888	3824	3419	2424	32124	7108
HCT-116-3							wt	420	2854	84654	8849	0	0	0	0	0
HCT-116-4							wt	883	0	98770	6562	0	0	0	0	0
HCT-116-5							wt	258	377	34035	13883	0	0	0	0	0
HCT-116-6							wt	0	249	33380	12796	0	0	0	0	0
A549-9							wt	0	4346	3330	7326	0	0	0	0	0
HT29-3							mutant	302	3771	40888	8815	0	0	0	0	0
EKVX-6							mutant	238	0	82983	8637	0	0	0	0	0
HT29-4							mutant	27	0	89030	8249	0	0	0	0	0
HT29-5							mutant	448	1309	25013	18178	0	0	0	0	0
HT29-6							mutant	304	0	84835	10800	0	0	0	0	0
KM12L4-3							wt	881	1386	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
OVCAR4-4							wt	329	427	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
OVCAR4-5							wt	45	[illegible]	[illegible]	[illegible]	0	[illegible]	0	[illegible]	0
OVCAR4-6							wt	41	322	28881	7181	0	0	0	0	0
SF539-3							wt	391	0	28682	9281	0	0	0	0	0
SF539-4							wt	408	0	34234	16617	0	0	0	0	0
SF539-5							wt	208	1468	16387	12742	0	0	0	0	0
SF539-6							wt	0	817	27867	14994	0	0	0	0	0
OVCAR5-3							mutant	848	2513	83162	8772	0	0	0	0	0
OVCAR5-4							mutant	0	2086	48488	10469	0	0	0	0	0
OVCAR5-6							mutant	512	444	8763	7282	0	0	0	0	0
ADR-RES-6							mutant	215	862	19634	7377	0	0	0	0	0
MCF-7-6							wt	711	2112	80711	12210	0	0	0	0	0
HeLa-5							HPV E6	0	0	82988	16788	0	0	0	0	0
H1299-6							mutant	253	354	21086	11987	0	0	0	0	0
SW480-3							mutant	828	228	80858	9787	0	0	0	0	0
SW480-4							mutant	84	2844	76480	17095	0	0	0	0	0
SW480-5							mutant	822	0	88518	28238	0	0	0	0	0
SW480-6							mutant	0	249	88918	23888	0	0	0	0	0
C33A-3							mutant	858	0	88806	21184	0	0	0	0	0
C33A-4							mutant	258	0	42319	25174	0	0	0	0	0
C33A-5							mutant	428	211	77746	11333	0	0	0	0	0
C33A-6							mutant	144	673	18218	8434	0	0	0	0	0
HuH-6							wt	203	0	8306	7627	0	0	0	0	0
U2OS-3							mutant	285	85	217325	20812	0	0	0	0	0
U2OS-4							mutant	817	2742	145703	12520	0	0	0	0	0
U2OS-5							mutant	836	1376	81355	17438	0	0	0	0	0
U2OS-6							mutant	454	528	110718	12778	0	0	0	0	0
WI 38-6							wt	26	4647	8880	8823	0	0	0	0	0
HuH-2							wt	232	4744	37188	10844	0	0	0	0	0
HuH-4							wt	1339	1334	57073	17844	0	0	0	0	0
SF-268-3							mutant	1761	748	88668	27637	0	0	0	0	0
SF-268-4							mutant	1145	8402	19847	21408	0	0	0	0	0
SF-268-5							mutant	821	1850	40558	20121	0	0	0	0	0
SF-268-6							mutant	874	1880	30621	13423	0	0	0	0	0
DuPong-13								1771	1629	127630	48848	0	0	0	0	0
Mixed-20								1617	8246	258833	83882	0	0	0	0	0
Mixed-21								1348	87	74348	83037	0	0	0	0	0
Mixed-22								1279	2814	130288	25282	0	0	0	0	0
OVCAR5-5							mutant	1063	0	86986	27874	0	0	0	0	0
Mixed-10								1287	18	18788	73612	0	0	0	0	0
Mixed-11								813	0	48488	87514	0	0	0	0	0
Mixed-12								1081	0	109632	88882	0	0	0	0	0
Mixed-13								2111	0	240881	27331	0	0	0	0	0
Mixed-14								2846	0	88383	28888	0	0	0	0	0
Mixed-15								738	0	104882	18747	0	0	0	0	0
Mixed-16								818	0	88748	13656	0	0	0	0	0
Mixed-17								676	0	40277	10300	0	0	0	0	0
Mixed-18								488	847	148788	18872	0	0	0	0	0
Mixed-19								844	4	300027	8470	0	0	0	0	0

Table 3 (cont'd)

Tissue	Tumor-sym	Normal-sym	Tumor - Ip	Tumor cells	Normal	Endos	p53	SEQ 17 AA	SEQ 20 SQ	SEQ 22 PT	SEQ 28 AA	SEQ 29 DR	SEQ 31 DR	SEQ 832 A	SEQ 40 NA	SEQ 844 T
adrenal gland - h		1						46820	1342	187762	8031	11409	2483	86050	560	4349
lymph node - h		2						64639	1004	373187	14301	80634	15380	139195	338	2871
bone marrow - h		3						63224	345	117799	11387	51933	6446	73638	0	284
mammary gland - h		4						26739	0	18847	1710	2723	266	5276	154	306
brain - h		5						84253	1826	159461	6878	829	1184	70036	3190	2311
pancreas - h		6						71698	2036	48828	7425	7287	2972	21495	4955	1246
cerebellum - h		7						82436	104	286725	18723	2748	2858	135678	6036	274
pituitary gland - h		8						67365	232	118587	13943	7314	2454	74670	3058	3477
fetal brain - h		9						183271	0	187662	22024	2638	1198	63217	7434	8836
placenta - h		10						90342	684	105463	8213	8436	6886	128884	1306	4169
fetal kidney - h		11						66084	6026	152578	10980	12234	2383	56346	8858	4617
prostate - h		12						78934	1446	84243	10884	17733	1143	36080	878	86
fetal liver - h		13						86877	3163	89895	11342	18732	3419	38384	278	2130
salivary gl. - h		14						80763	0	122833	2860	18787	2080	12800	0	233
fetal lung - h		15						82918	1478	187898	8127	18242	4178	87498	1544	3465
skeletal muscle - h		16						57631	171	576843	2744	1837	905	48674	1077	2017
heart - h		17						43684	0	236249	885	4858	2345	21339	1102	2174
small intestine - h		18						42979	1357	89581	3821	14338	3821	21878	632	1632
kidney - h		19						46325	6757	77677	1785	3302	1369	26570	2144	1494
spinal cord - h		20						84756	1319	53517	21234	8273	1063	21487	787	716
liver - h		21						46332	2639	53639	4414	2272	1234	34138	126	4123
Spleen - h		22						44988	0	129808	2530	30444	4683	17845	0	8227
[illegible]		23						37827	577	203801	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	457
[illegible]		24						18818	983	37850	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
testis - h		25						44859	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
thymus - h		27						45252	83	424519	19160	26880	8722	120548	1733	217
HPAEC		28				28		67087	0	3134	3884	2437	1616	0	728	0
thyroid gland - h		29						43676	842	181829	8252	4819	929	37702	0	765
RPTEC		30				30		42349	0	3012	5372	4387	356	418	0	0
trachea - h		31						78866	203	144782	8232	39484	3321	42087	682	2353
HMEC		32						69164	850	21473	3421	0	3872	7058	387	0
uterus - h		33						66878	354	142806	5371	8755	1002	37845	2648	3831
HCAEC		34						51717	273	22368	2138	118	580	198	242	0
Pancreas - h		35						48443	0	0	4314	13335	0	2548	0	1082
lymph node - h		36						84678	0	0	6698	83795	2110	3825	208	0
Skeletal muscle - h		37						38349	418	28836	4136	29	319	2006	812	0
fetal liver - h		38						26121	649	0	3467	9198	1606	745	347	288
Heart - h		39						47872	0	2818	2498	1134	0	4386	492	0
thymus - h		40						78722	0	0	2341	57019	1499	3872	220	0
Duodenum - h		41						42191	145	0	4383	4470	600	2529	10	3091
Fetal brain - h		42						66660	576	0	8154	4108	205	1081	284	386
Salivary gl. - h		43						26172	49	837	1319	17131	0	1205	0	0
testis - h		44						57084	129	294	2680	13574	462	2663	338	0
HT219-normal					385			12859	0	0	2384		87	0	298	0
HT213-normal					383			6344	77	0	344	222	247	327	284	0
HT157-normal					381			16338	0	0	348	163	0	842	0	6
Bov-13					358	358		82144	1084	0	23739	6795	7232	5308	1480	12
Bov-12					354	354		68687	88	0	42696	4027	1119	422	476	0
cerebellum - h					344			27729	0	0	220	839	50	0	0	71
brain - h					342			31402	280	0	0	88	79	0	0	0
RPTEC					334	334		21903	0	0	8084	8588	81	479	113	0
lymph node - h					332			38798	277	330	[illegible]	83857	253	367	0	9
h adult EMC 19Q14Q2 017					330			47389	237	0	789	41	0	223	94	0
Fetal brain - h					328			70808	0	6377	28065	18609	83	2749	1212	0
HT388-normal					327			66674	0	389	0	10836	264	202	1110	0
thymus - h					326			79626	0	834	42378	281101	721	750	526	119
HT149-normal					321			41371	416	0	0	0	43	166	325	0
HEPM 24 untreated					320			61610	0	10730	8706	2862	225	3880	232	0
uterus - h					318			66663	449	3041	24606	186533	8075	6242	1297	166
trachea - h					316			46846	276	0	23903	129636	7113	2740	883	440
thyroid gland - h					314			44988	0	1494	16891	84888	8246	1686	0	206
Salivary gl. - h					311			84587	0	0	3684	26082	1049	347	0	0
prostate - h					309			47808	825	0	380	23416	666	176	536	0
pituitary gland - h					307			24784	118	0	1592	19211	675	376	960	157
pancreas - h					305			44917	0	0	631	13638	1321	520	128	586
mammary gland - h					303			66451	1120	0	10462	186862	7974	407	323	0
bladder - h					302			73421	897	3700	5722	10239	184	4728	1068	89
[illegible]					[illegible]			83180	444	0	[illegible]	53042	8342	2816	1714	0
[illegible]					[illegible]			[illegible]	0	[illegible]	[illegible]	[illegible]	1462	[illegible]	[illegible]	[illegible]
[illegible]					[illegible]			63225	0	123	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible] cord - h					294			[illegible]	404	0	23722	[illegible]	[illegible]	1043	[illegible]	155
small intestine - h					292			41642	39	0	2123	14956	2308	[illegible]	0	133
skeletal muscle - h					290			66372	0	19	28791	62231	3867	2624	825	666
bone marrow - h					279			90667	27	0	0	27722	358	0	0	0
adrenal gland - h					277			84753	27	0	2306	8660	86	0	0	355
HPAEC					276	276		57168	0	0	0	1157	0	432	0	0
HT380-normal					268			36846	604	0	0	20358	0	741	596	0
HT382-normal					266			40114	0	1370	0	3833	0	308	0	605
Bov-11					239	239		73367	1154	0	1180	10286	1664	14	218	144
Bov-9					236	236		98453	381	525	108	2281	837	0	0	0
HT372-normal					234			78267	0	1186	2867	13736	0	0	0	0
Bov-7					233	233		71564	374	0	1852	1379	756	0	801	0
Bov-6					231	231		82712	0	307	0	1871	1227	0	73	198
Bov-2					229	229		46448	0	581	212	2316	748	0	875	0
Bov-1					227	227		41889	0	0	783	1630	862	0	0	0
bladder - h					222			33431	906	0	1290	6362	87	0	86	0
Heart - h					215			48688	0	226	744	1154	0	0	138	0
stomach - h					214			59601	0	767	69	63631	3007	323	579	0
fetal liver - h					213			38667	463	0	2249	360	43	338	131	0
placenta - h					212			43829	0	0	0	11419	2778	0	387	0
HCAEC					211	211		34737	280	38	1627	0	0	0	0	43
fetal brain - h					210			70127	0	0	23	8836	228	0	448	0
HMEC					208			48676	155	87	1200	2432	38	1108	0	0
Duodenum - h					205			38298	0	0	0	7386	36	322	336	120
Skeletal muscle - h					203			34118	0	0	882	34	0	0	323	286
Pancreas - h					201			33387	0	148	0	13233	0	865	0	0
testis - h					199			26853	0	0	178	8880	0	0	0	0
Salivary gl. - h					197			30898	0	8020	886	19857	0	2028	83	0
HEPM 24 TGFB1 detergent+Dhps					196			21219	328	548	1731	270	58	34	198	0
thymus - h					193			33113	309	0	14228	66431	8113	752	805	0
WI-38 72h					179			21345	0	0	0	75	0	608	0	0
lymph node - h					91			27301	0	0	267	38127	3087	218	83	0
lung - h					89			79836	980	0	2724	108563	7184	840	484	0
kidney - h					87			88006	0	0	0	7821	768	448	126	247
[illegible] - h					85			37503	0	99	107	16849	436	0	0	0
fetal lung - h					83			12835	0	0	779	2337	229	82	0	0
fetal liver - h					81			21581	48	0	382	7618	615	749	0	0
fetal kidney - h					48			21744	244	37	341	12404	168	141	280	328
HELA-2h-631800				79				38898	536	0	144	0	600	907	419	0
HELA-4h-631800				81				67302	0	0	79	462	1385	94	0	0
HELA-6h-631800				83				53322	0	0	0	0	158	0	714	0
HELA-8h-631800				86				28779	86	0	1042	0	827	830	0	0
HELA-8h-631800				88				68380	0	0	2037	986	291	298	185	0
HELA-8h-631800				90				88868	0	0	986	1267	1197	385	1438	0
HELA-10h-631800				92				62803	0	0	0	1258	2798	0	196	0
HELA-11h-631800				94				43462	0	0	0	836	982	428	0	0
HELA-12h-631800				96				34625	98	0	0	289	1008	0	313	0
NCI-H322M				146				16808	857	0	0	3844	3213	286	605	160
NCI-H460				148				32832	0	1137	0	719	1753	401	97	282
NCI-H522				150				20164	72	0	0	530	701	0	180	267
SNB-19				152				18878	0	211	281	390	2401	848	0	57
SNB-75				154				27275	0	796	0	15	4401	114	8838	175
SF-268				156				18225	0	383	232	155	882	0	0	0
SF-295				158				8330	114	0	187	110	388	24	743	141
CCRF-CEM				160				18635	280	0	334	408	254	0	29	0
DU-145				162				14305	121	0	60	317	923	281	0	778
HCT 116				164				13024	0	351	670	422	842	0	878	0

Table 3 (cont'd)

Tissue	Tumor-syn	Normal-syn	Tumor - No	Tumor cells	Normal	Endos	p53	SEQ 17 AA	SEQ 20 BO	SEQ 22 PT	SEQ 30 AA	SEQ 29 DR	SEQ 31 DR	SEQ 832 A	SEQ 40 M	SEQ 844 T
Caki-1				166				25841	1	0	727	471	4112	0	0	0
786-0				168				43253	1415	1044	2462	2283	6374	166	0	88
T-47D				169				52705	8	4622	638	771	1518	1169	0	134
Kan-3				171				30045	47	218	800	0	88	0	0	0
CRL 1441 RNA 8/30				181				11852	8	488	1471	242	339	32	197	176
791T untreated + DNase				183				21315	8	0	6	0	0	691	120	8
KB poly A+				194				22563	194	6	1630	2000	1096	288	0	0
HOB poly A+				196				38104	8	6	1156	3112	1662	145	46	30
ACHN				199				23616	8	1874	1888	823	874	730	371	126
UACC-62				200				19153	130	88	1284	812	840	0	858	0
MCF-7/ADR-RES				202				12891	214	0	714	406	215	178	0	435
UTC6 (Ahmed) poly a+				204				8408	8	0	1284	672	149	8	887	0
WISH (Collagen) poly A+				206				12860	8	8	14	6	82	8	308	0
439 nodule mRNA				208				83640	8	1841	3808	14082	411	8	411	8
CCL137 RNA 3/21/98				212				21190	8	863	0	631	47	0	488	8
WI-38 72h 0.5%FBS, 24h 10% FBS				219				28088	8	8	8	3727	0	148	176	134
CRL 1441 + TPA (24h) 8/30				220				14725	0	130	0	0	366	862	0	8
Kan-1				221				28116	84	8	1488	338	447	157	281	8
Kan-2				223				23646	88	0	383	0	235	0	8	8
Kan-4				225				37538	43	804	184	0	22	0	887	8
HOP-92				241				22240	0	0	88	726	740	63	0	8
MOLT-4				242				18708	0	13383	142	27	3864	836	0	88
EBVX				243				[illegible]	727	303	[illegible]	837	2757	371	0	0
[illegible]				244				[illegible]	[illegible]	0	8	[illegible]	4298	[illegible]	0	0
[illegible]				245				28842	[illegible]	981	308	[illegible]	914	[illegible]	[illegible]	142
[illegible] 8226				246				34425	0	0	[illegible]	[illegible]	1614	[illegible]	224	60
A549/ATCC				247				38618	8	8	665	0	8	[illegible]	612	401
SR				248				19568	8	1361	0	354	730	0	887	62
OVCAR-3				249				27443	30	208	869	852	1417	284	3025	288
HCT-15				250				34619	8	5278	813	1886	2386	1874	208	0
OVCAR-4				251				10333	478	1077	0	157	587	0	718	0
UO-31				252				13496	8	415	0	242	757	0	0	118
OVCAR-5				253				60257	8	3782	1757	584	7068	635	1034	271
SN12C				254				38550	119	3388	8	204	483	0	0	0
OVCAR-8				255				16467	190	573	882	812	215	819	104	0
LOX IMVI				256				49486	0	18804	8	784	8133	0	278	888
IGROV1				257				36126	121	280	749	373	1340	380	231	208
SK-MEL-2				258				34735	737	288	1017	0	536	377	73	0
SK-OV-3				259				17172	282	0	0	312	584	0	157	118
SK-MEL-5				260				13827	212	808	0	141	338	0	54	0
SF-539				261				38531	885	1771	824	855	3488	0	858	408
SK-MEL-28				262				34495	0	337	617	1130	2525	8	282	0
K-562				263				30125	198	11130	0	170	2880	888	55	336
UACC-257				264				25143	184	0	606	210	617	97	612	0
M14				265				10129	48	8	0	178	34	279	0	0
MCF7				267				68835	0	2880	488	807	1108	2558	449	583
MDA-MB-435				268				28815	0	878	815	40	803	8	8	0
HT279				270				38490	8	8	850	7537	0	418	1472	276
MDA-N				271				37574	727	7083	0	0	492	2143	424	625
Y79 poly A+				271				102506	872	2288	0	822	808	534	1228	0
SHOS poly A+				288				28603	44	8	9864	6283	4247	3083	147	0
HT836 24h TPA RNA 8/23				308				47107	8	8	850	3618	0	611	387	0
HELA-EXP 021999				313				19308	0	8	8	0	31	288	42	0
HT836 8h RNA				322				62888	109	8	7108	17288	2781	1124	803	0
HT347				323				40870	148	787	286	19626	0	1252	13	0
468 nodule RNA				324				60268	8	8	18772	8011	8	840	383	0
NCI-H226				326				23074	8	184	757	8	334	408	128	883
HOP-62				327				18884	0	187	1036	1027	2385	1532	231	0
MDA-MB-231				328				28882	0	8843	46452	11987	18823	8501	1838	1819
U251				339				23858	0	19508	13847	7782	63808	10227	1071	8180
PT cells poly A+				340				11887	71	108	0	8	1453	0	0	48
PC-3				341				23488	130	283	3488	825	813	388	0	282
HCC-2998				343				17788	8	881	1731	774	368	873	28	423
SW-620				345				15302	0	819	1383	688	203	481	1336	849
HT192				346				42880	87	0	2871	17388	2232	1485	0	73
COLO 205				347				12540	8	0	2265	8	108	0	707	0
HT29				348				28825	8	8	383	8440	8	[illegible]	8	0
KM-12				349				21718	8	1986	7178	779	[illegible]	[illegible]	531	348
HT1191				[illegible]				[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	611	379
[illegible]				351				[illegible]	0	[illegible]	[illegible]	0	152	[illegible]	848	[illegible]
[illegible]				352				[illegible]	483	[illegible]	[illegible]	[illegible]	2080	[illegible]	0	[illegible]
[illegible] 383				353				23448	0	0	[illegible]	[illegible]	2050	214	425	0
TK-10				365				40915	288	8636	22002	8242	8829	2488	23	678
[illegible]				357				74434	651	81082	18863	11088	21228	6343	1280	2753
Hs 578T				358				23716	71	2207	1888	834	1418	425	272	8
HT213			58					41738	0	808	282	12170	288	0	0	0
HT288			62					34614	610	8	3408	20846	288	8	0	0
HT130			64					37801	588	213	1671	0	0	104	55	143
HT156			58					37780	0	0	784	12374	28	0	581	88
HT163			59					38917	0	0	354	4844	0	408	141	0
HT170			60					38984	781	0	7384	50330	67	607	800	0
HT172			62					31376	8	0	871	3857	0	0	838	357
HT136			63					41881	0	343	0	17086	0	171	0	0
HT178			64					37107	0	0	238	1861	78	0	443	45
HT154			65					32270	0	0	0	11738	0	668	0	183
HT189			66					28571	8	0	881	3811	683	73	2343	37
HT188			67					30113	0	0	2883	1192	2544	0	1930	0
HT148			68					27823	287	0	1384	35	358	725	704	0
HT143			69					30413	0	475	385	0	8	0	0	257
HT198			70					19384	126	8	435	8121	8	0	539	19
HT145			71					27515	873	8	7047	23622	8	0	231	248
HT227			72					30808	0	8	2488	278	423	0	637	31
HT302			73					37706	0	0	1087	71833	781	0	200	0
HT314			74					38827	475	0	131	16888	313	0	0	0
HT317			76					66238	916	0	6015	62388	2800	0	428	0
Medulloblastoma 9/26 11/6			77					30458	0	8	142	119	8	286	0	0
HT323			78					91848	187	838	0	12817	182	0	8	0
HT327			80					43118	109	8	788	7645	97	183	840	0
HT335			82					47985	0	178	0	3129	8	330	168	40
HT146			86					13808	208	0	0	2507	8	183	26	90
HT348			87					91448	631	0	182	16307	8	126	725	88
HT311			170					37227	286	0	494	8888	88	0	0	114
HT388			186					38882	0	0	0	6827	1908	858	780	0
HT149			187					19306	0	0	0	453	8	0	307	78
HT281			188					36781	0	0	0	28196	184	0	1358	0
HT372			191					43132	0	0	30	1744	427	0	319	305
TCGP			207					38117	0	158	1	0	8	0	0	83
HT180			216					18433	205	283	1197	1329	0	8	244	8
HT367			217					17447	84	0	352	1273	353	0	0	142
HT309			224					38703	0	0	8188	19488	17	798	0	61
HT376			225					23028	0	0	216	10361	8	0	0	0
HT371			228					40677	8	1	0	8837	238	3	252	287
HT377			230					43688	438	187	0	12382	0	0	334	0
HT382			238					44408	0	8	1948	8181	0	327	427	0
[illegible]blastoma RNA			281					16888	288	8	8	63	0	0	0	0
HT334			298					68858	883	8	3888	25838	0	0	0	0
HT338			301					48347	335	0	3584	18153	145	473	221	0
HT382			315					17827	253	8	885	1837	0	383	0	0
HT384			317					39888	448	115	2383	48438	0	784	714	534
HT312			318					37888	0	0	633	1822	888	184	378	0
HT192			325					29858	0	322	175	0	208	130	148	0
HT386			354					34867	88	0	2288	17888	0	488	215	0
HT157			368					67210	0	8	12307	18792	385	233	0	0
T-47D	163							28111	84	34126	2596	413	81	7881	788	0
MDA-N	161							28384	0	218885	2530	288	0	18184	88	740
MDA-MB-435	159							34704	658	138840	2347	2104	326	15825	104	385
MDA-MB-231	157							48858	712	15181	24031	4452	1312	23542	140	412

Table 3 (cont'd)

Tissue	Tumor-cyno	Normal-cyno	Tumor - ln	Tumor cells	Normal	Endos	p53	SEQ 44 TI	SEQ 45 AA	SEQ 47 AA	SEQ 48 AA	SEQ 49 AA	SEQ 51 KU	SEQ 52 AA	SEQ 54 CO	SEQ 55 CL
DuPong-7								85383	571	729	0	0	0	0	0	0
DuPong-8								29488	348	374	0	0	0	0	0	0
DuPong-9								44303	738	138	0	0	0	0	0	0
DuPong-11								34887	0	628	0	0	0	0	0	0
DuPong-12								86743	0	485	0	0	0	0	0	0
DuPong-10								20110	284	211	0	0	0	0	0	0
DuPong-1								7884	864	23	0	0	0	0	0	0
DuPong-2								3139	281	38	0	0	0	0	0	0
DuPong-3								888	1703	255	0	0	0	0	0	0
DuPong-4								28852	334	0	0	0	0	0	0	0
DuPong-5								40888	0	51	0	0	0	0	0	0
DuPong-6								32908	20	0	0	0	0	0	0	0
A549-8							wt	1808	23	30	0	0	0	0	0	0
EKVX-8							mutant	859	212	0	0	0	0	0	0	0
HCT-116-7							wt	0	722	0	0	0	0	0	0	0
HCT-116-8							wt	771	122	65	0	0	0	0	0	0
HT29-1							mutant	310	0	144	0	0	0	0	0	0
HT29-7							mutant	0	0	25	0	0	0	0	0	0
HT29-8							mutant	0	0	51	0	0	0	0	0	0
SF539-7							wt	1387	837	38	0	0	0	0	0	0
SF539-8							wt	3338	7	130	0	0	0	0	0	0
SF-295-7							mutant	17078	882	0	0	0	0	0	0	0
[illegible]							mutant	13222	72	110	0	0	0	0	0	0
[illegible]-4-7							wt	1233	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
OVCAR-4-8							wt	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	0	[illegible]	[illegible]
OVCAR-5-7							mutant	4732	0	0	0	0	0	0	0	0
OVCAR-5-8							mutant	3132	0	4	0	0	0	0	0	0
MCF-7-8							wt	3375	440	0	0	0	0	0	0	0
ADR-RES-8							mutant	538	0	0	0	0	0	0	0	0
HeLa-8							HPV E6	1087	88	0	0	0	0	0	0	0
SW480-7							mutant	1822	717	22	0	0	0	0	0	0
SW480-8							mutant	412	4	72	0	0	0	0	0	0
H1299-8							mutant	0	182	10	0	0	0	0	0	0
C33A-7							mutant	0	235	4	0	0	0	0	0	0
C33A-8							mutant	444	0	0	0	0	0	0	0	0
U2OS-7							mutant	28619	143	84	0	0	0	0	0	0
U2OS-8							mutant	4768	418	0	0	0	0	0	0	0
Hs68-7							wt	1383	0	0	0	0	0	0	0	0
Hs68-8							wt	512	334	0	0	0	0	0	0	0
WI 38-8							wt	1504	41	0	0	0	0	0	0	0
HSB module RNA								0	0	0	70	5793	2686	309	598	9888
CRL1572 3/17/00								340	0	0	134	1830	255	0	517	661
Bov-4						84		842	0	0	188	8574	0	88	0	12425
HT380								0	0	0	801	4678	0	0	7	16708
HT378								0	0	34	0	4412	215	0	0	2036
HT383								19732	0	0	0	5567	8257	81	158	8810
HT388								0	0	0	0	8143	188	0	0	24662
Bov-3						173		83	0	7	0	3031	438	329	297	1815
Bov-8						175		0	0	58	34	1425	843	284	0	83
Bov-9						177		0	0	7	17	2354	228	0	0	1298
h keratinocytes 3/29/00 #10								0	0	93	13	3675	0	112	0	198
Bov-10						237		0	0	19	123	4085	180	40	281	3522
HTB18								0	0	0	0	7631	0	421	550	1825
h fibroblasts 3/31/00 #12								0	0	39	23	4648	0	0	208	883
prostate, h								0	0	0	81	2883	0	0	0	5850
MM4G-OS poly A+								918	0	0	0	2857	281	84	0	2243
SA-OS (Hunsky) poly A+								0	0	0	86	1148	0	176	0	1586
MK poly A+								0	0	57	0	2820	0	257	0	5073
HCT-116-3							wt	288	22	0	0	0	0	0	0	0
HCT-116-4							wt	438	1211	0	0	0	0	0	0	0
HCT-116-5							wt	127	204	28	0	0	0	0	0	0
HCT-116-6							wt	1178	0	0	0	0	0	0	0	0
A549-6							wt	0	0	4	0	0	0	0	0	0
HT29-3							mutant	16858	0	247	0	0	0	0	0	0
EKVX-6							mutant	881	0	0	0	0	0	0	0	0
HT29-4							mutant	0	17	28	0	0	0	0	0	0
HT29-5							mutant	1878	0	344	0	0	0	0	0	0
HT29-[illegible]							mutant	0	[illegible]	62	0	0	0	0	0	0
[illegible]							wt	[illegible]	723	30	0	0	[illegible]	[illegible]	[illegible]	[illegible]
OVC[illegible]-4							wt	[illegible]	0	0	0	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
OVCAR-4-5							wt	[illegible]	271	[illegible]	[illegible]	[illegible]	[illegible]	0	[illegible]	[illegible]
OVCAR-4-6							wt	0	0	[illegible]	0	0	0	0	[illegible]	[illegible]
SF539-3							wt	4462	146	148	0	0	0	0	0	0
SF539-4							wt	3258	281	32	0	0	0	0	0	0
SF539-5							wt	881	0	38	0	0	0	0	0	0
SF539-6							wt	1280	312	0	0	0	0	0	0	0
OVCAR-5-3							mutant	2388	0	116	0	0	0	0	0	0
OVCAR-5-4							mutant	0	0	37	0	0	0	0	0	0
OVCAR-5-6							mutant	241	0	0	0	0	0	0	0	0
ADR-RES-6							mutant	80	6	129	0	0	0	0	0	0
MCF-7-6							wt	629	846	80	0	0	0	0	0	0
HeLa-6							HPV E6	1297	1521	0	0	0	0	0	0	0
H1299-6							mutant	0	288	0	0	0	0	0	0	0
SW480-3							mutant	0	303	138	0	0	0	0	0	0
SW480-4							mutant	1137	629	67	0	0	0	0	0	0
SW480-5							mutant	3274	0	38	0	0	0	0	0	0
SW480-5							mutant	885	725	0	0	0	0	0	0	0
C33A-3							mutant	180	0	80	0	0	0	0	0	0
C33A-4							mutant	4870	0	0	0	0	0	0	0	0
C33A-5							mutant	0	678	80	0	0	0	0	0	0
C33A-6							mutant	3886	0	0	0	0	0	0	0	0
Hs68-6							wt	0	0	59	0	0	0	0	0	0
U2OS-3							mutant	71887	280	0	0	0	0	0	0	0
U2OS-4							mutant	4626	0	6	0	0	0	0	0	0
U2OS-5							mutant	7831	148	17	0	0	0	0	0	0
U2OS-6							mutant	0	0	49	0	0	0	0	0	0
WI 38-6							wt	2111	0	242	0	0	0	0	0	0
Hs68-3							wt	2882	0	87	0	0	0	0	0	0
Hs68-4							wt	83108	1282	248	0	0	0	0	0	0
SF-295-3							mutant	123828	0	0	0	0	0	0	0	0
SF-295-4							mutant	70501	1548	0	0	0	0	0	0	0
SF-295-5							mutant	32299	292	0	0	0	0	0	0	0
SF-295-6							mutant	0	2127	0	0	0	0	0	0	0
DuPong-13								43164	628	760	0	0	0	0	0	0
Mikhail-20								9819	9543	71	0	0	0	0	0	0
Mikhail-21								6250	3048	128	0	0	0	0	0	0
Mikhail-22								7053	9867	288	0	0	0	0	0	0
OVCAR-5-5							mutant	2918	783	112	0	0	0	0	0	0
Mikhail-10								2788	1330	113	0	0	0	0	0	0
Mikhail-11								2188	781	46	0	0	0	0	0	0
Mikhail-12								6385	61	388	0	0	0	0	0	0
Mikhail-13								4834	133	1023	0	0	0	0	0	0
Mikhail-14								4037	0	881	0	0	0	0	0	0
Mikhail-15								9848	0	1013	0	0	0	0	0	0
Mikhail-16								3877	3	0	0	0	0	0	0	0
Mikhail-17								1275	0	168	0	0	0	0	0	0
Mikhail-18								1218	3480	885	0	0	0	0	0	0
Mikhail-19								2	0	0	0	0	0	0	0	0

Table 3 (cont'd)

Tissue	Tumor-sym	Normal-sym	Tumor - fx	Tumor cells	Normal	Endos	p43	SEQ 36 AA	SEQ 37 W	SEQ 60 AA	SEQ 63 NE	SEQ 66 CA	SEQ 68 NH	SEQ 110 R	SEQ 73 NR	SEQ 78 AA
adrenal gland - h		1						1179	45366	13724	16216	11737	18736	4759	24187	161827
lymph node - h		2						1882	70208	24506	33534	13083	27463	7408	31327	144050
bone marrow - h		3						57	89402	12041	24326	28126	21479	2888	88126	103884
mammary gland - h		4						102	8388	808	388	3138	2968	884	4197	30703
brain - h		5						1997	33241	2387	8570	113857	27944	3079	13512	88724
pancreas - h		6						2724	28449	11763	2543	14282	19704	3837	27534	88825
cerebellum - h		7						2187	88557	2020	28887	401142	55813	7287	38350	180188
pituitary gland - h		8						2771	88387	14888	10820	6242	28081	5844	23798	128708
fetal brain - h		9						2182	88083	14224	9117	115808	32885	5280	23345	130701
placenta - h		10						7864	98118	15882	8421	27303	21623	4144	28458	118827
fetal kidney - h		11						3088	45781	8852	12231	27388	42058	4885	38782	202884
prostate - h		12						2873	23487	18038	6127	8510	18409	4448	8670	180508
fetal liver - h		13						1982	31433	13743	10843	18727	24811	2114	47817	86705
salivary gl. - h		14						1279	20888	8416	1858	18858	18078	2253	23301	188829
fetal lung - h		15						4579	80513	8388	8440	27130	27710	3082	32855	173336
skeletal muscle - h		16						3544	34874	88	5882	8833	12917	1781	8575	128486
heart - h		17						1238	18128	3837	3249	17179	18473	2054	8412	108323
small intestine - h		18						2013	18561	17208	1848	8810	17382	1876	15805	254853
kidney - h		19						1838	23780	8098	19880	7388	28848	2088	17836	150384
spinal cord - h		20						2970	15871	6250	8888	3857	33464	1988	7081	138873
liver - h		21						4785	15711	8344	2177	3843	38372	2313	10324	118884
Spleen - h		22						1085	28779	16388	2832	3727	38754	2087	4861	114231
[illegible] - h		23						484	22182	6232	8714	4773	29012	[illegible]	1478	[illegible]
stomach - h		[illegible]						1819	18425	12130	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible] - h		[illegible]						8482	153115	[illegible]	[illegible]	[illegible]	[illegible]	4775	[illegible]	1229
Thymus - h		27						1976	57884	48046	18138	17258	18898	4763	30850	115427
HPAEC		28				28		284	14426	8	886	4186	12772	3612	0	80708
thyroid gland - h		29						2594	28474	2485	2182	11290	13291	3114	13887	88705
RPTEC		30				30		888	12784	748	1729	1801	19158	3849	13263	88054
trachea - h		31						8137	74825	8278	8113	34729	22943	3380	21168	714306
HMEC		32						18853	21782	28857	3363	0	25487	2887	9425	78553
uterus - h		33						1208	41625	3525	6885	34817	19410	2493	15380	68824
HCAEC		34						0	18816	752	8	435	17803	1982	4218	72012
Pancreas - h		35						884	11785	0	3382	280	8241	2332	8068	128381
lymph node - h		36						1746	12072	5882	2849	638	7798	3831	3205	77707
Skeletal muscle - h		37						621	3867	0	1071	2029	4638	805	2524	38353
fetal liver - h		38						0	9143	382	4811	1080	14388	2211	30874	78356
Heart - h		39						888	8877	0	6788	888	4678	846	1733	88107
Brain - h		40						1610	11513	1144	4800	63	8088	2118	8482	84284
Duodenum - h		41						827	6294	830	102	405	4145	1544	6178	85243
Fetal brain - h		42						1670	16310	0	5643	561	8088	3845	8281	124700
Salivary gl. - h		43						1388	4880	0	2304	0	4275	1481	3876	81428
testis - h		44						1808	17351	8	4360	0	13191	2161	10838	128853
HT219-normal					385			0	7137	125	78	130	138	1614	801	20873
HT213-normal					383			8	8044	8	1311	0	743	1102	0	24883
HT157-normal					381			431	3428	8	0	22	171	1881	336	38438
Dev-13					356	356		288	94127	484	1116	5137	18587	14131	14820	172795
Dev-12					354	354		1780	128846	8	21	2012	6887	7821	2525	85082
cerebellum - h					344			8	4508	72	83	228	429	2304	1811	30731
brain - h					342			0	1387	715	175	0	128	2380	443	32872
RPTEC					334	334		1348	21842	10883	0	357	701	4284	274	188421
lymph node - h					332			153	13413	0	1318	7	1938	3888	0	85380
h adult BMC 10/21/82 #17					330			0	8843	0	0	84	24	2800	0	43488
Fetal brain - h					328			236	84197	837	825	1883	12083	8885	3780	85415
HT308-normal					327			1215	4886	0	87	1	1803	1882	7784	38482
thymus - h					326			483	76773	0	287	5123	4823	8848	1180	88848
HT148 - normal					321			0	2317	87	0	1	1318	2530	152	37883
HEPM 24 untreated					320			1317	22830	0	848	214	8813	4217	2088	88214
uterus - h					318			0	65418	1050	1252	1531	16880	11203	38228	123875
trachea - h					316			8	40353	806	1859	2184	12222	8363	140780	104888
thyroid gland - h					314			1	42887	0	1848	131	10332	6871	88801	114788
salivary gl. - h					311			0	8808	0	0	0	2738	3519	4532	101244
prostate - h					308			8	6480	0	233	129	1622	3462	3068	70433
pituitary gland - h					307			858	14108	0	114	238	1127	2486	2133	38848
pancreas - h					306			0	6503	0	45	0	2836	2501	3386	65363
mammary gland - h					303			184	38315	888	487	220	6827	4345	18318	98788
bladder - h					302			1873	19158	0	3240	507	8250	4488	7821	86038
aorta - h					298			1747	103501	7298	480	1802	28319	7297	29073	148418
[illegible] - h					297			2867	40647	2131	730	[illegible]	8744	8236	[illegible]	[illegible]
Spleen - h					[illegible]			605	8815	0	137	[illegible]	2888	2770	[illegible]	[illegible]
[illegible] - h					294			205	[illegible]	1404	[illegible]	1208	[illegible]	[illegible]	[illegible]	11201
small intestine - h					292			108	7475	318	[illegible]	70	3841	2023	5381	84882
skeletal muscle - h					290			2187	53058	1408	547	843	11138	8446	28427	184587
bone marrow - h					279			0	785	1872	0	0	0	1803	1888	30233
adrenal gland - h					277			0	8180	88	375	0	405	2158	875	24322
HPAEC					275	275		182	3878	88	0	0	804	2487	0	38020
HT380-normal					268			0	3038	229	114	287	0	2137	407	52419
HT382-normal					265			2212	3888	0	162	162	1078	3610	2147	71288
Dev-11					238	238		823	8248	0	0	0	7388	4208	18805	157420
Dev-8					235	235		8	3824	0	0	0	2750	2873	1723	61030
HT372-normal					234			8	14411	412	420	0	17	3430	803	80887
Dev-7					233	233		3491	3138	40	116	227	1882	2888	4367	80874
Dev-6					231	231		778	4003	0	87	0	1458	2734	3814	21581
Dev-2					229	229		197	5734	0	0	33	1062	2808	2380	48128
Dev-1					227	227		1862	3874	0	148	198	1828	2485	8847	48717
bladder - h					222			258	4008	0	17	322	0	2880	383	44378
Heart - h					215			8	1810	0	0	28	8343	3087	1778	107387
stomach - h					214			8	4818	0	0	0	3148	3385	3834	81804
fetal liver - h					213			0	2888	8	0	328	468	2202	480	41568
placenta - h					212			136	3720	8	0	153	3470	2961	7783	68882
HCAEC					211	211		135	2157	8	0	117	0	2312	1	45378
fetal brain - h					210			8	6864	0	388	230	879	3280	4176	62140
HMEC					208			779	2084	0	4	188	0	2108	0	37886
Duodenum - h					205			319	3084	43	13	0	483	1652	238	40848
Skeletal muscle - h					203			333	3298	60	0	29	3	2208	124	43570
Pancreas - h					201			0	3135	383	98	0	188	2439	384	43068
aorta - h					199			385	8731	0	188	336	0	2248	300	44576
Salivary gl. - h					197			0	5748	886	132	411	2172	2782	2052	53185
HEPM 24 TGFB1 detergent-DNase					195			884	3783	8	0	32	538	1918	62	38673
thymus - h					193			0	29385	349	365	75	254	1356	2852	47888
WI-38 72h					179			8	3118	0	204	0	841	1383	72	22181
lymph node - h					91			8	4438	0	0	0	2083	838	879	36753
lung - h					99			8	18888	883	158	88	3840	2001	3287	125162
kidney - h					87			8	3419	0	887	0	2379	2158	3845	88857
heart - h					85			1172	7101	0	0	622	1020	2135	1888	47860
fetal lung - h					83			273	3213	0	0	0	0	777	822	35488
fetal liver - h					81			8	3087	0	188	178	0	1167	6005	39043
fetal kidney - h					49			388	3688	0	83	0	805	2198	5247	68106
HELA-2h-031800				79				888	7753	0	47	819	1798	2759	21228	73020
HELA-4h-031800				81				8876	2501	0	198	0	781	2339	8803	73885
HELA-6h-031800				83				301	2784	0	58	203	1276	2285	8212	78474
HELA-8h-031800				85				1883	2781	864	182	80	2720	1297	4070	33776
HELA-8h-031800				88				84	12542	253	0	81	0	1843	4388	70122
HELA-9h-031800				90				232	3278	0	185	82	883	1744	3048	61476
HELA-10h-031800				92				1224	8588	0	88	80	1344	1761	7822	88409
HELA-11h-031800				94				476	838	0	195	182	0	1728	3846	44188
HELA-12h-031800				96				328	847	0	0	0	831	1409	1828	78433
NCI-H322M				146				706	6767	8	2283	283	807	4188	47488	28844
NCI-H460				148				362	6027	0	703	88	432	3194	13322	28280
NCI-H522				150				0	3418	0	225	0	378	1871	2808	34403
SNB-19				152				258	3181	8	373	0	1914	2329	30387	28888
SNB-75				154				488	6471	0	783	40	2808	3295	17171	28881
SF-588				156				0	3779	432	238	0	1122	1851	8488	18046
SF-295				158				0	0	0	87	438	732	656	2043	12380
CCRF-CEM				160				385	1885	8	0	188	821	887	303	19083
DU-145				162				8	2180	8	144	40	1288	1957	13480	18145
HCT 116				164				8	4548	0	248	0	471	1321	10123	17384

Table 3 (cont'd)

Tissue	Tumor-xyz	Normal-xyz	Tumor - 1o	Tumor cells	Normal	Endo	p53	SEQ 17 AA	SEQ 20 SQ	SEQ 22 PT	SEQ 26 AA	SEQ 29 DR	SEQ 31 DR	SEQ 832 A	SEQ 40 IM	SEQ 444 T
Hs 578T	155							48043	143	111914	7308	2366	887	8945	0	388
MCF-7/ADR-RES	153							48543	0	70411	721	287	0	15558	0	858
MCF7	151							53849	934	30804	11924	2850	218	13820	0	0
M14	148							63383	371	22226	15025	2725	257	4184	975	73
UACC-257	147							38000	1050	72536	4818	111	0	32363	0	311
UACC-62	145							27441	0	7895	202	986	74	9800	306	251
SK-MEL-28	144							20851	71	10348	1482	2018	634	4087	176	284
UO-31	143							88230	0	13483	3316	644	1206	1827	1885	0
SK-MEL-5	142							26301	0	137878	1882	110	280	18800	490	134
KM-12	141							33882	287	8823	2025	5	65	1287	0	329
SK-MEL-2	140							30577	0	58284	3528	827	465	19863	0	188
HCT-15	139							84738	445	25382	2789	1572	287	8888	642	0
Malme-3M	138							48080	1468	86469	4322	243	284	12794	226	461
COLO 205	137							57738	433	19982	2538	488	0	9756	0	174
LOX IMVI	136							26018	0	101759	1512	680	862	28228	348	826
SW-620	135							38849	437	28579	780	203	188	8408	375	188
TK-10	134							43287	68	13876	1719	883	282	7088	72	48
HCT 116	133							32969	345	18778	1178	8	438	3812	721	68
786-0	132							34175	0	27823	0	534	157	6538	887	14
HCC-2998	131							62382	734	17230	0	198	238	3881	0	841
ACHN	130							38080	329	81730	1363	977	303	10448	25	238
PC-3	129							38282	33	80887	1005	195	457	8256	819	0
RXF 393	128							40444	305	82851	3148	2477	2841	28834	478	0
DU-145	127							37777	0	8182	8153	140	408	[illegible]	[illegible]	[illegible]
Caki-1	126							35257	331	[illegible]	8471	85	[illegible]	[illegible]	[illegible]	[illegible]
SR	125							[illegible]	0	[illegible]	7887	1172	[illegible]	[illegible]	156	0
A498	124							39184	0	[illegible]	4214	0	1885	2823	423	888
RPMI 8226	123							89465	737	8134	2800	2182	525	13014	0	0
SN12C	122							32578	65	44277	536	1473	150	23830	0	537
HL-60	121							39449	886	2818	0	325	771	707	88	380
MOLT-4	120							28309	782	17196	881	532	1823	4838	0	0
OVCAR-8	119							25375	0	42226	1986	337	1586	8852	888	77
K-562	118							54213	582	18149	2138	382	222	5444	0	0
OVCAR-4	117							42586	1500	108842	5320	2238	2583	8251	1238	1118
CCRF-CEM	116							38120	578	100822	2781	831	478	41580	0	0
OVCAR-3	115							52017	848	47881	1242	858	383	18348	2443	0
SF-539	114							34885	86	14022	2825	0	380	18293	0	252
HOP-62	113							19578	0	84830	1846	1198	808	7728	0	108
SF-295	112							40800	257	17808	700	708	1194	5388	417	637
A549/ATCC	111							47438	0	78738	1818	488	383	17919	1914	872
SF-268	110							30245	84	56487	972	185	75	13647	482	868
NCI-H522	109							44511	0	81828	985	813	278	8838	0	84
U251	108							94878	433	46758	573	124	718	17877	888	0
NCI-H460	107							38886	386	78178	438	405	803	17568	808	152
SNB-75	106							41104	0	17012	403	458	389	4782	884	316
NCI-H322M	105							48837	88	10250	3058	4822	461	28338	746	0
SNB-19	104							80854	442	13825	1417	451	2844	32854	136	625
NCI-H226	103							61887	833	9072	2208	1331	886	16328	743	68
SK-OV-3	102							33170	0	18886	3841	622	280	18881	343	61
NCI-H23	101							38481	0	5616	4702	140	203	28088	0	491
IGROV1	100							41888	442	11780	3881	229	303	11318	0	0
EKVX	99							28817	0	14573	1822	0	842	34177	0	0
OVCAR-5	98							31129	0	7825	48	101	197	8382	11	0
HOP-92	97							33000	0	18562	1074	386	488	12782	492	103
h fibroblasts 2/31/92 #12	46							32880	0	8173	1568	5270	341	481	200	186
h adult SMC 10/21/92 #17	47							30837	188	0	2166	0	150	0	883	127
h keratinocytes 3/25/92 #16	48							29428	86	23401	1117	0	82	10270	344	0
TCGP	38							22863	700	18108	7310	88	130	8277	1704	111
A549 - 1							wt	0	0	0	348	1138	4368	413	571	0
A549 - 3							wt	0	0	0	631	124	4678	538	1033	0
A549 - 4							wt	0	0	0	0	1294	7889	0	880	0
A549 - 5							wt	0	0	0	0	484	6086	143	0	0
A549 - 7							wt	0	0	0	0	813	8874	787	0	0
EKVX - 1							mutant	0	0	0	1340	3420	6820	475	2338	0
EKVX - 4							mutant	0	0	0	3088	4310	10881	330	180	0
EKVX - 3							mutant	0	0	0	1808	0	4881	0	705	0
EKVX - 5							mutant	0	0	0	284	1113	8887	137	0	0
EKVX - 7							mutant	0	0	0	0	[illegible]	7463	787	0	0
MCF-7 - 1							wt	[illegible]	[illegible]	[illegible]	463	[illegible]	110	344	155	0
MCF-7 - 3							wt	[illegible]	[illegible]	[illegible]	16	1868	3887	0	482	0
MCF-7 - 4							wt	0	0	0	876	927	3028	[illegible]	1360	0
MCF-7 - 6							wt	0	0	0	1191	[illegible]	4608	[illegible]	[illegible]	0
MCF-7 - 7							wt	0	0	0	0	588	433	887	629	0
ADR-RES - 1							mutant	0	0	0	0	3736	2782	4698	2888	0
ADR-RES - 3							mutant	0	0	0	1149	3462	4838	1886	0	0
ADR-RES - 4							mutant	0	0	0	112	0	2817	837	801	0
ADR-RES - 5							mutant	0	0	0	403	3308	862	0	0	0
ADR-RES - 7							mutant	0	0	0	2811	2986	1958	886	488	0
WI 38 - 1							wt	0	0	0	0	7788	3848	888	1831	0
WI 38 - 3							wt	0	0	0	886	6886	8259	197	0	0
WI 38 - 4							wt	0	0	0	1631	3008	8486	0	1503	0
WI 38 - 5							wt	0	0	0	1308	7877	3292	863	787	0
WI 38 - 7							wt	0	0	0	1486	3377	3828	312	0	0
HeLa - 1							HPV E6	0	0	0	880	0	1819	0	88	0
HeLa - 3							HPV E6	0	0	0	842	848	4257	848	0	0
HeLa - 4							HPV E6	0	0	0	258	281	8858	335	850	0
HeLa - 5							HPV E6	0	0	0	1177	1708	4044	1380	173	0
HeLa - 7							HPV E6	0	0	0	1943	274	4788	0	0	0
H1299 - 1							mutant	0	0	0	114	2886	2247	0	237	0
H1299 - 3							mutant	0	0	0	0	431	2212	842	846	0
H1299 - 4							mutant	0	0	0	287	122	4874	421	812	0
H1299 - 5							mutant	0	0	0	0	1438	2279	28	0	0
H1299 - 7							mutant	0	0	0	458	1863	1117	19	0	0
A549 - 2							wt	0	0	0	334	788	2812	286	834	0
EKVX - 2							mutant	0	0	0	1435	820	28773	0	0	0
HCT-116 - 1							wt	0	0	0	1136	330	6848	1848	298	0
HCT-116 - 2							wt	0	0	0	2980	2806	8284	149	811	0
HT29 - 2							mutant	0	0	0	1814	2541	1846	488	0	0
SF539 - 1							wt	0	0	0	313	2130	1819	0	847	0
SF539 - 2							wt	0	0	0	819	8447	744	780	179	0
SF-268-1							mutant	0	0	0	2143	3277	4430	835	0	0
SF-268-2							mutant	0	0	0	338	8072	4867	2856	1288	0
OVCAR-4 - 1							wt	0	0	0	1444	2283	19120	251	862	0
OVCAR-4 - 2							wt	0	0	0	0	1828	13774	409	441	0
OVCAR-5 - 1							mutant	0	0	0	1743	8653	2488	483	339	0
OVCAR-5 - 2							mutant	0	0	0	1288	3797	1735	635	0	0
MCF-7 - 2							wt	0	0	0	788	3082	0	288	0	0
ADR-RES - 2							mutant	0	0	0	778	1980	945	0	44	0
HeLa - 2							HPV E6	0	0	0	841	1919	8717	1522	0	0
SW480 - 1							mutant	0	0	0	438	1570	8813	1886	1823	0
SW480 - 2							mutant	0	0	0	1208	703	2887	0	4488	0
H1299 - 2							mutant	0	0	0	283	0	2816	1014	840	0
C33A - 1							mutant	0	0	0	205	4384	0	121	448	0
C33A - 2							mutant	0	0	0	804	1182	888	280	373	0
U2OS - 1							mutant	0	0	0	2846	7878	7873	853	3787	0
U2OS - 2							mutant	0	0	0	8100	11204	3330	1903	3826	0
[illegible] - 1							wt	0	0	0	1432	4881	6738	0	808	0
[illegible] - 2							wt	0	0	0	0	1983	2936	283	0	0
WI 38 - 2							wt	0	0	0	2585	8887	8771	442	12	0
[illegible] - 1								0	0	0	1158	3119	0	244	0	0
[illegible] - 2								0	0	0	4485	2081	0	406	0	0
[illegible] - 3								0	0	0	8429	11949	13408	0	1371	0
[illegible] - 4								0	0	0	8860	41855	4828	0	1837	0
[illegible] - 5								0	0	0	4620	2881	0	282	0	0
[illegible] - 6								0	0	0	1708	349	310	143	0	0
[illegible] - 8								0	0	0	3347	131	0	1175	119	0
[illegible] - 9								0	0	0	48	21722	273	603	0	0

Table 3 (cont'd)

Tissue	Tumor-syn	Normal-syn	Tumor - 3n	Tumor cells	Normal	Endos	p53	SEQ 17 AA	SEQ 25 SQ	SEQ 23 PT	SEQ 26 AA	SEQ 25 DR	SEQ 31 DR	SEQ 833 A	SEQ 40 MA	SEQ 844 T
DoPong-7								0	0	0	21884	8479	21386	2728	1224	0
DoPong-8								0	0	0	10085	8543	17854	1880	1078	0
DoPong-9								0	0	0	9122	1988	25873	1318	884	0
DoPong-11								0	0	0	7501	5218	14361	1857	888	0
DoPong-12								0	0	0	3497	3288	16748	1028	0	0
DoPong-10								0	0	0	6482	298	19429	311	210	0
DoPong-1								0	0	0	3941	17538	8787	832	17852	0
DoPong-2								0	0	0	3878	16380	6327	148	88825	0
DoPong-3								0	0	0	4794	2846	2782	3287	4773	0
DoPong-4								0	0	0	1944	4731	97	4214	903	0
DoPong-5								0	0	0	1170	2029	327	1917	2183	0
DoPong-6								0	0	0	12057	5246	0	2839	1453	0
A549-8							wt	0	0	0	0	1484	9852	0	427	0
EKVX-8							mutant	0	0	0	1873	2153	6486	588	17	0
HCT-116-7							wt	0	0	0	742	2307	3043	8498	619	0
HCT-116-8							wt	0	0	0	614	8117	2307	781	0	0
HT29-1							mutant	0	0	0	420	3088	3122	881	0	0
HT29-7							mutant	0	0	0	444	190	8	0	151	0
HT29-8							mutant	0	0	0	1091	2808	2178	0	1148	0
SF539-7							wt	0	0	0	0	8143	2843	1875	208	0
SF539-8							wt	0	0	0	88	10348	2922	882	0	0
SF-268-7							mutant	0	0	0	771	8881	2712	1138	1884	0
SF-268-8							mutant	0	0	[illegible]	1188	8034	4822	384	0	0
OVCAR-4-7							[illegible]	0	0	[illegible]	0	1284	8080	0	0	0
OVCAR-4-8							wt	0	0	0	[illegible]	2109	[illegible]	[illegible]	[illegible]	[illegible]
OVCAR-4-?							mutant	0	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
OVCAR-5-8							mutant	0	0	0	88	2853	1124	2083	0	0
MCF-7-8							wt	0	0	0	0	3539	1521	0	190	0
ADR-RES-8							mutant	0	0	0	495	672	3321	0	0	0
HeLa-8							HPV E6	0	0	0	1829	225	4795	1418	0	0
SW480-7							mutant	0	0	0	246	841	4842	0	1427	0
SW480-8							mutant	0	0	0	8	870	4328	0	1188	0
H1299-8							mutant	0	0	0	1485	4781	2495	298	49	0
C33A-7							mutant	0	0	0	0	3082	2719	1002	837	0
C33A-8							mutant	0	0	0	0	5883	451	885	0	0
U2OS-7							mutant	0	0	0	2235	4849	3018	877	1215	0
U2OS-8							mutant	0	0	0	31	4880	8016	0	0	0
Hs68-7							wt	0	0	0	1028	346	3165	144	0	0
Hs68-8							wt	0	0	0	1446	1183	3374	1882	0	0
WI 38-8							wt	0	0	0	1470	0	3574	0	455	0
458 module RNA								27888	0	4416	218	280	1447	6182	0	0
CRL 1572 2/17/99								25584	678	728	843	4685	27	579	18	58
Bov-4						84		88810	0	0	1087	3021	1952	0	338	0
HT368								22584	0	0	7887	21100	3573	29	0	301
HT376								37888	0	388	882	2880	8874	0	0	0
HT388								78812	0	0	14370	8858	1358	318	0	0
HT308								21782	851	0	0	33308	1103	185	873	574
Bov-3						173		38821	38	0	0	1954	1810	79	179	0
Bov-5						175		19800	0	0	0	311	80	0	771	18
Bov-9						177		38078	0	142	383	0	843	0	418	110
h keratinocytes 2/25/99 #10								80327	0	0	2040	586	48	0	1788	0
Bov-10						237		45182	287	0	245	733	3244	400	106	0
HT818								88248	0	0	1379	3383	0	0	0	0
h fibroblasts 3/31/99 #72								44374	88	0	0	4810	70	0	261	0
prostate, h								29036	7	0	0	5762	14	0	0	0
MNNG-OS poly A+								24878	238	1878	3882	3701	1721	1048	0	0
SA-OS (thyroid) poly A+								27087	0	0	10788	8681	674	0	0	0
MK poly A+								32124	0	281	13808	10417	478	1882	883	483
HCT-116-3							wt	0	0	0	11	1788	4484	297	24	0
HCT-116-4							wt	0	0	0	0	3319	7970	113	0	0
HCT-116-5							wt	0	0	0	1780	1880	3267	0	0	0
HCT-116-6							wt	0	0	0	588	2879	7818	287	248	0
A549-6							wt	0	0	0	0	2281	82	0	302	0
HT29-3							mutant	0	0	0	148	4824	7875	1143	813	0
EKVX-6							mutant	0	0	0	0	1948	2378	0	436	0
HT29-4							mutant	0	0	0	1238	323	3234	181	0	0
HT29-5							mutant	0	0	0	1070	[illegible]	3867	0	383	0
HT29-6							mutant	0	0	0	0	2080	[illegible]	800	0	3
OVCAR-4-?							[illegible]	[illegible]	0	[illegible]	1372	[illegible]	[illegible]	870	1955	0
OVCAR-4-?							[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
OVCAR-4-?							[illegible]	0	0	[illegible]	859	3034	[illegible]	1759	49	[illegible]
OVCAR-4-6							wt	0	0	[illegible]	[illegible]	10870	[illegible]	21	284	[illegible]
SF539-3							wt	0	0	0	1288	4103	1872	198	746	0
SF539-4							wt	0	0	0	0	1803	2226	0	188	0
SF539-5							wt	0	0	0	846	1292	2380	414	0	0
SF539-6							wt	0	0	0	888	8480	0	549	808	0
OVCAR-5-3							mutant	0	0	0	1847	8487	7120	0	111	0
OVCAR-5-4							mutant	0	0	0	0	2700	2418	28	400	0
OVCAR-5-6							mutant	0	0	0	236	388	1833	13	0	0
ADR-RES-6							mutant	0	0	0	638	2829	2287	433	0	0
MCF-7-6							wt	0	0	0	0	1884	2838	94	718	0
HeLa-6							HPV E6	0	0	0	1327	1884	4791	129	182	0
H1299-6							mutant	0	0	0	309	0	372	0	0	0
SW480-3							mutant	0	0	0	0	858	2500	283	2808	0
SW480-4							mutant	0	0	0	0	377	3879	882	1084	0
SW480-5							mutant	0	0	0	2318	1276	4398	380	14325	0
SW480-6							mutant	0	0	0	1702	1928	4538	80	1577	0
C33A-3							mutant	0	0	0	0	0	1983	0	298	0
C33A-4							mutant	0	0	0	72	778	451	0	808	0
C33A-5							mutant	0	0	0	0	5467	0	0	0	0
C33A-7							mutant	0	0	0	0	10	21372	0	0	0
Hs68-6							wt	0	0	0	578	41	8477	3651	284	0
U2OS-3							mutant	0	0	0	1439	11936	8821	10083	5193	0
U2OS-4							mutant	0	0	0	1189	6946	8884	1818	2083	0
U2OS-5							mutant	0	0	0	1794	6166	2888	0	2200	0
U2OS-6							mutant	0	0	0	606	17887	918	802	219	0
WI 38-6							wt	0	0	0	1929	2318	2946	388	0	0
Hs68-3							wt	0	0	0	2401	8497	7121	105	329	0
Hs68-4							wt	0	0	0	2780	6162	20868	1817	0	0
SF-268-3							mutant	0	0	0	1184	6180	8451	0	0	0
SF-268-4							mutant	0	0	0	1417	2882	4791	1874	22	0
SF-268-5							mutant	0	0	0	1835	3830	3241	0	0	0
SF-268-6							mutant	0	0	0	1814	4308	84	402	0	0
DoPong-13								0	0	0	8318	12563	12086	2259	8086	0
Mixed-20								0	0	0	4071	18817	12550	2887	7180	0
Mixed-21								0	0	0	3819	4867	7886	588	3387	0
Mixed-22								0	0	0	3863	3314	2830	7314	861	0
OVCAR-5-5							mutant	0	0	0	4583	8871	4413	380	2940	0
Mixed-10								0	0	0	3874	538	476	183	4383	0
Mixed-11								0	0	0	2320	0	12	305	4583	0
Mixed-12								0	0	0	1877	2762	1025	812	17008	0
Mixed-13								0	0	0	1770	11411	1191	2822	251	0
Mixed-14								0	0	0	3018	0	0	2028	61	0
Mixed-15								0	0	0	1200	12215	645	747	4238	0
Mixed-16								0	0	0	1737	882	4336	438	800	0
Mixed-17								0	0	0	2243	98	0	873	433	0
Mixed-18								0	0	0	2478	6886	4291	1120	502	0
Mixed-19								0	0	0	1954	12890	4413	653	1028	0

Table 3 (cont'd)

Tissue	Tumor-sym	Normal-sym	Tumor - ts	Tumor cells	Normal	Endos	p53	SEQ 844 T	SEQ 45 AA	SEQ 47 AA	SEQ 48 AA	SEQ 49 AA	SEQ 51 IO	SEQ 52 AA	SEQ 54 CO	SEQ 55 CL
adrenal gland - h		1						10624	0	205	168	7815	2253	1782	20262	37891
lymph node - h		2						2318	0	287	584	8674	7198	2170	7791	79790
bone marrow - h		3						1999	0	237	0	8863	3816	1381	1112	45217
mammary gland - h		4						441	0	0	0	2785	1143	280	0	3258
brain - h		5						4881	0	188	239	6436	608	887	11956	31129
pancreas - h		6						288	0	0	344	7076	3342	888	8722	44206
cerebellum - h		7						8698	0	70	0	7808	2836	3188	13788	85380
pituitary gland - h		8						10870	0	60	221	8528	6557	932	32295	38020
fetal brain - h		9						52140	0	237	89	7743	5814	3007	25437	47438
placenta - h		10						4424	0	51	87	8183	2380	2312	41080	35806
fetal kidney - h		11						2337	0	233	0	8334	8433	1376	30344	73806
prostate, h		12						2000	0	174	0	7873	3767	334	5551	21151
fetal liver - h		13						2876	0	110	160	6088	1682	810	4386	47110
salivary gl. - h		14						0	0	130	0	9806	3418	1128	5531	28823
fetal lung - h		15						8859	0	219	248	10713	6378	1758	20842	64752
skeletal muscle - h		16						32869	0	0	0	5706	1942	1180	2008	14612
heart - h		17						8442	0	18	181	8123	472	1022	2810	14787
small intestine - h		18						2779	0	16	144	7037	2865	443	4172	22380
kidney - h		19						0	0	181	225	8344	2082	781	7038	31845
spinal cord - h		20						0	0	136	0	8879	2866	568	1234	14331
liver - h		21						8348	0	0	0	4814	0	833	0	15780
Spleen - h		22						2383	0	0	188	8447	3308	631	987	19480
lung - h		23						2811	0	[illegible]	177	3868	[illegible]	673	3438	34017
stomach - h		24						[illegible]	[illegible]	[illegible]	0	2808	812	281	1243	17807
testis - h		25						[illegible]	[illegible]	[illegible]	408	9838	8251	[illegible]	321778	[illegible]
[illegible]		27						1202	0	47	23	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
HPAEC		28				28		388	0	0	35	8356	[illegible]	0	0	[illegible]
thyroid gland - h		29						806	0	158	0	8306	1800	552	8464	27800
RPTEC		30				30		188	0	19	98	4184	10744	84	0	8480
trachea - h		31						3411	0	79	0	8182	4182	1587	8588	34959
HMEC		32						0	0	33	188	4406	944	19	380	9798
uterus - h		33						2891	0	62	207	7257	7343	1386	7384	38540
HCAEC		34						194	0	28	70	5751	8835	219	881	4988
Pancreas - h		35						570	0	0	0	6208	0	0	17	21419
lymph node - h		36						1518	0	118	0	5373	20884	113	9807	25025
Skeletal muscle - h		37						389	0	14	0	3413	0	31	0	2243
fetal liver - h		38						8836	0	0	0	6881	9072	134	0	23891
Heart - h		39						988	0	17	30	4065	10804	4	0	2701
thymus, h		40						109	0	0	87	4633	8751	0	0	28458
Duodenum - h		41						92	0	0	0	3050	0	0	0	2973
Fetal brain - h		42						11823	0	0	0	9880	8204	145	0	18628
Salivary gl. - h		43						0	0	0	407	8511	1427	0	0	18266
testis - h		44						1732	0	27	63	7444	19662	115	12733	22783
HT218-normal					385			671	0	0	0	301	0	0	0	0
HT213-normal					383			0	0	0	0	285	0	22	0	482
HT152-normal					381			2188	0	0	47	1307	387	21	0	8462
Liv-13					356	356		5100	0	0	403	8850	2807	248	0	6825
Liv-12					354	354		6027	0	40	0	8406	346	316	330	2524
cerebellum - h					344			0	0	71	0	1962	487	88	388	6728
brain - h					342			0	0	0	0	1829	1179	0	288	7547
RPTEC					334	334		0	0	0	288	9040	117	0	0	0
lymph node - h					332			2714	0	0	0	4034	0	521	0	27818
h adult SMC 102182 P17					330			0	0	0	328	4482	0	87	0	591
Fetal brain - h					328			3625	0	250	10	7086	28	603	4350	19417
HT388-normal					327			0	0	118	176	4857	0	0	42	408
thymus, h					326			2912	0	0	200	5583	0	625	547	78037
HT140 - normal					321			348	0	0	0	3459	0	0	0	7102
HEPM 3d untreated					320			1442	0	0	0	3821	0	0	0	3857
uterus - h					318			2528	0	313	0	6330	8643	0	0	88984
trachea - h					316			1424	0	29	186	4057	2227	167	5861	22076
thyroid gland - h					314			3800	0	229	175	5272	443	383	5808	88638
salivary gl. - h					311			0	0	64	0	8080	810	27	0	17721
prostate, h					309			238	0	0	0	8486	708	0	0	11078
pituitary gland - h					307			0	0	0	370	3428	0	66	205	8806
pancreas - h					305			0	0	34	250	6133	2262	68	622	22026
mammary gland - h					303			3840	0	382	33	5370	4075	0	0	37185
bladder - h					302			1375	0	378	184	8051	1673	145	1017	7888
testis - h					299			8310	0	223	64	9808	12217	644	3187	37818
liver - h					297			3864	0	[illegible]	[illegible]	[illegible]	[illegible]	44	1270	[illegible]
Spleen - h					296			[illegible]	0	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
spinal cord - h					294			0	0	85	0	5311	[illegible]	304	843	[illegible]
small intestine - h					[illegible]			321	0	88	0	2812	[illegible]	77	13	15175
skeletal muscle - h					290			13803	0	205	0	5290	631	68	824	48825
bone marrow - h					279			0	0	88	338	8448	116	0	385	8531
adrenal gland - h					277			188	0	0	0	4734	1192	0	1346	18122
HPAEC					276	276		0	0	41	181	3704	674	83	0	0
HT380-normal					268			0	0	7	0	3582	242	348	0	6225
HT382-normal					266			1287	0	0	118	3680	303	94	474	11174
Ovy-11					239	239		0	0	180	0	7854	7082	0	1821	13792
Liv-9					235	235		80	0	194	0	4088	680	0	52	4582
HT372-normal					234			0	0	0	0	6158	642	888	0	3467
Liv-7					233	233		678	0	47	0	4896	0	0	0	5731
Liv-6					231	231		0	0	130	168	4138	2231	118	417	1492
Liv-2					229	229		0	0	80	198	3519	4888	152	0	6186
Liv-1					227	227		0	0	187	0	4156	717	0	0	4183
bladder - h					222			0	0	14	3	2450	0	83	0	6858
Heart - h					219			18777	0	0	134	9047	0	0	454	12723
stomach - h					214			1488	0	41	143	6036	1880	0	138	33040
fetal liver - h					213			0	0	30	78	3033	0	133	0	12807
placenta - h					212			1246	0	0	77	8011	1804	156	77	19098
HCAEC					211	211		107	0	0	0	5206	241	0	0	640
fetal brain - h					210			4482	0	173	0	5800	4194	160	681	18585
HMEC					209			38	0	11	0	2834	3235	38	586	316
Duodenum - h					205			5184	0	0	132	4247	0	0	0	3834
Skeletal muscle - h					203			1310	0	0	0	2630	0	118	0	278
Pancreas - h					201			752	0	29	0	3178	308	0	0	4186
testis - h					199			208	0	15	0	2838	0	20	0	12308
Salivary gl. - h					197			198	0	15	0	2207	19730	82	4298	23443
HEPM 3d TGFB1 [illegible]					196			0	0	44	0	1387	174	82	23	1613
thymus - h					193			118	0	23	0	3008	866	77	0	34871
WI-38 72h					179			0	0	0	0	1150	0	0	480	70
lymph node - h					91			0	0	0	88	3830	855	0	0	9800
lung - h					88			1428	0	0	0	7882	1000	0	0	28022
kidney - h					87			585	0	0	0	4677	2940	74	388	22338
heart - h					86			242	0	64	0	3084	247	78	0	8323
fetal lung - h					53			0	0	0	0	1718	142	0	837	410
fetal liver - h					51			174	0	22	242	2821	381	0	187	7087
fetal kidney - h					49			0	0	97	0	3083	2158	0	91	12023
HELA-2h-031800				79				0	0	0	70	4570	828	0	0	37510
HELA-4h-031800				81				0	0	82	2288	4853	257	0	21	3414
HELA-6h-031800				83				143	0	48	0	6886	4897	0	200	1978
HELA-8h-031800				86				686	0	38	0	3814	0	0	237	8884
HELA-8h-031800				88				298	0	0	383	7318	835	0	0	3846
HELA-9h-031800				90				0	0	183	0	8793	707	683	0	8370
HELA-10h-031800				92				53	0	70	52	8402	731	43	0	28215
HELA-11h-031800				94				485	0	0	0	6867	0	239	0	1053
HELA-12h-031800				96				1638	0	88	0	4358	4121	72	0	1788
NCI-H226				146				88	0	0	0	3197	679	0	5273	6625
NCI-H460				148				22	0	0	153	2184	80	143	1738	435
NCI-H522				150				0	0	38	0	1947	1863	194	798	2447
SNB-19				152				3872	0	0	347	2204	0	343	3370	2828
SNB-75				154				888	0	0	0	3823	1180	0	6086	5502
SF-268				156				0	0	42	247	1822	0	0	798	1022
SF-295				158				0	0	42	578	846	0	638	1114	0
CCRF-CEM				160				0	0	82	148	1729	1178	0	0	231
DU-145				162				0	0	43	0	1822	317	233	1036	1840
HCT 116				164				12084	0	0	0	1344	0	153	1606	4084

Table 3 (cont'd)

Tissue	Tumor-sym	Normal-sym	Tumor - 1o	Tumor cells	Normal	Endo	p53	SEQ 844 T	SEQ 46 AA	SEQ 47 AA	SEQ 48 AA	SEQ 49 AA	SEQ 51 KIA	SEQ 52 AA	SEQ 54 CC	SEQ 55 CL
Caki-1				169				0	0	47	88	4012	0	984	258	8449
786-0				168				4917	0	0	812	7988	46	0	21583	20885
T-47D				169				0	0	70	212	4498	73	295	6531	7187
Kan-3				171				0	0	0	75	1846	278	0	0	261
CRL 1441 RNA 8/30				181				0	0	0	682	1398	120	383	192	0
7811 untreated + DNase				183				0	0	31	0	867	0	1	212	418
KB poly A+				194				0	0	0	135	1653	24	52	211	7891
HOS poly A+				196				282	0	48	0	2437	0	84	84	3781
ACHN				198				0	0	0	0	2832	208	171	8142	2184
UACC-62				200				385	0	38	131	1288	0	0	1277	1373
MCF-7/ADR-RES				202				0	0	36	0	1357	700	0	1430	1020
UTOS (Mandy) poly a+				204				0	0	171	22	0	0	0	0	8430
WI38 (Collagen) poly A+				206				0	0	0	0	742	843	44	42	1191
458 medulla mRNA				208				6841	0	0	0	7137	0	0	0	8852
CCL137 RNA 3/21/88				218				0	0	80	141	1194	3	100	0	827
WI-38 72h 0.5%FBS, 24h 10% FBS				219				0	0	0	0	2130	0	77	0	882
CRL1441 + TPA (24h) 8/30				220				0	0	0	224	985	93	0	0	0
Kan-1				221				688	0	0	16	1572	0	0	0	1267
Kan-2				222				0	0	0	0	2235	330	85	0	1881
Kan-4				225				738	0	172	0	2728	0	0	0	1331
HOP-62				241				128	0	0	0	1124	372	0	0	1758
MOLT-4				242				1229	0	0	0	4198	1258	0	2452	8189
[illegible]				243				984	0	0	[illegible]	2740	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]				244				3	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	814	[illegible]	[illegible]
[illegible]				245				727	0	[illegible]	[illegible]	[illegible]	[illegible]	321	2362	6938
RPMI 8226				246				2	0	84	413	2887	[illegible]	[illegible]	0	[illegible]
A549/ATCC				247				0	0	86	0	2858	0	0	0	[illegible]
SR				248				0	0	0	0	2108	1910	33	281	2208
OVCAR-3				249				0	0	17	287	2491	0	48	183	644
HCT-15				250				1042	0	0	82	4088	1587	283	648	13641
OVCAR-4				251				83	0	83	15	562	0	7	880	847
UO-31				252				347	0	0	86	814	0	0	463	1847
OVCAR-5				253				0	0	89	722	6152	0	362	4788	6832
SN12C				254				811	0	0	0	3564	2301	0	10456	8668
OVCAR-8				255				322	0	0	13	2581	872	0	2102	1742
LOX IMVI				256				0	0	77	343	8201	4888	283	2850	8100
IGROV1				257				884	0	84	0	3888	571	3	2367	3837
SK-MEL-2				258				0	0	115	0	2345	401	338	1374	2004
SK-OV-3				259				0	0	0	0	1198	0	184	1499	1437
SK-MEL-5				260				0	0	0	472	1328	198	0	198	1488
SF-539				261				1273	0	188	458	8873	2291	0	7414	2088
SK-MEL-28				262				867	0	0	0	3780	861	0	2858	2083
K-562				263				187	0	86	31	8148	4328	218	2537	1782
UACC-257				264				888	0	0	0	2881	0	42	0	1288
M14				266				0	0	74	0	877	151	181	0	1458
MCF7				267				3828	0	0	28	8238	0	0	17404	29882
MDA-MB-435				268				0	0	88	227	1824	0	0	744	1343
HT279				270				1743	0	0	0	1668	2583	67	0	2884
MDA-N				271				0	0	17	0	4127	0	283	1252	2025
179 poly A+				272				8085	0	137	0	7232	1880	43	858	18372
10406 poly A+				286				2788	0	18	288	3285	32	284	879	8284
HT838 24h TPA RNA 8/23				288				0	0	18	0	2952	646	171	88	8878
HELA-EXP-031888				313				0	0	19	48	2177	645	24	0	10840
HT838 8h RNA				322				838	0	0	198	4184	806	428	773	4214
HT267				323				447	0	0	0	2448	3872	0	188	88352
458 medulla RNA				324				2289	0	16	0	2484	0	11	781	1101
NCI-H226				336				0	0	0	38	2886	0	100	0	1148
HOP-92				337				0	0	0	357	3132	301	181	5222	2879
MDA-MB-231				338				7880	0	22	0	8113	4666	0	8564	28831
U251				339				18348	0	68	0	11880	18318	202	141803	38708
PT cells poly A+				340				0	0	0	0	1888	0	0	2491	2808
PC-3				341				0	0	0	227	3870	708	83	884	818
HCC-2998				343				31	0	0	0	2188	0	138	0	1370
SW-620				345				0	0	72	83	2072	0	108	18	0
HT182				346				578	0	80	23	4300	808	0	3475	18731
COLO 205				347				0	0	28	45	703	688	0	0	0
HT218				348				4211	0	0	0	1703	0	0	0	1055
KM-12				349				0	0	44	137	1724	842	102	0	1138
HT[illegible]				[illegible]				0	0	30	202	3787	[illegible]	288	0	[illegible]
[illegible]				[illegible]				[illegible]	[illegible]	0	[illegible]	[illegible]	0	[illegible]	[illegible]	[illegible]
HT[illegible]				[illegible]				185	0	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	0	[illegible]
RXF 393				[illegible]				0	0	[illegible]	0	[illegible]	0	0	[illegible]	[illegible]
TK-10				356				5344	0	0	0	7888	2228	0	3006	[illegible]
Malme-3M				357				2846	0	0	0	26180	16870	313	37531	7453
Hs 578T				358				0	0	0	0	1888	0	0	588	1108
HT213			50					0	0	162	0	18822	1275	37	0	4385
HT208			52					195	0	187	0	8482	437	0	429	48848
HT138			54					0	0	0	31	3341	0	0	0	2708
HT136			56					0	0	114	0	3081	0	0	0	12178
HT163			58					337	0	35	28	3236	938	0	0	248
HT170			60					0	0	28	0	8032	0	0	0	12850
HT172			62					0	0	6	0	4071	0	84	104	2203
HT138			63					1382	0	0	0	3571	121	0	0	28749
HT178			64					0	0	0	201	3034	0	0	0	2801
HT134			65					1835	0	0	0	8175	1983	0	0	1773
HT160			66					0	0	73	0	4848	0	0	0	2834
HT168			67					0	0	0	8	884	24	45	283	1388
HT169			68					0	0	28	5	4352	0	440	0	3848
HT163			69					3	0	0	1176	3324	0	57	0	888
HT190			70					2888	0	81	0	4240	876	190	834	4448
HT145			71					280	0	0	0	6818	0	0	0	3886
HT227			72					0	0	20	114	4036	0	0	0	4727
HT262			73					430	0	0	133	8415	57	32	419	8464
HT214			74					429	0	0	0	4709	6214	0	0	5802
HT317			76					543	0	27	0	8318	2871	0	0	20250
[illegible] 8/25 118			77					285	0	33	328	3198	575	220	287	2212
HT323			78					88	0	110	0	5528	3804	197	0	5220
HT327			80					0	0	128	0	3771	1778	80	14	2370
HT335			82					0	0	71	0	4488	11873	0	422	17130
HT146			86					432	0	120	0	1141	0	419	0	388
HT348			87					0	0	0	0	5314	18455	0	304	21360
HT311			170					388	0	38	0	3141	4853	255	0	5243
HT388			185					0	0	188	0	3280	0	228	0	3488
HT149			187					0	0	0	0	612	0	0	0	308
HT291			188					0	0	244	0	2857	1134	0	0	847
HT372			191					0	0	88	342	3358	203	347	0	451
TCOP			207					0	0	0	212	3836	484	0	611	1517
HT180			216					131	0	0	0	891	0	202	428	2230
HT307			217					0	0	115	0	1315	0	0	0	4418
HT388			224					0	0	45	15	3538	0	50	827	3308
HT370			226					1627	0	22	0	2962	44	134	844	11808
HT371			228					0	0	58	27	4211	0	0	291	9810
HT377			230					486	0	23	0	3752	779	282	0	16806
HT382			234					288	0	28	0	3820	408	0	827	7888
[illegible] RNA			281					0	0	0	887	0	0	0	0	0
HT304			289					0	0	32	0	4472	0	0	0	33816
HT308			301					0	0	0	3	3010	0	202	0	6382
HT382			316					844	0	0	71	2188	0	0	0	2810
HT384			317					0	0	0	102	2127	10712	3	0	9879
HT312			319					2877	0	0	108	2304	65	0	80	9812
HT192			325					0	0	18	0	1411	0	193	0	0
HT388			328					0	0	0	0	5212	295	0	182	4313
HT157			392					795	0	5	336	3318	426	0	374	12146
T-47D	163							810	0	0	0	4107	304	253	18636	9108
MDA-N	161							228	0	48	0	4886	0	338	132888	7874
MDA-MB-435	160							1148	0	58	130	5380	618	808	74636	8480
MDA-MB-231	157							3004	0	0	103	4223	381	200	141	8801

Table 3 (cont'd)

Tissue	Tumor-cyto	Normal-cyto	Tumor - fa	Tumor cells	Normal	Endo	p53	SEQ 44 T	SEQ 45 AA	SEQ 47 AA	SEQ 48 AA	SEQ 49 AA	SEQ 51 AA	SEQ 52 AA	SEQ 54 CO	SEQ 55 CL
Hs 578T	155							4159	0	84	0	4775	0	670	1536	18385
MCF-7/ADR-RES	153							0	0	0	186	3752	0	110	1947	4808
MCF7	151							3033	0	181	0	7051	0	1602	0	27225
M14	149							0	0	150	0	3887	1661	802	0	8825
UACC-257	147							0	0	0	0	6335	566	0	813	14836
UACC-62	145							0	0	47	45	3386	319	84	1253	4501
SK-MEL-28	144							865	0	181	0	4238	190	22	86	8388
UO-31	143							755	0	0	0	6134	1814	428	0	8086
SK-MEL-5	142							808	0	14	0	4782	879	464	1913	6211
KM-12	141							1860	0	8	29	3860	238	437	868	1798
SK-MEL-2	140							0	0	4	0	3883	380	177	1547	18358
HCT-15	139							0	0	6	0	6167	0	386	370	16881
Malme-3M	138							1858	0	0	0	4847	23	311	1087	6770
COLO 205	137							2153	0	222	336	5649	0	0	0	6236
LOX IMVI	136							6438	0	0	181	3835	886	93	0	11410
SW-620	135							1038	0	37	0	3684	1187	384	858	3488
TK-10	134							1885	0	0	18	3828	1883	344	885	11184
HCT 116	133							519	0	107	104	3883	1088	193	0	4867
786-0	132							2701	0	7	118	3530	0	370	374	8085
HCC-2998	131							1371	0	0	0	6532	767	281	770	2945
ACHN	130							0	0	0	184	4886	827	102	880	8837
PC-3	129							0	0	0	0	3888	819	250	248	9808
[illegible]	[illegible]							3345	0	11	212	3357	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	127							456	0	8	43	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	126							0	0	[illegible]	[illegible]	[illegible]	[illegible]	289	[illegible]	7762
DR	125							1045	0	2	0	3578	0	0	629	7913
A498	124							2388	0	126	305	4481	0	732	4011	12181
RPMI 8226	123							0	0	0	84	3852	1414	102	8477	5880
SN12C	122							0	0	0	288	4346	1762	358	1148	10454
HL-60	121							0	0	0	144	3536	0	203	0	7486
MOLT-4	120							594	0	24	0	3217	850	83	3283	4867
OVCAR-5	119							576	0	96	38	4828	0	65	4365	7988
K-562	118							0	0	0	0	7270	0	372	2107	2843
OVCAR-4	117							1705	0	0	0	8408	2352	302	4352	12834
CCRF-CEM	116							818	0	70	0	3841	180	1813	862	14584
OVCAR-3	115							2336	0	88	0	3837	0	188	281	5028
SF-539	114							861	0	2	0	3003	843	0	183	4037
HOP-62	113							577	0	0	188	3830	208	25	811	14232
SF-295	112							678	0	0	210	8431	2146	387	1058	18818
A549/ATCC	111							1174	0	0	193	8431	1777	654	1208	11838
SF-268	110							863	0	0	112	2861	432	102	1883	5808
NCI-H522	109							0	0	21	0	8381	1871	403	863	8165
U251	108							1887	0	0	474	4637	880	331	1216	7834
NCI-H460	107							294	0	221	41	4688	651	345	0	8432
SNB-75	106							863	0	76	3	2867	633	308	0	1015
NCI-H322M	105							0	0	0	28	2880	134	348	0	8885
SNB-19	104							28	0	63	0	2171	1878	481	2088	4580
NCI-H226	103							4486	0	19	0	7057	1991	244	1819	7164
SK-OV-3	102							842	0	58	0	3732	2018	625	0	11044
NCI-H23	101							200	0	142	0	3780	1388	492	1790	6447
IGROV1	100							0	0	0	0	4188	1818	788	0	4586
EKVX	99							783	0	14	187	3052	0	443	38	8847
OVCAR-8	98							0	0	72	285	3056	79	46	151	2451
HOP-62	97							0	0	8	108	3868	1347	54	446	4634
h fibroblasts 3/31/82 #12	48							1168	0	123	0	3077	1635	88	1336	2846
h adult SMC 10/21/82 #17	47							2236	0	112	0	4184	0	86	742	4832
h keratinocytes 2/25/82 #10	46							1043	0	0	328	3112	734	276	0	2214
TCGP	28							0	0	115	0	3382	7036	256	311870	3115
A549 - 1							wt	487	48	37	0	0	0	0	0	0
A549 - 3							wt	317	106	0	0	0	0	0	0	0
A549 - 4							wt	0	28	153	0	0	0	0	0	0
A549 - 5							wt	321	109	62	0	0	0	0	0	0
A549 - 7							wt	0	236	48	0	0	0	0	0	0
EKVX - 1							mutant	5881	2136	285	0	0	0	0	0	0
EKVX - 4							mutant	2147	841	0	0	0	0	0	0	0
EKVX - 3							mutant	2885	0	480	0	0	0	0	0	0
EKVX - 5							mutant	1030	0	0	0	0	0	0	0	0
EKVX - 7							mutant	0	1073	0	0	0	0	0	0	0
MCF-7 - 1							wt	0	0	0	0	0	0	0	0	0
MCF-7 - 3							wt	403	6	46	0	0	0	0	0	0
MCF-7 - 4							wt	150	[illegible]	115	0	0	0	0	0	0
MCF-7 - 6							wt	3134	0	0	0	0	0	0	0	0
MCF-7 - 7							wt	840	0	0	0	0	0	0	0	0
ADR-RES - 1							mutant	0	1818	135	0	0	0	0	0	0
ADR-RES - 3							mutant	30834	0	290	0	0	0	0	0	0
ADR-RES - 4							mutant	4757	279	308	0	0	0	0	0	0
ADR-RES - 6							mutant	536	872	84	0	0	0	0	0	0
ADR-RES - 7							mutant	748	281	11	0	0	0	0	0	0
WI 38 - 1							wt	2519	84	176	0	0	0	0	0	0
WI 38 - 3							wt	1880	0	30	0	0	0	0	0	0
WI 38 - 4							wt	0	0	0	0	0	0	0	0	0
WI 38 - 6							wt	3088	0	37	0	0	0	0	0	0
WI 38 - 7							wt	812	0	43	0	0	0	0	0	0
HeLa - 1							HPV E6	0	385	7	0	0	0	0	0	0
HeLa - 3							HPV E6	852	0	38	0	0	0	0	0	0
HeLa - 4							HPV E6	848	0	115	0	0	0	0	0	0
HeLa - 6							HPV E6	2847	388	172	0	0	0	0	0	0
HeLa - 7							HPV E6	429	880	7	0	0	0	0	0	0
H1299 - 1							mutant	0	0	27	0	0	0	0	0	0
H1299 - 3							mutant	1149	0	193	0	0	0	0	0	0
H1299 - 4							mutant	1155	0	36	0	0	0	0	0	0
H1299 - 6							mutant	819	63	106	0	0	0	0	0	0
H1299 - 7							mutant	0	0	71	0	0	0	0	0	0
A549 - 2							wt	781	281	208	0	0	0	0	0	0
EKVX - 2							mutant	21741	2830	208	0	0	0	0	0	0
HCT-116 - 1							wt	848	0	208	0	0	0	0	0	0
HCT-116 - 2							wt	8208	882	436	0	0	0	0	0	0
HT29 - 2							mutant	407	256	86	0	0	0	0	0	0
SF539 - 1							wt	1107	281	0	0	0	0	0	0	0
SF539 - 2							wt	533	202	71	0	0	0	0	0	0
SF-268-1							mutant	5794	164	138	0	0	0	0	0	0
SF-268-2							mutant	11614	4311	203	0	0	0	0	0	0
OVCAR-4 - 1							wt	3888	781	0	0	0	0	0	0	0
OVCAR-4 - 2								0	0	0	0	0	0	0	0	0
OVCAR-5 - 1							mutant	705	0	0	0	0	0	0	0	0
OVCAR-5 - 2							mutant	367	448	0	0	0	0	0	0	0
MCF-7 - 2							wt	2184	0	43	0	0	0	0	0	0
ADR-RES - 2							mutant	418	747	83	0	0	0	0	0	0
HeLa - 2							HPV E6	2741	0	83	0	0	0	0	0	0
SW480 - 1							mutant	883	1079	308	0	0	0	0	0	0
SW480 - 2							mutant	813	718	80	0	0	0	0	0	0
H1299 - 2							mutant	322	871	0	0	0	0	0	0	0
C33A - 1							mutant	318	0	57	0	0	0	0	0	0
C33A - 2							mutant	8488	0	75	0	0	0	0	0	0
U2OS - 1							mutant	3301	1141	0	0	0	0	0	0	0
U2OS - 2							mutant	3542	1266	0	0	0	0	0	0	0
HepG2 - 1							wt	2216	164	46	0	0	0	0	0	0
HepG2 - 2							wt	4302	734	18	0	0	0	0	0	0
WI 38 - 2							wt	0	831	21	0	0	0	0	0	0
Mixed - 1								513	0	72	0	0	0	0	0	0
Mixed - 2								310	0	2786	0	0	0	0	0	0
Mixed - 3								88334	0	0	0	0	0	0	0	0
Mixed - 4								84782	808	0	0	0	0	0	0	0
Mixed - 5								8018	0	0	0	0	0	0	0	0
Mixed - 6								8086	728	311	0	0	0	0	0	0
Mixed - 8								2854	0	37	0	0	0	0	0	0
Mixed - 9								2088	0	8	0	0	0	0	0	0

Table 3 (cont'd)

Tissue	Tumor-cyto	Normal-cyto	Tumor - fn	Tumor cells	Normal	Endos	p53	SEQ 30 AA	SEQ 37 W	SEQ 68 AA	SEQ 83 NE	SEQ 86 CA	SEQ 68 NH	SEQ 110 R	SEQ 73 NR	SEQ 78 AA
Caki-1				185				865	4675	157	1036	972	1529	1954	17285	29406
786-0				190				533	8526	227	878	272	8856	5304	82251	93576
T-47D				206				8605	8618	0	1074	352	880	2801	19722	38601
Ken-3				171				0	1853	0	234	13	137	1787	138	37872
CRL 1441 RNA 8/30				181				278	3104	0	24	0	0	1858	0	13078
791T untreated + DMem				193				197	1800	0	82	0	0	843	230	14562
KB poly A+				194				0	8084	0	108	0	1488	1818	808	31810
HOS poly A+				196				287	3265	8277	0	0	828	2815	868	52776
ACHN				198				0	6583	0	358	0	1158	4807	14597	28142
UACC-62				200				1482	9883	0	212	0	475	2225	2825	17274
MCF-7/ADR-RES				202				185	2228	756	0	11	281	1444	2582	14607
UTOS (blank) poly A+				204				0	7812	0	104	0	0	1038	617	9807
WISH (Collagen) poly A+				208				190	0	0	84	188	883	679	725	11442
K58 medulla mRNA				209				0	18176	0	623	83	0	2382	2915	60583
CCL 137 RNA 3/21/88				218				219	1868	0	208	0	281	1447	916	23844
WI-38 72h 0.5%FBS, 24h 10% FBS				216				271	3187	1190	0	34	403	2260	0	41474
CRL 1441 + TPA (24h) 8/30				220				0	6582	0	31	683	0	1086	63	18180
Ken-1				221				2280	2513	0	0	0	453	2919	158	45286
Ken-2				223				705	2806	0	118	0	302	2129	41	41277
Ken-4				225				521	4048	0	31	0	1303	2242	88	30345
HOP-62				241				0	2382	0	218	0	87	1773	13338	18884
MOLT-4				242				846	6384	782	483	481	3828	3182	38413	23872
EKVX				243				0	13083	0	328	73	3130	6482	108714	30253
HL-60				244				0	14211	886	23	431	2402	[illegible]	[illegible]	[illegible]
CCRF-CEM				245				[illegible]	13057	572	2041	167	[illegible]	6334	[illegible]	[illegible]
RPMI 8226				246				0	1353	488	173	0	[illegible]	2272	18378	20888
A549/ATCC				247				88	3450	0	819	384	881	1991	2386	18871
SR				248				0	1814	383	0	23	344	2887	10201	17287
OVCAR-3				249				0	7397	0	214	120	1028	2424	7704	20878
HCT-15				250				0	18765	598	1456	0	3628	4642	106630	27662
OVCAR-4				251				223	314	1330	0	188	473	805	1481	7813
UO-31				252				372	3404	0	0	0	143	547	1109	6008
OVCAR-5				253				2586	8638	1811	825	62	1738	3348	12208	24804
SN12C				254				0	6112	504	178	188	3326	2875	26805	18317
OVCAR-8				255				0	3608	888	733	0	1122	1350	25633	14140
LOX IMVI				256				622	17298	405	606	61	8803	5283	30147	38648
IGROV1				257				1194	8362	756	715	88	2832	3844	28834	31764
SK-MEL-2				258				0	5305	0	19	0	0	853	4882	15816
SK-OV-3				259				85	3527	0	200	0	1880	3782	8318	17004
SK-MEL-5				260				135	3811	0	48	103	1340	1148	3811	13562
BT-549				261				2652	12225	0	884	180	7673	6550	62279	81606
SK-MEL-28				262				0	7037	0	384	0	1713	1981	8611	34907
K-562				263				867	8300	1849	1686	98	8058	4576	195684	61730
UACC-257				264				0	6275	0	408	0	1580	2388	3498	25085
M14				265				0	2838	0	0	214	984	916	1179	17725
MCF7				267				829	18845	820	888	804	4888	6719	78777	80830
MDA-MB-435				268				144	8376	477	543	0	958	1857	1149	28187
HT270				270				14	4480	0	0	0	891	2525	281	41481
MDA-N				271				276	7085	0	354	82	1298	1838	5866	18606
Y79 poly A+				273				0	6884	0	378	0	3785	6025	24854	77861
SOHOS poly A+				286				0	20759	17445	271	226	6786	4275	38086	78861
HT1080 24h TPA RNA 8/23				309				783	3881	0	1458	0	2298	2482	221	31917
HELA-EXP-8/31/88				313				634	1812	0	247	0	1380	2848	4181	38714
HT1080 0h RNA				322				1461	24464	0	0	886	2512	8180	3044	81484
HT347				323				404	4646	0	0	0	2808	3484	15822	40401
468 medulla RNA				324				1327	40673	0	0	248	880	4386	476	68088
NCI-H226				336				672	6161	721	345	0	1815	2111	2329	37119
HOP-62				337				0	15388	0	808	78	2808	1717	38488	21036
MDA-MB-231				338				1106	69815	1217	8728	1217	23352	13718	208035	103178
U251				339				132	90374	1171	18298	382	76764	33880	2025348	111922
PT cells poly A+				340				483	1482	0	467	0	1987	2005	45052	16298
PC-3				341				177	13679	62	382	2330	6703	6884	40354	71886
HCC-2998				343				82	8308	0	852	988	1782	2288	23873	21576
SW-620				345				25	7776	0	621	200	1251	2048	10731	24715
HT192				346				1001	7290	408	182	0	1412	5254	2082	65025
COLO 205				347				182	8047	0	308	8	0	688	1304	8815
HT219				348				448	4819	0	77	158	0	1385	381	28848
KM-12				349				49	17062	0	408	0	881	1115	34840	17488
HT161				[illegible]				138	[illegible]	[illegible]	0	0	773	3737	497	45600
A430				351				757	[illegible]	0	[illegible]	1544	[illegible]	2826	4743	30375
HT380				352				728	18335	[illegible]	0	0	[illegible]	[illegible]	[illegible]	[illegible]
PDF 283				353				0	8872	0	114	73	[illegible]	2729	724	34306
TK-10				355				736	78806	884	3780	1673	23030	12524	128790	71862
Malme-3M				357				2111	83276	13887	38286	2444	58479	34872	201421	150808
Hs 578T				359				0	9184	0	68	82	2381	2875	8581	46882
HT213			50					0	6740	47	0	0	878	1700	28	57671
HT240			52					179	8087	0	0	272	783	2581	7941	84143
HT130			54					821	8343	0	4	635	0	1806	276	65037
HT155			56					0	6880	0	281	632	2394	2121	2121	61017
HT165			58					1082	1302	384	0	253	281	1598	940	81343
HT170			60					37	19871	0	252	0	1862	4224	13427	83008
HT172			62					0	3376	0	0	17	384	975	0	46345
HT182			63					0	2621	0	0	43	797	1070	4034	45881
HT176			64					31	3165	0	0	145	348	974	800	51453
HT184			65					0	1277	2364	0	44	308	1138	0	62719
HT188			66					276	2607	0	82	0	862	865	197	43129
HT186			67					427	4848	0	0	229	289	655	1238	39880
HT189			68					69	4866	388	122	0	348	1043	3308	79481
HT143			69					2087	348	0	0	0	181	828	42	39405
HT190			70					0	6719	864	68	0	0	1654	0	66009
HT145			71					1653	3381	530	0	74	3262	1933	230	66667
HT227			72					0	8796	0	83	183	2486	1828	257	65948
HT362			73					0	19129	0	439	112	0	2881	685	84881
HT314			74					0	10943	138	0	41	279	1796	1196	81087
HT317			76					275	25780	0	2002	651	69	6151	5403	160831
Metastatic tumor HT25_11B			77					0	3181	0	128	250	0	3011	815	69844
HT327			78					0	7807	0	1120	58	335	3764	1841	107547
HT322			80					224	3260	0	267	41	834	1737	888	52009
HT226			83					0	7044	112	1	201	2486	2234	812	70437
HT149			86					2887	780	545	143	0	898	5900	881	32152
HT248			87					2360	6064	1312	380	203	3888	1570	2273	46848
HT211			170					1602	2027	0	0	0	806	3081	1136	57169
HT249			185					2942	11424	803	258	0	0	1958	814	31322
HT149			187					0	2198	0	317	70	864	1607	0	19444
HT261			188					0	7338	0	37	0	0	1916	0	41150
HT372			191					841	2888	0	130	104	0	1932	708	88862
TCGP			207					186	2445	0	114	33	130	1578	0	18184
HT160			216					0	1880	383	0	107	740	937	0	36841
HT367			217					0	3179	0	0	210	1083	1057	731	21628
HT300			224					0	12133	0	125	177	858	2374	878	40414
HT376			226					64	2885	0	0	180	1017	1958	0	27470
HT379			228					887	4802	0	0	0	1523	2322	1348	34933
HT377			230					0	3361	0	58	0	884	1678	443	25063
HT362			238					116	8719	818	0	0	3205	2838	1824	43216
normal lung RNA			281					0	19149	0	0	298	186	683	0	5483
HT334			289					0	20876	0	859	0	6867	8479	14342	67294
HT338			301					130	13101	313	0	0	880	2548	2000	34862
HT382			315					48	4833	0	0	48	1318	1461	8518	30163
HT384			317					1372	6204	188	248	21	1008	2951	11844	48292
HT312			319					278	3848	0	5847	0	880	2685	0	35234
HT162			325					357	2817	0	308	0	0	1241	866	22977
HT386			354					853	9137	0	0	0	1105	2121	3677	60581
HT157			360					0	10089	0	21	0	4816	4803	1407	140477
T-47D	183							2806	38724	847	1579	2021	6844	1538	13780	45383
MDA-N	181							1387	29148	1829	1361	6882	17212	1168	8784	36475
MDA-MB-435	159							847	17867	3441	2565	5842	17246	1815	13088	33644
MDA-MB-231	157							878	80840	2818	2248	1727	42150	2891	10358	68885

Table 3 (cont'd)

Tissue	Tumor-sym	Normal-sym	Tumor - fx	Tumor cells	Normal	Endos	p53	SEQ 36 AA	SEQ 37 W	SEQ 38 AA	SEQ 63 NE	SEQ 66 CA	SEQ 68 HM	SEQ 110 R	SEQ 73 HR	SEQ 79 AA
Hs 578T	155							0	41445	847	1886	3442	20751	2987	8385	65874
MCF-7/ADR-RES	153							2256	18577	3382	2919	488	22338	1868	3882	84013
MCF7	151							3886	38688	168	1808	2944	11888	3495	22510	81798
M14	149							778	16702	0	704	437	6271	3880	4821	88408
UACC-257	147							908	14878	9934	7209	193	8907	2195	17873	61725
UACC-62	145							808	9415	0	2145	8	8453	1388	4231	41288
SK-MEL-28	144							48	12812	4856	577	770	5176	1071	2980	58831
UO-31	143							448	8850	1716	638	88	14005	2232	3834	105891
SK-MEL-5	142							1182	27382	1884	1844	2808	13115	1215	8595	42911
KM-12	141							325	6737	9512	104	0	1881	1317	64	48588
SK-MEL-2	140							1987	14488	3221	795	1827	7348	1576	7479	82671
HCT-15	139							740	12279	771	857	808	4827	2087	7421	71190
Malme-3M	138							1725	28340	2546	2881	2863	10072	2038	7321	42587
COLO 205	137							2884	9100	2786	438	1948	12401	1681	2407	88313
LOX IMVI	136							303	37237	202	3101	4339	32433	882	8061	33734
SW-620	135							838	6811	0	1807	1808	18151	1195	2788	28388
TK-10	134							646	8427	1317	1508	1082	23888	1771	11381	42220
HCT 116	133							1815	7308	0	148	413	11794	2813	1498	38586
786-0	132							888	8319	827	1162	947	28088	1670	7153	41803
HCC-2998	131							1700	8388	0	387	1115	8212	1984	3255	74595
ACHN	130							619	8838	1426	1253	845	21377	1488	7825	48258
PC-3	129							577	10302	0	33	808	14288	1480	3151	46670
[illegible]	128							1027	12027	[illegible]	4327	377	20888	1884	13038	43831
DU-145	127							1300	9843	103	128	178	4882	2174	3858	46334
CAKI-1	126							981	13876	881	2888	334	[illegible]	[illegible]	[illegible]	[illegible]
SR	125							0	5723	0	1086	[illegible]	1754	2308	4870	44877
A498	124							8313	18840	351	295	0	14129	2475	18888	49887
RPMI 8226	123							0	5481	0	1	112	580	3030	5708	85179
SN12C	122							0	17333	0	2502	134	6784	2447	10677	75056
HL-60	121							280	4211	841	118	240	1354	2057	2980	88254
MOLT-4	120							226	4486	2179	561	811	5801	1313	7213	70156
OVCAR-5	119							858	10544	8273	3442	877	12121	888	32826	40584
K-562	118							1044	4812	2234	380	888	6276	1771	8528	58038
OVCAR-4	117							2174	13867	4108	240	1040	14315	1408	21344	44825
CCRF-CEM	116							1588	31473	868	4834	881	4841	1438	7738	58657
OVCAR-3	115							855	8082	2388	1091	178	2448	1421	29044	42501
SF-539	114							1113	7238	0	888	834	10017	1247	4855	41079
HOP-62	113							0	4086	2082	8258	887	16786	888	24881	25387
SF-295	112							208	7264	304	1051	2776	8751	878	18884	47318
A549/ATCC	111							1371	14728	0	3749	2445	18286	1303	68884	51944
SF-268	110							1333	11508	0	2308	1054	18314	1000	8620	32508
NCI-H522	109							335	10129	1946	3385	1263	17062	2084	15365	42495
U251	108							1814	8800	2187	374	1811	28319	2228	10888	53640
NCI-H460	107							1081	11984	2326	8788	870	15224	1305	22430	40200
SNB-75	106							252	7382	327	838	25	20030	1080	1580	40388
NCI-H322M	105							3883	13867	3336	3512	473	11000	2188	20863	58294
SNB-19	104							0	7540	1418	888	328	14888	3884	8129	52718
NCI-H226	103							822	18491	1382	2867	372	7863	4474	13488	103482
SK-OV-3	102							0	10857	671	740	482	8154	2780	8202	51778
NCI-H23	101							872	12935	1798	5827	716	1781	2129	30267	54401
IGROV1	100							872	10801	3057	295	885	3356	3272	7830	58870
EKVX	99							0	8485	888	3388	217	4085	2078	21182	42470
OVCAR-8	98							347	7233	2432	887	874	8534	1948	4824	48858
HOP-92	97							474	12057	2267	2887	782	12382	2385	31301	88830
h fibroblasts 3/31/92 #12	48							1806	4800	0	2536	215	24750	1914	5368	92800
h adult BMC 10/21/92 #17	47							37	3414	0	477	80	28787	1464	18148	75029
h keratinocytes 3/23/92 #10	46							4753	18827	0	2620	7914	18844	1176	5181	73676
TCOP	28							888	12483	55	30815	781	9829	2428	9414	61036
A549 - 1							wt	0	2808	887	13218	0	1876	331	14888	18083
A549 - 3							wt	0	3582	0	383	0	317	314	3847	10181
A549 - 4							wt	0	3788	0	1886	0	823	157	11425	18882
A549 - 5							wt	0	4433	0	2173	0	488	242	15448	13382
A549 - 7							wt	0	3415	0	679	0	1983	281	12240	20201
EKVX - 1							mutant	0	7818	218	10485	0	2358	602	27454	14020
EKVX - 4							mutant	0	8808	0	7448	0	2803	1003	70154	19451
EKVX - 3							mutant	0	4185	0	8833	0	1342	387	7118	18830
EKVX - 5							mutant	0	3062	442	1804	0	2086	781	18082	27288
EKVX [illegible]							mutant	0	8308	1404	40	0	1233	1386	5245	26418
MCF-7 [illegible]							wt	[illegible]	[illegible]	0	307	0	736	307	11222	18811
MCF-7 - 3							wt	0	[illegible]	0	[illegible]	0	[illegible]	[illegible]	18275	11347
MCF-7 - 4							wt	0	[illegible]	[illegible]	[illegible]	0	[illegible]	[illegible]	18884	[illegible]
MCF-7 - 5							wt	0	4888	[illegible]	314	0	0	[illegible]	24367	[illegible]
MCF-7 - 7							wt	0	2879	0	341	0	380	118	8134	14350
ADR-RES - 1							mutant	0	13125	0	4485	0	1135	880	48482	43329
ADR-RES - 3							mutant	0	7886	206	1943	0	883	715	8378	15827
ADR-RES - 4							mutant	0	3613	612	79	0	1947	635	10884	22884
ADR-RES - 5							mutant	0	1814	0	5874	0	572	116	18216	11906
ADR-RES - 7							mutant	0	9037	0	1519	0	535	310	4844	17985
WI 38 - 1							wt	0	11854	0	1743	0	480	816	23088	21030
WI 38 - 3							wt	0	9568	317	2832	0	2774	777	23798	13274
WI 38 - 4							wt	0	6781	0	134	0	2280	786	25808	14200
WI 38 - 5							wt	0	8853	0	1887	0	1877	760	6838	17103
WI 38 - 7							wt	0	8181	481	887	0	888	1033	12862	13382
HeLa - 1							HPV E6	0	2872	1045	125	0	783	381	8880	13285
HeLa - 3							HPV E6	0	8135	208	2588	0	226	308	18037	12311
HeLa - 4							HPV E6	0	1802	787	1330	0	283	819	11308	10796
HeLa - 5							HPV E6	0	8774	348	2858	0	2129	834	38267	18512
HeLa - 7							HPV E6	0	8057	0	1984	0	1873	880	18576	19187
H1299 - 1							mutant	0	6732	0	1828	0	488	788	13208	13828
H1299 - 3							mutant	0	7988	0	3838	0	581	847	4848	12467
H1299 - 4							mutant	0	11978	0	3883	0	1887	867	32388	18525
H1299 - 5							mutant	0	3280	0	2088	0	1547	852	9875	17847
H1299 - 7							mutant	0	6748	87	2847	0	888	234	13878	13714
A549 - 2							wt	0	1778	0	7823	0	388	478	7747	14837
EKVX - 2							mutant	0	4310	0	1255	0	888	386	16174	16880
HCT-116 - 1							wt	0	802	0	1151	0	1887	1882	13042	61832
HCT-116 - 2							wt	0	10450	0	3282	0	8188	888	84456	12001
HT29 - 2							mutant	0	1416	606	2288	0	1581	581	26757	15828
SF539 - 1							wt	0	7391	187	102	0	774	285	8028	18847
SF539 - 2							wt	0	18809	0	813	0	0	247	10468	14833
SF-268-1							mutant	0	11788	0	1106	0	3283	1120	18384	18521
SF-268-2							mutant	0	6717	0	10847	0	2007	1179	22525	14385
OVCAR-4 - 1							wt	0	2886	705	1387	0	1686	678	8858	24251
OVCAR-4 - 2							wt	0	4382	688	3277	0	1872	683	23042	58483
OVCAR-5 - 1							mutant	0	3130	380	238	0	881	388	12738	11007
OVCAR-5 - 2							mutant	0	2876	0	829	0	288	278	6088	11588
MCF-7 - 2							wt	0	2288	281	4687	0	630	122	7463	11768
ADR-RES - 2							mutant	0	6143	0	2038	0	814	834	9841	10802
HeLa - 2							HPV E6	0	8488	2267	5388	0	4474	842	40273	13088
SW480 - 1							mutant	0	6848	33	2511	0	1800	1182	44883	22143
SW480 - 2							mutant	0	3858	0	3388	0	815	538	28875	18486
H1299 - 2							mutant	0	7812	0	1835	0	1502	864	23857	24451
C33A - 1							mutant	0	8878	0	0	0	679	230	47320	12514
C33A - 2							mutant	0	3255	804	428	0	878	208	8221	8813
U2OS - 1							mutant	0	18292	0	5788	0	2118	1888	52566	21188
U2OS - 2							mutant	0	6288	748	8373	0	3282	1081	98322	27447
Hs68 - 1							wt	0	7177	447	1091	0	1135	416	11483	11884
Hs68 - 2							wt	0	8434	403	2884	0	3208	748	8788	17887
WI 38 - 2							wt	0	13825	488	1883	0	1880	732	11784	15250
[illegible] - 1								0	8888	0	2718	0	1113	388	12581	14913
[illegible] - 2								0	12728	0	128	0	1818	386	13386	14118
[illegible] - 3								0	12108	0	285	0	688	488	44133	14838
[illegible] - 4								0	23882	0	0	0	1887	848	4312	28874
[illegible] - 5								0	9406	0	0	0	0	494	0	11982
[illegible] - 6								0	12634	0	0	0	3388	1258	6031	21144
[illegible] - 8								0	15347	0	6882	0	3784	1358	28829	23861
[illegible] - 9								0	12135	0	308	0	2077	1080	4931	20944

Table 3 (cont'd)

Tissue	Tumor-cyto	Normal-cyto	Tumor-tis	Tumor cells	Normal	Endos	p53	SEQ 38 AA	SEQ 57 WS	SEQ 60 AA	SEQ 63 NS	SEQ 66 CA	SEQ 68 NS	SEQ 110 N	SEQ 73 NS	SEQ 76 AA
DuPang-2								0	80728	3124	2303	0	2775	1021	16539	11945
DuPang-5								0	35381	84	3297	0	2819	588	23678	14951
DuPang-8								0	28319	0	4208	0	4247	714	62757	13234
DuPang-11								0	40836	0	8022	0	3724	1096	49300	13179
DuPang-12								0	16274	0	1652	0	2814	582	59083	11807
DuPang-16								0	18015	0	1366	0	4279	801	34082	11401
DuPang-1								0	11739	0	21443	0	2076	1022	20201	22149
DuPang-2								0	8371	0	13765	0	1538	783	15252	18136
DuPang-3								0	6893	1171	8515	0	503	823	31807	25588
DuPang-4								0	4889	0	610	0	1748	680	20143	25155
DuPang-5								0	3723	0	216	0	1016	548	8031	17544
DuPang-6								0	28084	0	0	0	466	462	1929	8985
A549-8							wt	0	4018	837	1675	0	2280	388	18012	13833
EKVX-8							mutant	0	5749	0	8081	0	4381	803	24268	14160
HCT-116-7							wt	0	2845	807	88	0	812	478	8413	12883
HCT-116-8							wt	0	5165	2414	808	0	302	381	11432	18808
HT29-1							mutant	0	2474	0	1583	0	1484	451	22618	21737
HT29-7							mutant	0	1083	0	84	0	307	208	9185	13162
HT29-8							mutant	0	4333	0	2902	0	709	584	16207	19784
SF539-7							wt	0	8802	0	888	0	1074	1088	12408	17888
SF539-8							wt	0	6856	0	150	0	856	811	14376	16086
SF-295-7							mutant	0	8910	1888	708	0	1316	420	14248	15443
SF-295-[illegible]							mutant	[illegible]	[illegible]	[illegible]	1486	0	[illegible]	808	17101	16434
OVCAR4-7							wt	0	[illegible]	[illegible]	807	0	801	100	3378	14258
OVCAR4-8							wt	0	[illegible]	758	12121	0	2077	733	172[illegible]	[illegible]
OVCAR[illegible]-7							mutant	0	8291	0	1178	[illegible]	18	1330	[illegible]	14871
OVCAR[illegible]-8							mutant	0	3810	11046	46	[illegible]	2223	288	807	10551
MCF-7-8							wt	0	4047	348	1389	0	842	451	15891	15873
ADR-RES-8							mutant	0	4033	465	2605	0	478	[illegible]	7075	12882
HeLa-8							HPV E6	0	4132	944	1678	0	1623	706	11493	19006
SW480-7							mutant	0	3841	808	846	0	1026	212	13765	11469
SW480-8							mutant	0	3866	386	1133	0	218	438	19627	16513
H1299-8							mutant	0	8441	8274	1442	0	887	480	8507	12888
C33A-7							mutant	0	8465	0	131	0	804	331	1088	11768
C33A-8							mutant	0	4384	0	408	0	1880	1422	8025	26088
U2OS-7							mutant	0	6463	208	863	0	1824	231	21545	18594
U2OS-8							mutant	0	4223	197	1921	0	2485	614	32498	11280
Hs68-7							wt	0	4235	17844	462	0	888	614	10886	18314
Hs68-8							wt	0	4538	0	1101	0	673	583	3589	17784
WI38-8							wt	0	8888	0	0	0	2236	880	7101	12515
450 mobility RNA								219	19478	0	4887	322	11843	2288	4332	123811
CRL1572 2/17/99								0	1425	70	288	0	8	1492	988	33047
Bov-4						84		1358	7179	0	471	66	4171	2041	13126	60734
HT388								415	10878	388	182	228	1211	1804	86	81232
HT376								384	1670	0	48	43	878	1344	481	64588
HT385								2884	23778	1062	187	825	1895	3482	3771	110825
HT308								484	4382	0	0	167	1806	2814	7488	73383
Bov-3						173		142	2803	0	88	40	1463	2683	2513	47784
Bov-8						175		1326	887	0	54	8	83	1843	678	27812
Bov-9						177		0	1832	818	108	0	315	1821	783	37803
h keratinocytes 2/23/82 #16								8	8382	0	0	878	1031	1484	280	44387
Bov-10						237		1180	3331	811	95	31	1233	2831	1885	63844
HTB10								0	6868	288	827	0	604	8317	197	84103
h fibroblasts 2/21/82 #12								185	4732	0	30	8	1843	2487	119	83251
prostate, h								87	709	88	151	47	840	1828	0	71280
MNNG-OS poly A+								0	8876	1806	300	186	2523	2810	8344	68836
SA-OS (Rhesus) poly A+								888	31235	0	101	1871	2813	2883	3873	62848
MK poly A+								272	28863	0	38	1131	4200	3844	5141	46333
HCT-116-3							wt	0	2284	630	2801	0	808	457	8081	14136
HCT-116-4							wt	0	3670	177	630	0	288	241	10348	13244
HCT-116-5							wt	0	6838	208	724	0	477	388	13863	18472
HCT-116-6							wt	0	5158	1378	2077	0	383	483	11650	12866
A549-6							wt	0	777	0	42	0	888	315	2191	14884
HT29-3							mutant	0	3211	1117	2366	0	1884	511	16881	15822
EKVX-6							mutant	0	819	80	0	0	367	636	8049	16148
HT29-4							mutant	0	771	1454	676	0	888	408	13686	21159
HT29-5							mutant	0	3498	1303	4081	0	1383	1083	[illegible]	27154
HT29-6							mutant	0	3159	811	2404	0	143	1080	28041	38150
[illegible]4-7							wt	0	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]							wt	0	[illegible]	0	1105	0	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]4-[illegible]							[illegible]	[illegible]	[illegible]	[illegible]	4308	[illegible]	[illegible]	173	[illegible]	[illegible]
OVCAR4-[illegible]							wt	0	3879	1244	0	[illegible]	[illegible]	84	[illegible]	15714
SF539-3							wt	0	8084	177	708	0	828	188	8632	15388
SF539-4							wt	0	11231	435	204	0	413	194	14888	10833
SF539-5							wt	0	12548	388	488	0	842	352	4084	13677
SF539-6							wt	0	5758	0	0	0	2221	382	14823	20785
OVCAR5-3							mutant	0	4328	288	1241	0	1507	27	8822	14804
OVCAR5-4							mutant	0	2508	0	1061	0	849	488	8731	13888
OVCAR5-6							mutant	0	2838	0	88	0	708	106	319	11271
ADR-RES-6							mutant	0	3371	328	1832	0	555	195	8837	10873
MCF-7-6							wt	0	2788	0	222	0	0	141	20834	15834
HeLa-6							HPV E6	0	8105	0	2138	0	1130	874	28825	22168
H1299-6							mutant	0	1457	70	10	0	1108	448	8018	16346
SW480-3							mutant	0	1342	0	5328	0	383	304	15618	14858
SW480-4							mutant	0	4798	0	3808	0	481	843	47025	14272
SW480-5							mutant	0	7857	582	8867	0	1248	684	37825	18108
SW480-6							mutant	0	4158	0	1304	0	0	285	30247	17087
C33A-3							mutant	0	4870	885	185	0	823	173	7118	8840
C33A-4							mutant	0	2863	0	831	0	888	838	8045	7717
C33A-5							mutant	0	4227	188	2852	0	1128	484	11378	13418
C33A-6							mutant	0	1881	0	0	0	467	686	8887	17806
Hs68-6							wt	0	6868	0	384	0	881	835	4848	13083
U2OS-3							mutant	0	6180	8848	13081	0	1448	473	84886	18082
U2OS-4							mutant	0	4248	2379	8586	0	818	588	38448	17858
U2OS-5							mutant	0	8188	4213	4881	0	1083	478	89416	21279
U2OS-6							mutant	0	9431	0	0	0	1883	288	38463	18157
WI38-6							wt	0	8088	837	888	0	1854	840	2085	12848
Hs68-3							wt	0	10577	10235	1233	0	2412	888	20817	13348
Hs68-4							wt	0	17277	1853	3875	0	2413	1982	28235	20880
SF-295-3							mutant	0	4453	0	2302	0	1910	482	9438	17468
SF-295-4							mutant	0	8837	760	11168	0	1348	925	16808	18347
SF-295-5							mutant	0	13125	0	2499	0	844	1137	27879	18888
SF-295-6							mutant	0	4088	0	0	0	288	408	2400	18754
DuPang-13								0	15808	8	38388	0	3018	852	32106	24788
Mithel-20								0	15885	0	4210	0	2461	740	11291	20883
Mithel-21								0	14060	0	7219	0	2419	777	19057	20805
Mithel-22								0	13676	8	3119	0	2879	887	44815	21250
OVCAR5-5							mutant	0	7348	1	8016	0	1187	823	16827	16178
Mithel-10								0	6712	0	3809	0	2858	387	1837	7830
Mithel-11								0	6278	0	4708	0	837	129	888	4271
Mithel-12								0	10844	0	2880	0	2290	828	43027	19805
Mithel-13								0	13881	0	883	0	1883	810	87512	17026
Mithel-14								0	18619	0	1380	0	432	1229	21693	17484
Mithel-15								0	10792	0	3886	0	834	868	20174	15732
Mithel-16								0	7817	0	56	0	1777	710	18220	12001
Mithel-17								0	8770	0	288	0	1223	678	1888	18522
Mithel-18								0	13084	8	224	0	2444	1438	12988	21852
Mithel-19								0	9081	0	0	0	1173	840	22262	14100

Table 3 (cont'd)

Tissue	Tumor-cyto	Normal-cyto	Tumor - To	Tumor cells	Normal	Endo	p53	SEQ 79 AA	SEQ 80a	SEQ 82 NU	SEQ 84 NU	SEQ 88 AA	SEQ 90 AA	SEQ 90 NU	SEQ 93 TS	SEQ 94 AA
adrenal gland - h		1						0	330	18727	28487	188725	3877	1368	305	13731
lymph node - h		2						0	180	25286	28056	133216	11022	818	281	22717
bone marrow - h		3						0	487	8624	22689	80880	8274	447	0	12523
mammary gland - h		4						0	0	4132	3261	30833	30	24	100	2064
brain - h		5						0	0	11468	8976	138488	6167	3520	61	12108
pancreas - h		6						0	630	9084	17822	100224	2001	1052	241	11588
cerebellum - h		7						0	236	18449	41688	84237	10828	4741	488	21132
pituitary gland - h		8						127	182	5828	87715	134453	6087	4401	28	11637
fetal brain - h		9						171	354	10858	23841	182430	3445	612	65	23358
placenta - h		10						717	386	10004	74254	187867	6384	358	201	16661
fetal kidney - h		11						236	830	28118	28184	87528	6311	903	224	14839
prostate - h		12						51	88	11315	8847	222874	217	1870	74	11687
fetal liver - h		13						436	207	10229	8486	118434	1804	430	268	8814
salivary gl. - h		14						0	632	13840	7798	102290	6580	2038	75	9465
fetal lung - h		15						0	608	27774	19719	188848	6148	1076	177	13841
skeletal muscle - h		16						191	1988	184818	11019	194752	1836	22813	58	3341
heart - h		17						308	1084	119083	8508	82887	2298	6781	0	4512
small intestine - h		18						230	288	25312	14109	183840	3380	1228	48	7578
kidney - h		19						318	6	8142	18392	81561	3888	388	0	6850
spinal cord - h		20						85	340	7758	11084	84387	7382	877	61	3802
liver - h		21						372	254	4038	13851	185877	1734	304	500	2807
spleen - h		22						78	286	8082	14888	85380	2284	345	333	4083
[illegible]		23						179	842	19806	[illegible]	88815	[illegible]	317	[illegible]	[illegible]
[illegible]		24						0	79	[illegible]	[illegible]	[illegible]	[illegible]	3227	0	3447
[illegible]		25						[illegible]	377	[illegible]	[illegible]	[illegible]	[illegible]	856	892	[illegible]
thymus - h		27						171	456	21276	[illegible]	112730	[illegible]	700	[illegible]	7479
HPAEC		28				28		0	138	6798	13178	184784	240	329	[illegible]	[illegible]
thyroid gland - h		29						0	229	13848	8088	110349	7238	1484	322	10434
RPTEC		30				30		122	0	0	4221	115750	11	378	7	6048
trachea - h		31						0	438	15832	13708	88718	2751	1477	1621	15045
HMEC		32						0	787	16748	8112	158844	1837	388	421	28117
uterus - h		33						105	1371	81570	11729	84358	3828	1884	81	18387
HCAEC		34						30	0	11182	3718	222488	298	320	0	8100
Pancreas - h		35						0	138	20503	3244	127701	2384	1828	0	7344
lymph node - h		36						0	104	7145	4641	17634	818	0	84	2580
Skeletal muscle - h		37						0	0	23826	1929	167218	302	313	0	3018
fetal liver - h		38						438	27	6837	8863	85009	411	0	0	8085
Heart - h		39						134	232	20525	4808	129875	888	27	333	4438
thymus - h		40						382	0	2423	14735	15108	423	168	0	4408
Duodenum - h		41						0	0	0	4472	83200	79	87	88	6253
Fetal brain - h		42						834	204	5307	18212	1837	1026	238	280	7798
Salivary gl. - h		43						4	170	4203	8635	110729	1347	86	187	3286
testis - h		44						441	218	5877	17240	33387	4086	370	384	8357
HT210-normal					398			168	34	0	1327	1611	0	384	40	2873
HT213-normal					363			0	0	0	1226	0	0	208	62	883
HT152-normal					361			44	0	0	5086	0	226	15	67	4004
Bro-13					366	366		2541	0	0	4870	38818	47	1438	180	8885
Bro-12					364	364		4181	44	166	8008	36483	830	675	363	19148
endothelium - h					344			78	41	0	3834	0	618	86	0	2827
brain - h					342			255	156	239	2481	0	226	83	0	3843
RPTEC					334	334		280	0	0	8463	4048	0	423	0	216
lymph node - h					332			18	0	0	15025	0	106	82	0	884
h adult SMC 10/21/82 #17					330			0	0	803	6185	0	128	0	0	1881
Fetal brain - h					329			846	0	8021	28080	83713	442	886	147	7317
HT289-normal					327			88	0	272	2277	0	0	118	146	2882
thymus - h					328			2882	85	417	17258	28188	198	571	0	8888
HT148-normal					321			0	20	0	2856	0	0	248	0	2382
HEPM 3d untreated					320			263	0	8488	8511	77932	1048	207	204	1880
uterus - h					318			447	2480	8784	17780	110827	6284	1031	131	13281
trachea - h					316			327	250	28285	8849	19058	2828	880	78	8714
thyroid gland - h					314			230	470	20840	12886	4852	10045	1002	273	14507
salivary gl. - h					311			80	52	43	7346	316	173	0	153	1713
prostate - h					309			0	21	300	2837	0	145	48	0	1643
pituitary gland - h					307			258	0	325	6466	19	188	570	159	1446
pancreas - h					306			0	11	186	4777	857	436	86	0	2540
mammary gland - h					303			148	756	3409	7475	735	1802	158	341	3067
bladder - h					302			0	868	27864	14481	181733	503	400	10	3883
testis - h					298			3408	1134	7086	11747	8708	3876	2377	1281	15783
liver - h					292			1374	344	14841	7284	[illegible]	1179	1089	[illegible]	[illegible]
[illegible]					295			[illegible]	244	70	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
spinal cord					294			168	45	114	[illegible]	[illegible]	[illegible]	[illegible]	331	[illegible]
small intestine - h					291			125	80	1630	4522	129	419	331	152	[illegible]
skeletal muscle - h					290			633	1806	30460	19470	8700	2133	1328	224	19788
bone marrow - h					279			0	0	0	1113	0	18	0	188	1019
adrenal gland - h					277			0	0	650	1687	746	28	0	0	3444
HPAEC					275	275		118	124	87	2787	172	0	0	73	1817
HT392-normal					268			0	0	0	1285	0	113	82	108	5486
HT383-normal					266			0	0	0	2508	0	0	19	0	7822
Bro-11					238	238		0	1802	0	8325	887	18	11	31	7455
Bro-8					236	236		527	98	213	4726	1702	313	17	130	6438
HT372-normal					234			188	0	0	4079	2161	734	0	52	2239
Bro-7					233	233		182	112	0	2948	0	136	64	0	5213
Bro-6					231	231		0	0	194	6488	0	179	82	0	4789
Bro-3					229	229		0	0	347	3875	0	50	50	171	6802
Bro-1					227	227		208	82	0	1779	208	10	0	32	5127
bladder - h					222			61	0	1081	3512	0	188	133	40	2038
heart - h					218			200	0	0	7286	674	0	131	0	1979
stomach - h					214			0	284	0	6474	0	1257	215	108	2652
fetal liver - h					213			36	0	0	3881	0	125	0	0	843
placenta - h					212			0	83	243	29838	198	888	153	79	3836
HCAEC					211	211		0	0	0	2921	1	190	0	38	1167
fetal brain - h					210			188	145	0	4763	0	873	108	182	5873
HMEC					208			115	0	88	2386	0	198	0	70	2719
Duodenum - h					205			235	80	125	2970	0	1786	72	18	2887
Skeletal muscle - h					203			128	15	328	3074	183	63	30	0	831
Pancreas - h					201			0	0	194	2780	0	83	101	7	2300
testis - h					198			188	25	0	3811	0	154	83	0	1428
Salivary gl. - h					197			33	48	2102	2498	12588	193	119	0	3808
HEPM 3d TGFB1 [illegible]					196			0	30	658	1988	2238	787	117	0	841
thymus - h					190			444	155	213	5844	0	368	0	78	2851
WI-38 72h					179			0	67	0	1834	0	349	71	0	712
lymph node - h					91			0	67	0	1946	0	0	172	0	2303
lung - h					89			488	386	447	2183	0	1374	867	25	13413
kidney - h					67			0	213	191	3330	0	977	475	112	4580
heart - h					68			186	198	3427	2346	0	889	281	404	4283
fetal lung - h					53			149	113	486	28	0	0	0	21	844
fetal liver - h					61			0	83	204	1747	28	262	188	0	2802
fetal kidney - h					49			0	79	260	5458	1233	275	215	0	5812
HELA-2h-031999				79				213	887	121	3227	805	61	190	0	8488
HELA-4h-031999				81				72	174	0	3629	0	0	80	0	5410
HELA-6h-031999				83				0	253	215	2881	208	0	218	0	8647
HELA-8h-031999				85				83	0	287	2876	0	0	298	0	4962
HELA-8h-031999				88				140	388	0	8084	2788	0	347	0	4351
HELA-9h-031999				90				242	203	0	5776	0	84	0	163	7038
HELA-10h-031999				92				33	615	616	5088	0	182	0	0	7081
HELA-11h-031999				94				138	143	224	4108	0	0	0	0	3838
HELA-12h-031999				96				43	0	388	8810	0	109	67	0	3080
NCI-H222M				146				0	0	13071	1104	3218	514	285	38	8838
NCI-H460				148				0	18	8702	787	1588	1738	38	0	8485
NCI-H522				150				0	78	9166	1557	248	71	0	38	2277
SNB-19				152				0	158	8865	730	4151	918	0	0	1808
SNB-75				154				91	108	24358	888	800	1175	68	184	5215
SF-268				156				242	0	3462	0	884	37	192	0	1168
SF-295				158				52	0	1780	705	0	87	3	27	857
CCRF-CEM				160				0	0	883	445	8	287	0	121	1619
DU-145				162				88	0	7045	178	6522	186	202	57	880
HCT 116				164				0	30	1437	817	372	0	0	147	781

Table 3 (cont'd)

Tissue	Tumor-cyto	Normal-cyto	Tumor - Tn	Tumor cells	Normal	Endos	p53	SEQ 79 AA	SEQ 80a	SEQ 82 NA	SEQ 84 NA	SEQ 86 AA	SEQ 88 AA	SEQ 90 NA	SEQ 92 TX	SEQ 94 AA
Caki-1				165				278	236	16781	1332	0	792	0	0	1360
786-0				166				132	88	25330	4542	2050	4182	138	0	3888
T-47D				169				0	236	13638	3870	85	2558	414	0	11608
Kan-3				171				40	0	0	1822	8713	0	61	0	2573
CRL1441 RNA 8/28				181				0	244	0	0	1791	0	1	128	843
761T untreated + DNase				183				29	0	0	321	111	0	0	0	284
KB poly A+				184				114	0	541	2325	0	50	136	0	2763
HOS poly A+				185				218	0	1363	3288	0	0	101	190	3434
ACHN				198				0	122	16872	1171	849	147	150	83	1871
UACC-62				200				166	0	3877	0	2173	244	0	183	4027
MCF-7/ADR-RES				202				100	0	1487	402	215	148	0	0	2877
UTOS (Steroid) poly A+				204				112	0	0	330	0	79	252	124	498
WISH (Collagen) poly A+				208				0	289	613	837	315	0	0	0	1578
458 medulla mRNA				209				1149	0	2134	2543	838	880	0	107	8071
CCL137 RNA 3/21/98				210				0	0	282	1884	0	25	143	0	2128
WI-38 72h 0.5%FBS, 24h 10% FBS				211				0	0	181	3383	416	835	184	0	2256
CRL1441 + TPA (24h) 8/28				220				0	184	0	177	0	0	5	71	1172
Kan-1				221				18	66	0	2177	0	0	41	84	2556
Kan-2				222				85	0	45	1182	144	0	133	0	2250
Kan-4				225				0	230	0	822	0	11	20	0	1278
HOP-92				241				0	0	1780	1888	863	186	216	0	2936
MOLT-4				242				86	183	8863	1038	2886	153	180	48	5219
[illegible]				243				0	0	22076	[illegible]	886	311	[illegible]	[illegible]	[illegible]
[illegible]				244				0	226	14080	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]				245				0	1087	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
RPMI 8226				246				0	0	0	611	838	57	0	7	26
A549/ATCC				247				0	0	4447	266	0	166	68	0	2944
SR				248				0	183	18413	855	1882	500	17	0	2103
OVCAR-3				249				0	148	8885	1324	168	0	80	218	4524
HCT-15				250				328	0	46256	1488	201	588	0	66	9053
OVCAR-4				251				171	0	2361	84	0	148	0	167	1032
UO-31				252				208	0	307	480	0	38	0	191	1421
OVCAR-5				253				0	88	577	3408	0	1477	8	0	4319
SN12C				254				498	0	6836	173	0	0	322	192	4185
OVCAR-8				255				181	66	17488	496	0	98	129	0	1781
LOX IMVI				256				0	2838	82575	1953	3615	1383	0	134	5249
IGROV1				257				140	73	32874	1388	565	128	0	226	4424
SK-MEL-2				258				0	167	4482	234	1864	0	48	567	1288
SK-OV-3				259				0	19	4761	313	1949	681	0	71	1009
SK-MEL-5				260				0	101	3676	172	0	38	0	41	1817
SF-539				261				159	0	73032	1663	2888	825	486	174	4144
SK-MEL-28				262				187	0	14342	548	0	0	86	0	1275
K-562				263				0	118	38831	825	1578	433	74	48	2880
UACC-257				264				0	82	8688	1800	775	91	109	0	1237
M14				265				0	21	1255	673	3737	0	121	0	2708
MCF7				267				126	286	23780	5288	7080	0	718	0	14882
MDA-MB-435				268				0	0	8791	383	0	147	290	126	4085
HT279				270				38	26	0	1084	0	67	170	29	3872
MDA-N				271				0	0	14738	415	0	441	336	0	4136
Y79 poly A+				273				11	361	6684	4474	0	1320	0	345	17179
KHOS poly A+				288				25	380	18880	8570	1854	2113	1861	0	21810
HT1080 24h TPA RNA 6/23				300				71	0	0	8286	0	0	40	153	766
HELA-EXP-601669				313				37	62	0	4774	0	0	153	97	3084
HT1080 6h RNA				322				344	0	916	8852	14719	0	800	0	4427
HT347				323				282	0	38	4100	270	277	482	83	5453
459 medulla RNA				324				942	14	0	8157	8087	481	558	170	1863
NCI-H226				326				282	21	11463	1217	1915	0	171	0	0
HOP-62				337				0	0	10827	2336	0	236	139	0	3071
MDA-MB-231				338				833	1127	131888	15988	28722	8588	1867	48	13815
U251				339				488	1748	724467	8066	80562	28673	1674	0	19852
PT cells poly A+				340				0	112	6025	779	0	445	128	27	2086
PC-3				341				613	215	25675	1044	10117	1417	1087	0	5852
HCC-2998				343				0	3	7506	1212	708	179	529	0	3085
SW-620				345				68	6	23634	1150	1401	32	243	0	2487
HT182				346				46	0	1886	8307	0	15	245	0	6888
COLO 205				347				17	80	3655	846	634	0	481	0	840
HT29				348				1	0	912	5285	0	72	0	0	2281
[illegible]				349				0	81	8008	[illegible]	913	0	198	0	7180
[illegible]				[illegible]				31	202	382	[illegible]	0	182	304	[illegible]	[illegible]
[illegible]				[illegible]				[illegible]	11	[illegible]	2774	2335	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]				[illegible]				273	121	0	14919	119	[illegible]	[illegible]	[illegible]	3522
HOP 383				353				253	0	[illegible]	2129	[illegible]	182	219	0	2967
TK-10				355				2370	1831	88088	4836	38193	4080	868	173	6282
Malme-3M				357				1422	1373	162135	14630	51277	8889	987	88	6366
Hs 578T				358				184	46	21138	1288	1167	1033	150	12	629
HT213			50					8	0	797	2103	0	880	336	0	14318
HT288			52					146	0	647	3338	0	88	804	0	16288
HT130			54					174	0	0	2329	0	80	307	27	5084
HT155			56					0	0	13	2383	0	0	88	0	15006
HT183			58					275	0	119	1588	0	412	181	117	6436
HT170			60					713	0	2417	1494	1888	0	719	0	13133
HT172			62					111	0	85	2348	0	0	29	0	8824
HT138			63					384	24	82	3379	0	0	0	0	8539
HT178			64					0	78	147	3414	0	621	40	0	6823
HT184			65					208	0	374	2620	0	6	607	0	12319
HT192			66					43	122	437	3888	0	6	0	46	3531
HT199			67					0	119	0	1891	0	0	240	182	2809
HT189			68					43	836	2833	3850	0	684	83	78	8023
HT143			69					327	0	0	2861	0	0	182	0	632
HT139			70					382	71	1388	6365	0	208	288	0	1531
HT146			71					84	88	2084	4726	0	0	238	0	838
HT227			72					12	0	215	3473	0	1015	404	0	2504
HT302			73					143	0	2818	7366	1888	4134	721	174	25415
HT314			74					230	0	674	3847	0	838	348	0	11481
HT317			75					285	0	348	7388	708	979	886	228	13108
Rhabdomyosarcoma 6/25 11/8			77					0	0	0	2882	2	0	88	0	87
HT323			78					0	0	808	4865	0	292	198	0	3445
HT327			80					0	83	238	1542	1133	0	18	45	2807
HT335			82					0	0	8	4194	8	288	8	0	6152
HT146			85					48	6	93	0	0	38	8	182	1384
HT348			87					80	198	190	5629	8	1017	0	0	3434
HT311			178					238	0	0	2176	0	130	5	111	5105
HT388			186					673	0	0	1128	1616	0	382	0	8821
HT140			187					230	117	0	0	8	0	188	139	746
HT281			188					303	0	0	1384	388	0	301	8	406
HT372			191					43	220	0	2713	0	298	133	144	438
TCGP			207					94	17	0	1460	0	0	10	0	3112
HT180			216					0	0	80	1385	308	0	40	0	1331
HT307			217					0	80	0	2222	0	48	149	0	4198
HT368			226					343	0	0	884	12719	127	327	115	4898
HT370			228					116	0	0	1345	0	0	0	0	3848
HT373			229					170	888	32	1671	0	0	128	0	8422
HT377			230					38	181	122	3488	87	135	53	0	3819
HT382			236					185	81	0	4306	183	820	208	132	2718
Lymphoblastoma RNA			281					0	0	103	855	0	38	41	0	283
HT334			290					0	127	0	6791	1382	86	123	8	8378
HT338			301					616	82	0	2712	0	185	241	278	6756
HT382			316					198	0	2290	322	394	187	31	208	3177
HT384			317					83	3474	0	8804	0	981	188	0	7782
HT312			319					208	88	184	3247	0	17	38	198	9742
HT182			325					415	0	228	2151	0	0	0	0	20
HT385			358					388	808	0	3119	0	0	0	0	3471
HT197			369					488	0	0	4418	1881	3885	88	0	585
T-47D	183							437	128	38188	3858	178878	3816	113	0	2821
MDA-N	181							485	135	90418	6919	157582	1446	523	171	4281
MDA-MB-435	188							78	0	95236	4848	124701	2831	197	0	3868
MDA-MB-231	157							810	282	82876	3858	384882	7811	523	445	4871

Table 3 (cont'd)

Tissue	Tumor-sym	Normal-sym	Tumor-fo	Tumor cells	Normal	Endos	p53	SEQ 79 AA	SEQ 082a	SEQ 83 MI	SEQ 84 RI	SEQ 86 AA	SEQ 89 AA	SEQ 90 MI	SEQ 93 TS	SEQ 94 AA
Hs 578T	155							225	196	133345	4802	281680	3072	326	83	9383
MCF-7/ADR-RES	153							454	0	62589	3763	173587	940	234	71	4802
MCF7	151							0	88	22491	3843	218251	402	453	56	8546
M14	149							34	0	103835	5728	88626	734	463	78	8105
UACC-257	147							0	189	44884	4488	48559	1177	177	77	5052
UACC-62	145							0	33	108680	6515	47818	1123	348	0	8145
SK-MEL-28	144							0	103	36141	6515	65330	875	133	34	1529
UO-31	143							808	108	20849	9249	73274	520	188	275	4295
SK-MEL-5	142							104	0	29587	6758	73371	1055	79	11	2580
KM-12	141							418	0	3484	2364	80853	108	127	182	3168
SK-MEL-2	140							171	0	22919	3246	134829	27	167	132	2782
HCT-15	139							0	47	15008	3813	104830	898	0	103	7884
Malme-3M	138							148	160	22488	5785	137580	877	279	0	3758
COLO 205	137							0	213	21911	8843	114441	642	9	74	8403
LOX IMVI	136							158	1464	58887	3350	112298	1478	0	0	3197
SW-620	135							188	0	11585	3817	184847	798	0	210	8271
TK-10	134							0	137	23887	4146	75724	1989	130	0	4536
HCT 116	133							1060	58	7185	2816	119724	702	83	283	7445
786-0	132							225	0	28315	3030	102477	3214	0	42	6256
HCC-2998	131							0	180	17887	5588	127791	485	18	0	9803
ACHN	130							0	136	30733	4256	97808	473	165	144	2382
PC-3	129							180	184	8373	2715	80476	1017	348	0	7408
RXF 393	128							134	204	38880	3502	88563	377	798	65	[illegible]
[illegible]	127							0	79	8334	2631	17432	228	[illegible]	8	[illegible]
[illegible]	126							0	137	12187	7748	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
SR	125							0	[illegible]	8485	2594	[illegible]	[illegible]	150	41	12012
A498	124							0	13	28496	2800	84336	15	1192	0	6887
RPMI 8226	123							34	0	88	2814	12804	102	473	168	4276
DNT2C	122							0	0	36753	7382	38841	542	572	84	11656
HL-60	121							613	188	825	8301	450	388	314	173	21438
MOLT-4	120							0	0	888	8372	83742	1346	27	0	3085
OVCAR-5	119							425	0	828	4872	41219	4613	1282	171	1432
K-562	118							258	0	10818	4887	188477	2277	87	70	6878
OVCAR-4	117							664	246	21840	2514	133148	8857	231	0	3791
CCRF-CEM	116							0	0	18280	3482	113784	6877	144	0	5340
OVCAR-3	115							464	37	13087	2885	86832	1896	33	0	3081
SF-539	114							217	0	14108	3652	85279	2383	110	0	6806
HOP-62	113							404	153	36838	1330	72188	3886	0	0	6448
SF-295	112							281	0	21130	3578	88198	3313	0	5	13804
A549/ATCC	111							1008	321	44888	4814	138108	3808	223	0	6885
SF-268	110							0	0	22677	2917	128788	868	446	416	2835
NCI-H522	109							384	213	33098	3465	81138	2552	225	113	4126
U251	108							282	0	24503	9808	148817	1984	183	253	7311
NCI-H460	107							170	219	27831	3888	48573	3814	27	0	4305
SNB-75	106							0	335	6881	1862	88012	9808	143	0	6291
NCI-H322M	105							212	0	23147	4126	72818	1184	8	0	6616
SNB-19	104							138	58	6408	2362	17270	1803	0	67	6179
NCI-H226	103							271	119	21914	8830	11321	4083	0	298	10800
SK-OV-3	102							0	0	9804	2381	18880	8044	212	171	5881
NCI-H23	101							318	432	81716	2984	2378	1014	187	84	9311
IGROV1	100							0	262	8150	2107	13131	1772	413	219	12734
EKVX	99							82	132	28183	4584	5729	613	373	0	8752
OVCAR-8	98							168	23	8123	8395	2988	2072	116	0	8109
HOP-92	97							0	284	18887	7181	3804	18079	366	0	12900
lo fibroblasts 3/31/82 #12	48							315	280	22448	6764	180648	4888	414	0	4865
lo adult BMC 10/21/82 #17	47							0	0	1888	7348	122385	424	458	298	4362
lo keratinocytes 2/28/82 #18	46							0	0	13008	8192	188018	116	117	0	5780
TCCP	38							0	16	11088	6238	81485	341	236	0	14132
A549-1							wt	0	48	2053	83185	0	3072	0	48	110
A549-3							wt	0	22	0	48138	0	0	0	276	888
A549-4							wt	0	82	116	46247	0	1843	0	242	794
A549-5							wt	0	208	2508	72867	0	2142	0	0	1102
A549-7							wt	0	50	821	38880	0	888	0	0	1377
EKVX-1							mutant	0	256	3888	88834	0	4758	0	132	330
EKVX-4							mutant	0	223	714	150881	0	18081	0	128	1800
EKVX-3							mutant	0	308	48	77788	0	6784	0	0	834
EKVX-5							mutant	0	18	1206	37831	0	888	0	187	2282
EKVX-7							mutant	0	1153	80	74385	0	[illegible]	0	0	4888
MCF-7-1							wt	0	[illegible]	0	41807	0	[illegible]	0	0	1186
MCF-7-3							wt	0	77	0	37944	0	[illegible]	0	134	[illegible]
MCF-7-[illegible]							wt	0	162	1028	[illegible]	0	[illegible]	0	[illegible]	[illegible]
MCF-7-[illegible]							wt	0	0	0	[illegible]	0	[illegible]	0	0	650
MCF-7-7							wt	0	284	20	27895	0	0	0	0	867
ADR-RES-1							mutant	0	744	1810	88435	0	2747	0	912	1776
ADR-RES-3							mutant	0	811	2487	43852	0	860	0	175	1127
ADR-RES-4							mutant	0	448	218	40637	0	1142	0	0	1422
ADR-RES-5							mutant	0	0	4	38517	0	1779	0	24	249
ADR-RES-7							mutant	0	473	4304	27946	0	1096	0	0	994
WI 38-1							wt	0	853	3884	87821	0	18038	0	110	2042
WI 38-3							wt	0	382	1016	43671	0	18258	0	0	1308
WI 38-4							wt	0	0	1422	44081	0	8338	0	0	1232
WI 38-5							wt	0	18	1564	48542	0	2404	0	0	1857
WI 38-7							wt	0	27	268	32873	0	18729	0	188	1050
HeLa-1							HPV E6	0	287	0	38078	0	857	0	140	1118
HeLa-3							HPV E6	0	143	1254	46790	0	788	0	0	842
HeLa-4							HPV E6	0	80	3830	41446	0	803	0	0	833
HeLa-5							HPV E6	0	148	884	73772	0	1303	0	0	679
HeLa-7							HPV E6	0	0	140	48884	0	858	0	151	1152
H1299-1							mutant	0	887	330	22779	0	1806	0	0	858
H1299-3							mutant	0	1745	1070	28134	0	4888	0	0	441
H1299-4							mutant	0	2384	1828	35508	0	14841	0	84	1827
H1299-5							mutant	0	0	80	15450	0	6835	0	0	1528
H1299-7							mutant	0	813	4827	23888	0	1127	0	115	577
A549-2							wt	0	0	2762	38578	0	1188	0	0	811
EKVX-2							mutant	0	1047	85	73357	0	8238	0	80	1408
HCT-116-1							wt	0	1082	308	62248	0	1884	0	0	1781
HCT-116-2							wt	0	17	84	122523	0	7838	0	0	1283
HT29-2							mutant	0	148	858	34858	0	121	0	170	877
SF539-1							wt	0	0	830	22587	0	2052	0	0	488
SF539-2							wt	0	182	21	23348	0	4928	0	0	731
SF-268-1							mutant	0	0	3888	43016	0	3529	0	438	1744
SF-268-2							mutant	0	258	1236	66884	0	6088	0	170	383
OVCAR-4-1							wt	0	1448	220	42306	0	7178	0	220	1914
OVCAR-4-2							wt	0	8383	780	40888	0	1149	0	388	3834
OVCAR-5-1							mutant	0	253	0	30086	0	913	0	0	475
OVCAR-5-2							mutant	0	1238	0	25746	0	623	0	53	1084
MCF-7-2							wt	0	0	0	28132	0	93	0	0	923
ADR-RES-2							mutant	0	982	82	18243	0	0	0	297	1312
HeLa-2							HPV E6	0	0	800	18042	0	585	0	187	815
SW480-1							mutant	0	2207	1291	61906	0	9198	0	0	1342
SW480-2							mutant	0	1156	432	34859	0	8880	0	16	180
H1299-2							mutant	0	2438	0	28010	0	7738	0	113	982
C33A-1							mutant	0	817	0	38805	0	205	0	47	823
C33A-2							mutant	0	677	0	28147	0	484	0	34	858
U2OS-1							mutant	0	1684	8649	88348	0	4086	0	0	2314
U2OS-2							mutant	0	276	1546	68820	0	1257	0	0	777
[illegible]-1							wt	0	106	87	60212	0	3856	0	71	389
[illegible]-2							wt	0	124	4293	88967	0	18711	0	87	2035
WI 38-2							wt	0	2108	894	65770	0	13181	0	334	2020
[illegible]-1								0	0	245	23671	0	8	0	0	973
[illegible]-2								0	0	0	48133	0	79	0	92	164
[illegible]-3								0	0	0	148384	0	252	0	0	1068
[illegible]-4								0	0	0	69686	0	232	0	145	480
[illegible]-5								0	0	0	1588879	0	82	0	179	483
[illegible]-6								0	0	131	50757	0	0	0	72	1086
[illegible]-8								0	0	0	82530	0	14485	0	3535	1386
[illegible]-9								0	200	0	77265	0	1094	0	0	1986

Table 3 (cont'd)

Tissue	Tumor-cyto	Normal-cyto	Tumor - fo	Tumor cells	Normal	Endos	p53	SEQ 79 AA	SEQ 883n	SEQ 83 AA	SEQ 84 NS	SEQ 86 AA	SEQ 89 AA	SEQ 90 NS	SEQ 93 TS	SEQ 94 AA
OvPong-7								0	1147	2287	84087	0	7232	0	238	1539
OvPong-8								0	2758	83	73828	0	8613	0	48	633
OvPong-9								0	2323	15	38855	0	14281	0	103	780
OvPong-11								0	11	2578	73686	0	6704	0	0	1249
OvPong-12								0	0	1983	47635	0	7889	0	0	1779
OvPong-10								0	34	0	33803	0	18777	0	0	813
OvPong-1								0	257	704	80021	0	2318	0	88	309
OvPong-2								0	408	286	146848	0	1211	0	48	383
OvPong-3								0	213	8567	108848	0	2713	0	0	384
OvPong-4								0	52	581	68193	0	660	0	364	801
OvPong-5								0	2855	0	48709	0	0	0	349	622
OvPong-6								0	1896	0	84800	0	68	0	19	482
A549-8							wt	0	28	4742	86151	0	2089	0	0	845
EKVX-8							mutant	0	184	4821	74538	0	7705	0	0	2327
HCT-116-7							wt	0	173	836	22298	0	1578	0	72	1588
HCT-116-8							wt	0	205	779	28048	0	2302	0	0	1781
HT29-1							mutant	0	167	1381	47837	0	276	0	315	852
HT29-7							mutant	0	0	80	14674	0	80	0	88	441
HT29-8							mutant	0	45	843	38188	0	342	0	0	499
SF539-7							wt	0	254	114	28009	0	1532	0	124	933
SF539-8							wt	0	1007	178	38188	0	4118	0	0	1851
SF-268-7							mutant	0	0	2813	53411	0	2540	0	167	1488
SF-268-8							mutant	0	1365	1825	38782	0	4138	0	128	1371
OVCAR4-7							wt	0	108	0	34881	0	534	0	140	2428
OVCAR4-8							wt	0	0	2405	25308	0	8738	0	[illegible]	[illegible]
OVCAR5-7							mutant	0	1341	880	98880	[illegible]	2132	0	[illegible]	[illegible]
OVCAR5-8							mutant	0	79	476	13621	[illegible]	1	0	0	971
MCF-7-8							wt	0	284	0	40587	0	208	0	0	342
ADR-RES-8							mutant	0	108	0	23303	0	181	0	323	1287
HeLa-8							HPV E6	0	1303	1836	31862	0	884	0	288	651
SW480-7							mutant	0	236	483	28435	0	1176	0	88	1435
SW480-8							mutant	0	1133	0	27332	0	1872	0	330	879
H1299-8							mutant	0	215	7288	20150	0	2881	0	53	728
C33A-7							mutant	0	1088	204	18811	0	0	0	0	850
C33A-8							mutant	0	7777	323	70434	0	3388	0	215	1883
U2OS-7							mutant	0	720	1487	83571	0	3482	0	113	879
U2OS-8							mutant	0	1325	826	33247	0	112	0	38	858
[illegible]-7							wt	0	88	622	78358	0	8382	0	0	855
[illegible]-8							wt	0	0	538	40810	0	1024	0	0	1105
WI 38-8							wt	0	55	0	82606	0	142	0	8	980
[illegible] RNA								86	348	18715	14788	157513	855	88	0	2438
CRL1572 3/17/00								0	0	154	1378	908	83	21	0	2241
Bov-4						84		110	70	107	3788	816	805	234	0	12872
HT388								0	33	0	4338	137	22	888	640	7852
HT378								0	30	0	4042	10	0	44	0	3843
HT386								893	115	251	5218	14108	1123	1190	133	10527
HT308								308	186	874	5219	0	287	298	0	6483
Bov-3						173		105	0	0	1404	249	0	0	0	4087
Bov-5						175		48	115	220	154	44	0	0	0	2716
Bov-8						177		0	0	0	1798	0	84	0	103	2493
h lymphocytes 2/23/00 #19								18	0	0	2182	2734	0	81	80	5086
Bov-10						237		87	88	0	4051	850	416	154	77	2480
HT810								48	73	821	8012	740	165	181	8	1821
h fibroblasts 3/21/00 #12								0	0	381	3370	0	818	0	111	1882
prostate, h								0	0	0	4530	0	0	0	0	474
MHNG-OS poly A+								236	87	4388	4880	286	485	375	11	12888
SA-OS (Moody) poly A+								832	0	2811	1291	6082	49	788	349	6795
MK poly A+								838	0	7825	1853	8843	271	1030	147	4771
HCT-116-3							wt	0	0	817	38808	0	1747	0	0	0
HCT-116-4							wt	0	211	234	32187	0	8246	0	52	307
HCT-116-5							wt	0	7	37	34680	0	3413	0	0	1034
HCT-116-6							wt	0	188	383	36888	0	1888	0	88	1308
A549-6							wt	0	0	0	21787	0	0	0	0	887
HT29-3							mutant	0	302	1678	18879	0	193	0	188	888
EKVX-6							mutant	0	0	41	24371	0	187	0	82	1103
HT29-4							mutant	0	132	0	25088	0	484	0	0	2528
HT29-5							mutant	0	31	1363	78872	0	628	0	0	822
HT29-6							mutant	0	470	0	42341	0	152	[illegible]	0	1229
OVCAR4-3							wt	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	8217	0	0	[illegible]
OVCAR4-4							wt	[illegible]	[illegible]	[illegible]	30781	0	2982	0	0	[illegible]
OVCAR4-5							wt	0	100	[illegible]	38312	[illegible]	8880	0	65	[illegible]
OVCAR4-6							wt	0	[illegible]	452	18032	[illegible]	312	0	515	8821
SF539-3							wt	0	112	4586	32580	0	1861	0	0	1253
SF539-4							wt	0	0	2488	27211	0	2208	0	38	1087
SF539-5							wt	0	38	178	22884	0	1847	0	236	1238
SF539-6							wt	0	211	1013	88830	0	0	0	282	827
OVCAR5-3							mutant	0	181	882	27675	0	1461	0	0	424
OVCAR5-4							mutant	0	402	884	18852	0	1206	0	362	817
OVCAR5-6							mutant	0	183	418	8373	0	483	0	0	477
ADR-RES-6							mutant	0	34	87	24285	0	806	0	0	578
MCF-7-6							wt	0	182	0	30348	0	32	0	84	881
HeLa-6							HPV E6	0	72	873	40487	0	1186	0	72	862
H1299-6							mutant	0	0	0	28441	0	4028	0	0	881
SW480-3							mutant	0	1787	444	24371	0	2777	0	88	884
SW480-4							mutant	0	797	50	38290	0	2235	0	0	1810
SW480-5							mutant	0	1245	884	82347	0	5886	0	289	1571
SW480-6							mutant	0	84	1207	31434	0	884	0	79	1880
C33A-3							mutant	0	1553	0	44178	0	1673	0	32	185
C33A-4							mutant	0	1129	155	28446	0	288	0	18	135
C33A-5							mutant	0	1088	711	29882	0	0	0	93	855
C33A-6							mutant	0	80	378	21348	0	86	0	30	350
[illegible]-6							wt	0	434	0	33074	0	0	0	123	412
U2OS-3							mutant	0	58	2847	82229	0	6382	0	0	1217
U2OS-4							mutant	0	885	884	80322	0	4818	0	202	1229
U2OS-5							mutant	0	197	3251	78404	0	8848	0	120	1287
U2OS-6							mutant	0	44	369	25411	0	83	0	0	1748
WI 38-6							wt	0	68	0	16781	0	112	0	0	578
[illegible]-3							wt	0	0	856	46605	0	4873	0	0	838
[illegible]-4							wt	0	72	4286	88882	0	10191	0	481	2144
SF-268-6							mutant	0	111	148	47208	0	8536	0	33	718
SF-268-4							mutant	0	1	226	48802	0	4135	0	0	805
SF-268-5							mutant	0	80	981	54194	0	8455	0	0	1182
SF-268-8							mutant	0	0	804	27680	0	7780	0	0	814
OvPong-43								0	0	1183	136780	0	4570	0	0	353
[illegible]-20								0	0	239	221297	0	1384	0	213	785
[illegible]-21								0	0	0	98785	0	8061	0	114	1116
[illegible]-22								0	0	0	118088	0	8653	0	0	1115
OVCAR5-6							mutant	0	81	0	85862	0	2188	0	0	588
[illegible]-10								0	53	0	27408	0	888	0	0	418
[illegible]-11								0	12	1	18844	0	232	0	22	0
[illegible]-12								0	28	887	81131	0	8219	0	0	1103
[illegible]-13								0	32	0	73783	0	3887	0	84	884
[illegible]-14								0	93	16	88828	0	8887	0	231	1108
[illegible]-15								0	0	0	88153	0	6341	0	228	1552
[illegible]-16								0	0	0	48282	0	6586	0	73	1048
[illegible]-17								0	170	0	257777	0	17808	0	0	1258
[illegible]-18								0	0	2254	218278	0	6806	0	148	1116
[illegible]-19								0	141	88	45120	0	7770	0	0	822

Table 3 (cont'd)

Tissue	Tumor-cyto	Normal-cyto	Tumor - ts	Tumor cells	Normal	Endos	p53	SEQ 95 AA	SEQ 96 AA	SEQ 97 NA	SEQ 100 A	SEQ 101 A	SEQ 110 A	SEQ 111 A	SEQ 112 A	SEQ 114 N
adrenal gland - h		1						0	620	8217	18583	5311	3706	32946	560	18327
lymph node - h		2						143	1220	11829	24718	19827	8388	19401	882	19488
bone marrow - h		3						0	833	3258	4084	6045	4161	18644	1113	4801
mammary gland - h		4						121	306	949	403	452	1581	1216	553	3851
brain - h		5						488	947	2461	11046	2517	8005	85845	745	12780
pancreas - h		6						543	805	1776	11768	4269	4387	15743	1117	11146
cerebellum - h		7						342	1137	14444	44712	4832	2800	76814	1388	51364
pituitary gland - h		8						815	831	4652	21432	8817	4163	27271	1158	19044
fetal brain - h		9						0	1302	3571	20240	4881	7301	98138	1549	38240
placenta - h		10						863	818	7524	4384	8283	3481	51723	1725	38256
fetal kidney - h		11						1088	1190	8450	16797	9588	4328	34771	2075	49585
prostate - h		12						583	1311	788	7308	810	2872	14850	1414	30916
fetal liver - h		13						246	1238	3869	4142	1438	4358	14560	907	11285
salivary gl. - h		14						841	488	2624	7760	2508	9846	20032	1128	18188
fetal lung - h		15						1184	808	2215	12136	8087	8322	18162	1636	87915
skeletal muscle - h		16						249	805	808	3018	633	2580	113112	1787	13497
heart - h		17						22	708	3722	2385	1138	1481	41333	1154	37256
small intestine - h		18						0	624	2431	8421	3280	2070	10871	1713	19816
kidney - h		19						881	386	8028	14631	4876	4912	28886	1331	12278
spinal cord - h		20						1080	284	1535	4310	1780	846	16408	1058	8030
liver - h		21						0	428	1811	8137	1885	2116	19447	1435	4737
spleen - h		22						331	348	4882	8027	3412	1301	6880	1888	4258
lung - h		23						[illegible]	[illegible]	[illegible]	8947	4177	1821	13028	892	28815
stomach - h		24						0	[illegible]	[illegible]	3228	1851	2145	6009	1775	[illegible]
[illegible] - h		25						16438	2814	[illegible]	4231	29181	[illegible]	67389	[illegible]	3885
[illegible] - h		27						700	414	6038	18072	21136	[illegible]	11803	[illegible]	13111
HPAEC		28				28		703	187	0	239	1182	4888	4272	331	0
thyroid gland - h		29						681	880	1230	4784	3196	2800	21887	818	24486
RPTEC		30				30		181	816	0	380	1052	3123	1220	723	0
trachea - h		31						586	740	4384	8881	10717	2086	13172	1555	86886
HMEC		32						0	844	260	95	115	3044	1023	1182	2038
uterus - h		33						0	818	2915	8459	2889	1347	20080	1100	67098
HCAEC		34						0	298	0	454	0	3408	1110	806	0
Pancreas - h		35						0	461	0	312	222	1827	980	830	0
lymph node - h		36						746	473	442	201	11	1081	883	948	1325
Skeletal muscle - h		37						0	375	169	0	0	1441	1986	720	0
fetal liver - h		38						0	842	0	363	0	3211	1382	1654	901
Heart - h		39						0	338	1343	0	0	1184	3383	868	149
thymus - h		40						143	622	0	488	363	2819	841	1219	0
Duodenum - h		41						906	290	618	138	11	2938	0	1884	0
Fetal brain - h		42						629	408	0	573	464	1788	377	2223	0
Salivary gl. - h		43						0	421	154	0	145	1888	1341	1283	0
testis - h		44						1653	636	2190	425	3878	2371	978	1846	0
HT218-normal					385			0	323	0	0	0	734	53	348	0
HT212-normal					383			0	0	288	151	0	120	0	134	0
HT197-normal					381			0	0	0	18	0	83	2494	165	0
Bov-13					366	366		4165	8888	345	634	323	8777	296	2419	16347
Bov-12					354	354		7286	3210	1258	308	80	4808	182	1521	16388
cerebellum - h					344			0	254	82	225	35	297	64	858	0
brain - h					342			0	0	32	288	0	348	0	462	264
RPTEC					334	334		0	348	0	0	0	798	0	1088	0
lymph node - h					332			0	0	11	19	24	84	45	836	0
h adult SMC 1021/02 817					330			80	81	0	87	0	71	0	887	0
Fetal brain - h					328			1807	3885	0	1912	109	3829	438	1452	7258
HT388-normal					327			0	881	0	171	0	118	411	429	0
thymus - h					326			309	4778	86	727	0	1388	82	1824	8521
HT149 - normal					321			216	45	0	0	0	0	72	765	0
HEPM 24 untreated					320			0	780	0	283	238	2579	21	1311	0
uterus - h					318			2810	1322	774	2029	2189	4202	471	1087	2888
trachea - h					316			812	74	0	1132	1683	2843	0	701	1532
thyroid gland - h					314			184	271	0	749	2547	2342	333	730	2522
salivary gl. - h					311			0	0	0	163	47	68	251	1072	0
prostate - h					309			58	591	47	135	342	108	187	462	0
pituitary gland - h					307			306	610	158	464	88	1874	0	401	0
pancreas - h					306			0	78	0	387	200	626	535	749	0
mammary gland - h					303			0	1878	0	1884	675	1378	48	833	0
bladder - h					302			0	0	3904	123	72	306	2554	888	228
[illegible]					298			7748	6576	2195	2085	3779	4087	1271	[illegible]	4479
[illegible] - h					297			2206	[illegible]	0	[illegible]	[illegible]	2776	[illegible]	[illegible]	1872
[illegible]					295			0	[illegible]	0	[illegible]	[illegible]	[illegible]	[illegible]	801	[illegible]
spinal cord - h					294			1237	1442	0	1800	[illegible]	[illegible]	75	[illegible]	488
small intestine - h					292			0	0	0	1413	265	313	0	946	85
skeletal muscle - h					280			1434	482	0	3317	886	1887	277	801	2240
bone marrow - h					279			2288	171	0	0	0	865	288	485	0
adrenal gland - h					277			0	744	0	0	248	1362	374	884	0
HPAEC					276	276		0	14	887	0	0	407	181	801	0
HT383-normal					288			0	7	0	508	113	288	184	863	0
HT282-normal					288			0	0	1147	181	0	0	246	738	762
Bov-11					238	238		0	300	222	357	889	834	2867	1460	0
Bov-8					235	235		0	88	88	127	40	0	481	791	0
HT373-normal					234			78	1472	0	191	184	1276	0	1532	0
Bov-7					233	233		0	338	447	153	0	70	1884	862	0
Bov-6					231	231		0	835	385	217	81	228	2538	817	0
Bov-2					229	229		316	818	0	12	25	884	484	719	0
Bov-1					227	227		184	287	0	0	2	82	1087	847	0
bladder - h					222			0	57	0	0	86	849	46	483	0
Heart - h					216			0	408	0	0	0	314	0	1007	0
stomach - h					214			0	208	281	193	230	741	883	876	0
fetal liver - h					213			36	84	147	0	67	0	182	1042	0
placenta - h					212			0	338	0	387	814	832	533	865	0
HCAEC					211	211		0	67	0	0	88	0	259	793	0
fetal brain - h					210			0	179	0	288	0	188	541	580	0
HMEC					209			0	317	0	181	0	284	0	751	0
Duodenum - h					205			0	180	92	0	0	733	0	765	21
Skeletal muscle - h					202			0	141	279	68	0	115	0	881	0
Pancreas - h					201			87	473	0	125	0	668	0	725	0
testis - h					199			95	104	0	111	148	123	0	481	0
Salivary gl. - h					197			143	0	0	222	110	43	422	636	0
HEPM 3d TGFB1 [illegible]					185			0	88	0	158	78	238	0	387	0
thymus - h					183			453	452	0	348	119	2341	107	608	0
WI-38 72h					179			0	178	0	0	78	388	0	377	0
lymph node - h					61			0	873	0	0	169	1190	64	839	0
lung - h						59		0	2301	0	778	748	2537	383	858	0
kidney - h					57			0	482	240	142	182	808	52	787	0
heart - h					55			64	625	0	279	119	338	0	522	0
fetal lung - h					53			681	408	855	88	0	814	0	447	0
fetal liver - h					51			0	0	214	30	45	456	386	325	0
fetal kidney - h					49			0	92	311	213	138	482	0	798	0
HELA-2h-031000				79				0	408	115	288	0	336	454	774	278
HELA-4h-031000				81				0	337	0	201	0	888	102	779	0
HELA-6h-031000				83				0	243	0	212	0	381	321	1274	0
HELA-8h-031000				85				491	887	0	255	51	483	0	846	0
HELA-8h-031000				86				294	888	0	448	76	8211	1347	2176	0
HELA-9h-031000				90				346	228	0	200	211	2441	178	1088	302
HELA-10h-031000				92				0	0	0	285	219	288	313	1114	36
HELA-11h-031000				94				0	138	0	123	11	0	788	1073	0
HELA-12h-031000				96				104	210	328	18	121	172	247	1208	0
NCI-H322M				146				540	77	248	330	2183	677	42	170	0
NCI-H460				148				0	0	0	238	1214	168	98	431	0
NCI-H522				150				273	154	185	144	1241	0	0	362	0
SNB-19				152				0	121	0	134	553	1020	81	220	283
SNB-75				154				0	343	0	260	527	881	277	808	0
SF-268				156				0	448	898	173	819	838	0	182	0
SF-295				158				0	87	0	221	342	0	0	742	4819
CCRF-CEM				160				231	343	486	175	256	20	252	484	1672
DU-145				162				346	0	0	0	238	352	0	294	0
HCT 116				164				322	205	344	55	102	0	0	138	0

Table 3 (cont'd)

Tissue	Tumor-cyto	Normal-cyto	Tumor - 1o	Tumor cells	Normal	Endos	p53	SEQ 95 AA	SEQ 96 AA	SEQ 97 NA	SEQ 100 A	SEQ 101 A	SEQ 110 A	SEQ 111 A	SEQ 112 A	SEQ 114 N
Caki-1				186				6	377	308	131	1114	713	82	303	0
786-0				188				238	355	21	45	4121	1818	0	1856	0
T-47D				169				0	152	14	104	5001	1079	0	708	0
Ken-3				171				0	3	150	85	0	336	8	530	0
CRL 1441 RNA 8/30				181				31	447	8	1	81	747	8	528	0
786T untreated + DNase				183				0	203	8	0	122	64	236	303	0
503 poly A+				194				0	0	253	278	1030	237	0	446	0
HOS poly A+				196				8	0	131	130	183	258	0	474	0
ACHN				198				118	283	0	87	1046	885	0	853	0
UACC-62				200				227	891	0	64	1408	1221	167	808	0
MCF-7/ADR-RES				202				0	78	137	0	167	130	172	257	0
UTOS (Mandy) poly a+				204				305	524	948	8	73	3426	158	431	0
WI38 (Collagen) poly A+				206				0	0	888	8	283	474	0	197	10
458 medulla mRNA				208				712	1711	0	361	288	1345	0	858	0
CCL137 RNA 3/21/00				218				347	181	680	27	168	0	0	452	8
WI-38 72h 0.5%FBS, 24h 10% FBS				219				0	186	0	111	30	115	8	386	8
CRL 1441 + TPA (24h) 8/30				220				0	0	92	138	41	322	8	477	6
Ken-1				221				0	80	0	8	42	212	184	577	0
Ken-2				223				0	140	181	117	180	117	0	478	815
Ken-4				225				8	172	305	31	0	86	8	487	8
HOP-62				241				0	0	197	165	385	80	8	86	1800
MOLT-4				242				10	0	173	804	2918	787	824	294	8
[illegible]				243				[illegible]	302	[illegible]	[illegible]	[illegible]	720	320	[illegible]	0
[illegible]				244				[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	330	86	18	817
NCI-H23				245				[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	183	8	337	6
RPMI 8226				246				6	450	847	146	1617	0	[illegible]	[illegible]	0
A549/ATCC				247				225	108	8	312	837	249	8	[illegible]	881
SR				248				0	122	8	229	298	823	8	425	0
OVCAR-3				249				0	0	1127	321	3870	467	215	306	270
HCT-15				250				18	423	64	448	1543	831	382	484	8887
OVCAR-4				251				8	84	421	79	463	453	0	186	0
UO-31				252				197	270	8	207	62	34	8	41	0
OVCAR-5				253				0	816	8	73	8728	1339	0	351	305
SN12C				255				880	388	882	8	1418	388	452	687	0
OVCAR-8				256				783	0	0	19	193	265	8	276	0
LOX IMVI				258				227	841	454	732	2188	814	367	703	0
IGROV1				257				8	880	864	458	1087	288	189	826	0
SK-MEL-2				258				0	212	0	83	47	246	8	204	0
SK-OV-3				259				8	572	8	8	634	448	415	853	0
SK-MEL-5				260				211	0	0	8	1528	325	8	463	0
SF-539				261				0	252	8	158	2048	1851	8	1121	0
SK-MEL-28				262				8	884	1838	0	1332	1027	0	837	0
K-562				263				82	8	780	287	473	91	32	844	302
UACC-257				265				0	0	0	78	2168	805	8	483	0
M14				266				408	0	0	70	414	119	114	186	8
MCF7				267				472	8	0	2572	17838	1425	8	1304	8
MDA-MB-435				269				0	73	0	136	1853	108	8	88	0
HT278				270				8	838	0	41	0	1085	0	800	480
MDA-N				271				78	278	0	0	1378	488	847	221	0
Y79 poly A+				272				0	810	327	218	1924	1367	0	1481	1821
IOH26 poly A+				288				0	158	147	1711	2315	1851	0	513	0
HT1080 24h TPA RNA 8/23				308				0	383	85	218	37	0	0	404	0
HELA-EXP-6/14/00				313				0	0	207	141	0	6	0	288	0
HT1080 6h RNA				322				808	1211	0	129	225	1286	0	1375	3086
HT347				323				0	246	0	222	211	117	0	749	0
458 medulla RNA				324				338	1804	0	0	58	1282	0	901	4155
NCI-H226				326				0	77	0	0	3462	484	8	814	0
HOP-62				332				0	0	219	857	413	388	0	16	0
MDA-MB-231				336				883	8	0	836	32087	4881	0	1033	3276
T221				339				2821	1873	83	2315	28387	11887	1195	1018	3184
PT cells poly A+				340				136	0	0	282	858	228	28	144	0
PC-3				341				383	1328	0	842	3008	1872	0	1051	858
HCC-2998				343				300	846	280	44	1152	482	0	485	0
SW-620				345				207	1338	0	20	1834	792	0	423	0
HT192				346				0	232	109	0	217	0	7	88	0
COLO 205				347				0	845	0	168	822	87	113	386	0
HT210				348				0	308	41	8	0	272	0	446	0
KM12				349				0	1263	8	68	880	227	180	181	0
[illegible]				350				3	476	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]				351				[illegible]	2884	628	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
HT385				352				0	[illegible]	[illegible]	435	54	700	[illegible]	[illegible]	[illegible]
SNF 26J				353				173	1824	0	98	448	185	279	[illegible]	485
TK-10				356				4314	2783	0	858	3338	4922	482	1378	8137
Malme-3M				357				1133	4380	0	1484	22112	4881	1835	1824	2340
Hs 578T				358				0	459	0	8	327	205	142	945	354
HT213			50					0	861	848	257	17	1388	0	248	0
HT288			62					0	502	0	8	2784	1622	180	438	0
HT138			64					8	646	130	37	0	355	0	354	0
HT156			66					8	280	0	8	387	782	0	825	0
HT183			66					0	288	0	47	0	870	0	482	0
HT170			68					482	2258	0	412	28	1722	72	1138	8
HT172			60					0	1113	0	8	41	822	0	608	8
HT138			63					8	812	78	234	0	8	0	552	0
HT176			88					8	148	0	163	28	0	78	600	37
HT184			66					0	194	65	64	270	852	0	383	8
HT180			66					8	0	0	384	81	881	0	679	8
HT188			67					8	919	0	179	7	888	0	451	301
HT189			68					329	428	8	77	139	180	189	1829	0
HT143			68					8	20	65	28	0	61	0	728	8
HT198			70					8	288	668	478	27	418	0	1892	0
HT145			71					449	880	0	338	84	1127	0	2057	277
HT227			72					312	1880	358	187	781	1787	83	1137	708
HT302			73					0	184	8	284	118	2888	1837	828	0
HT314			74					0	33	8	222	8	834	727	812	8
HT317			76					180	588	8	750	180	2488	782	887	8
Medulloblastoma (425_118)			77					8	2	8	388	8	448	0	388	8
HT322			78					0	616	0	488	7	838	438	1116	0
HT323			80					281	873	280	112	0	880	173	887	6
HT336			82					45	348	8	128	0	576	181	808	0
HT198			86					0	0	288	20	0	219	0	173	0
HT348			87					0	480	8	128	51	112	373	1349	182
HT311			176					221	27	0	0	28	0	101	846	138
HT288			186					0	1887	0	52	0	887	0	846	0
HT190			187					0	277	0	185	0	858	0	517	0
HT301			188					0	0	0	63	0	881	0	453	0
HT372			191					0	581	7	197	0	300	0	576	0
TCGP			207					421	888	0	109	86	375	142	863	8
HT188			216					0	0	0	45	84	135	67	345	8
HT307			217					8	8	0	275	203	403	0	291	1888
HT388			224					224	1098	172	384	0	1186	0	773	2380
HT370			228					8	218	0	0	85	408	0	856	8
HT371			228					0	347	0	386	1	882	256	720	0
HT377			230					0	172	0	290	88	207	87	774	0
HT380			238					8	71	286	88	11	0	88	738	8
[illegible] RNA			281					8	38	0	8	8	287	298	842	8
HT334			290					0	1249	828	383	758	787	241	1030	8
HT338			301					0	2030	0	796	0	880	137	802	8
HT362			315					570	44	8	288	182	347	0	400	8
HT304			317					0	0	0	105	0	127	18	471	8
HT312			319					0	38	8	8	28	147	281	549	488
HT182			325					388	0	8	8	34	0	174	408	0
HT308			358					0	0	8	106	0	0	100	880	8
HT157			388					0	0	8	10	14	470	8	888	6
T-47D	163							4583	188	845	825	1180	8222	1028	868	1143
MDA-N	161							1843	308	871	1441	814	8740	8767	730	8208
MDA-MB-435	158							4884	379	1184	1887	938	8884	4457	878	2808
MDA-MB-231	157							11137	2218	0	1828	1858	28345	3387	1579	388

Table 3 (cont'd)

Tissue	Tumor-sym	Normal-sym	Tumor - 1o	Tumor cells	Normal	Endo	p53	SEQ 95 AA	SEQ 96 AA	SEQ 97 AA	SEQ 100 A	SEQ 101 A	SEQ 110 A	SEQ 111 A	SEQ 113 A	SEQ 114 A
Hs 578T	155							2529	943	0	1798	2080	12004	10483	665	14282
MCF-7/ADR-RES	153							491	817	1977	881	686	10679	6354	882	0
MCF7	151							8433	1236	160	8806	3880	25834	2094	1308	2238
M14	149							3631	0	450	2401	1983	3478	1359	1035	0
UACC-257	147							4023	388	1208	2278	2137	11053	6220	678	947
UACC-62	146							2546	157	726	798	1215	4403	2488	589	429
SK-MEL-28	144							8634	60	2606	1173	721	3089	1531	805	2945
UO-31	143							5324	487	2107	604	442	3000	1020	1536	11007
SK-MEL-5	142							1338	0	1009	2281	2826	18384	2804	691	3386
KM-12	141							281	319	0	488	0	3403	379	443	0
SK-MEL-2	140							2814	186	1844	1741	479	18872	1717	918	3811
HCT-15	139							4882	486	656	1930	388	8858	682	979	1620
Malme-3M	138							1290	46	865	2381	1148	7970	2364	843	2899
COLO 205	137							3538	181	1983	1864	1417	11150	231	1214	1103
LOX IMVI	136							3634	82	1973	1538	677	23802	2457	867	1885
SW-620	135							4581	483	1385	1190	828	13216	571	850	1756
TK-10	134							4848	318	1863	886	484	9544	2033	821	1147
HCT 116	133							1236	384	579	1534	323	6848	365	768	0
786-0	132							2284	182	1883	638	792	11840	2319	732	0
HCC-2998	131							2884	28	0	1232	719	9839	868	904	0
ACHN	130							2287	488	2088	1078	836	38009	2863	852	0
PC-3	129							8813	370	0	719	646	13846	2588	643	0
[illegible]	128							614	317	8314	911	640	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	127							1412	63	671	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
CAKI-1	126							2183	[illegible]	[illegible]	[illegible]	[illegible]	8405	[illegible]	[illegible]	1386
SR	125							3471	223	0	811	[illegible]	19003	1193	246	911
A498	124							8481	0	1125	1867	368	20834	10429	828	1032
RPMI 8226	123							1851	48	44	228	364	1928	0	863	654
SN12C	122							2088	184	800	178	1633	11749	11038	834	837
HL-60	121							830	0	0	294	649	2184	395	634	0
MOLT-4	120							6883	0	1010	622	1507	4271	793	1206	0
OVCAR-5	119							1380	119	1730	1886	2515	8853	1800	825	6825
K-562	118							3767	0	0	880	252	8345	1008	1091	289
OVCAR-4	117							1258	284	0	1029	2228	11490	3863	1253	867
CCRF-CEM	116							6823	86	1588	2572	1638	29882	2716	881	1348
OVCAR-3	115							2088	150	1653	834	1582	12158	1242	842	0
SF-539	114							2627	457	10	717	387	16856	883	882	1468
HOP-62	113							455	0	1559	873	285	19246	3408	282	1027
SF-295	112							3017	538	75	1118	801	17864	1980	841	0
A549/ATCC	111							1880	840	1723	2304	1701	30228	3221	1074	781
SF-268	110							2250	208	1443	583	1814	11939	4509	843	1886
NCI-H522	109							1284	0	1176	1767	1721	7210	1486	876	1034
U251	108							2200	208	729	877	738	8651	3618	538	2250
NCI-H460	107							2274	448	1277	828	838	17629	1892	676	0
SNB-75	106							1148	228	0	405	288	4322	1304	722	0
NCI-H322M	105							3388	436	0	3825	1847	20442	338	559	327
SNB-19	104							2008	316	0	1883	436	4368	2108	812	1908
NCI-H226	103							8463	125	0	1140	758	4785	1852	1081	0
SK-OV-3	102							6185	418	0	1085	815	13274	5271	587	3219
NCI-H23	101							8803	311	0	1182	841	7912	446	380	0
IGROV1	100							212	0	0	1883	888	10757	0	480	0
EKVX	99							1881	178	77	1733	816	17099	1357	340	842
OVCAR-8	98							3654	0	477	422	150	7006	376	782	0
HOP-92	97							2307	158	0	886	828	13230	8619	887	481
h fibroblasts [illegible] #12	48							334	84	16	280	21	1718	823	1434	0
h adult SMC [illegible] #17	47							288	10	108	221	0	1288	602	1342	0
h keratinocytes [illegible] #16	46							534	306	0	193	62	6234	8718	1436	7862
TCGP	28							1080	737	4716	402	636	2721	1945	24	1762
A549-1							wt	0	0	0	8421	18	0	363	825	0
A549-3							wt	0	0	0	4212	30	0	0	402	0
A549-4							wt	0	0	0	6323	48	0	687	404	0
A549-5							wt	0	0	0	2872	210	0	88	636	0
A549-7							wt	0	0	0	182	118	0	630	580	0
EKVX-1							mutant	0	0	0	1343	0	0	438	817	0
EKVX-4							mutant	0	0	0	43880	11	0	657	705	0
EKVX-3							mutant	0	0	0	934	0	0	0	708	0
EKVX-5							mutant	0	0	0	0	207	0	283	768	0
EKVX-7							mutant	0	0	0	1576	72	0	126	802	0
MCF-7-1							wt	0	0	0	719	64	0	[illegible]	[illegible]	0
MCF-7-3							wt	0	[illegible]	0	[illegible]	85	[illegible]	[illegible]	[illegible]	[illegible]
MCF-7-4							wt	0	[illegible]	0	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
MCF-7-5							wt	0	[illegible]	[illegible]	[illegible]	180	0	0	[illegible]	0
MCF-7-7							wt	0	0	0	1337	145	0	[illegible]	638	0
ADR-RES-1							mutant	0	0	0	3885	0	0	[illegible]	2343	0
ADR-RES-3							mutant	0	0	0	525	88	0	168	886	0
ADR-RES-4							mutant	0	0	0	851	0	0	0	835	0
ADR-RES-5							mutant	0	0	0	472	112	0	0	588	0
ADR-RES-7							mutant	0	0	0	7982	0	0	329	670	0
WI 38-1							wt	0	0	0	0	222	0	2187	854	0
WI 38-3							wt	0	0	0	217	672	0	581	558	0
WI 38-4							wt	0	0	0	751	79	0	648	548	0
WI 38-5							wt	0	0	0	3721	114	0	1814	829	0
WI 38-7							wt	0	0	0	4617	0	0	0	956	0
HeLa-1							HPV E6	0	0	0	12821	108	0	0	1073	0
HeLa-3							HPV E6	0	0	0	843	263	0	74	884	0
HeLa-4							HPV E6	0	0	0	3311	270	0	585	871	0
HeLa-5							HPV E6	0	0	0	1186	816	0	1402	1159	0
HeLa-7							HPV E6	0	0	0	1048	460	0	0	801	0
H1299-1							mutant	0	0	0	0	0	0	0	703	0
H1299-3							mutant	0	0	0	0	0	0	212	808	0
H1299-4							mutant	0	0	0	2070	330	0	147	1342	0
H1299-5							mutant	0	0	0	1806	183	0	868	878	0
H1299-7							mutant	0	0	0	0	0	0	0	719	0
A549-2							wt	0	0	0	4278	141	0	408	585	0
EKVX-2							mutant	0	0	0	2083	86	0	0	373	0
HCT-116-1							wt	0	0	0	8687	143	0	1327	1078	0
HCT-116-2							wt	0	0	0	3758	44	0	2853	816	0
HT29-2							mutant	0	0	0	1380	186	0	1005	1046	0
SF539-1							wt	0	0	0	1840	198	0	220	858	0
SF539-2							wt	0	0	0	2474	10	0	387	719	0
SF-268-1							mutant	0	0	0	317	2004	0	1212	886	0
SF-268-2							mutant	0	0	0	560	282	0	451	853	0
OVCAR-4-1							wt	0	0	0	89	819	0	375	1271	0
OVCAR-4-2							wt	0	0	0	1543	186	0	714	1200	0
OVCAR-5-1							mutant	0	0	0	581	154	0	430	914	0
OVCAR-5-2							mutant	0	0	0	10	80	0	535	632	0
MCF-7-2							wt	0	0	0	1433	48	0	0	430	0
ADR-RES-2							mutant	0	0	0	731	138	0	23	786	0
HeLa-2							HPV E6	0	0	0	0	107	0	1170	780	0
SW480-1							mutant	0	0	0	0	632	0	0	865	0
SW480-2							mutant	0	0	0	7828	1023	0	843	879	0
H1299-2							mutant	0	0	0	2573	18	0	1147	1143	0
C33A-1							mutant	0	0	0	18707	0	0	0	856	0
C33A-2							mutant	0	0	0	1155	1	0	114	748	0
U2OS-1							mutant	0	0	0	85	186	0	568	887	0
U2OS-2							mutant	0	0	0	0	183	0	1008	871	0
[illegible]-1							wt	0	0	0	882	487	0	40	667	0
[illegible]-2							wt	0	0	0	886	0	0	846	931	0
WI 38-2							wt	0	0	0	3476	0	0	881	1129	0
[illegible]-1								0	0	0	285	57	0	178	638	0
[illegible]-2								0	0	0	3267	402	0	0	872	0
[illegible]-3								0	0	0	886	388	0	1724	610	0
[illegible]-4								0	0	0	0	143	0	178	583	0
[illegible]-5								0	0	0	0	71	0	319	481	0
[illegible]-6								0	0	0	8430	1	0	0	414	0
[illegible]-8								0	0	0	1887	8531	0	2588	867	0
[illegible]-9								0	0	0	0	0	0	0	1734	0

Table 3 (cont'd)

Tissue	Tumor-syn	Normal-syn	Tumor - fx	Tumor cells	Normal	Endos	p53	SEQ 96 AA	SEQ 96 AA	SEQ 97 NS	SEQ 100 A	SEQ 101 A	SEQ 110 A	SEQ 111 A	SEQ 112 A	SEQ 114 N
DuPong-7								0	0	0	4153	258	0	1186	786	0
DuPong-8								0	0	0	0	72	0	1136	384	0
DuPong-9								0	0	0	352	17	0	2407	903	0
DuPong-11								0	0	0	2910	477	0	1191	732	0
DuPong-12								0	0	0	0	90	0	6703	388	0
DuPong-10								0	0	0	11437	112	0	810	863	0
DuPong-1								0	0	0	0	86	0	130	638	0
DuPong-2								0	0	0	282	0	0	208	737	0
DuPong-3								0	0	0	8086	88	0	337	870	0
DuPong-4								0	0	0	3678	67	0	3608	784	0
DuPong-5								0	0	0	217	72	0	1060	843	0
DuPong-6								0	0	0	0	40	0	62	1067	0
A549-8							wt	0	0	0	1853	79	0	59	822	0
EKVX-8							mutant	0	0	0	6488	207	0	334	847	0
HCT-116-7							wt	0	0	0	0	209	0	84	573	0
HCT-116-8							wt	0	0	0	846	122	0	176	676	0
HT29-1							mutant	0	0	0	3501	0	0	855	844	0
HT29-7							mutant	0	0	0	2147	20	0	214	833	0
HT29-8							mutant	0	0	0	467	0	0	200	788	0
SF539-7							wt	0	0	0	373	55	0	21	864	0
SF539-8							wt	0	0	0	0	252	0	21	883	0
SF-268-7							mutant	0	0	0	448	164	0	706	829	0
SF-268-8							mutant	0	0	0	0	183	0	303	848	0
OVCAR-4-7							wt	0	0	[illegible]	1305	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]							[illegible]	0	[illegible]	[illegible]	1327	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
OVCAR-8-7							[illegible]	[illegible]	[illegible]	[illegible]	328	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
OVCAR-8-8							mutant	0	0	0	0	216	0	811	808	0
MCF-7-8							wt	0	0	0	740	184	0	810	880	0
ADR-RES-8							mutant	0	0	0	3013	0	0	295	1032	0
HeLa-8							HPV E6	0	0	0	2343	117	0	138	875	0
SW480-7							mutant	0	0	0	1081	452	0	0	1625	0
SW480-8							mutant	0	0	0	7328	417	0	302	712	0
H1299-8							mutant	0	0	0	2363	0	0	0	737	0
C33A-7							mutant	0	0	0	3128	0	0	183	760	0
C33A-8							mutant	0	0	0	1813	0	0	538	1083	0
U2OS-7							mutant	0	0	0	2184	0	0	13	831	0
U2OS-8							wt	0	0	0	0	167	0	468	888	0
Hs68-7							wt	0	0	0	4534	808	0	171	615	0
Hs68-8							wt	0	0	0	4487	0	0	301	578	0
WI 38-8							wt	0	0	0	67	0	0	904	973	0
408 module RNA								0	380	134	304	1664	1336	1421	1814	0
CRL 1972 3/17/99								0	104	0	32	0	42	443	338	1013
Bm-1						91		274	484	0	75	153	872	2372	1229	2096
HT368								1326	1327	0	217	70	6103	0	922	0
HT378								28	184	0	163	65	723	0	939	0
HT388								278	2601	0	670	60	4081	375	1937	3835
HT308								0	234	0	440	0	484	95	2633	62094
Bm-2						172		0	0	186	34	115	0	0	637	0
Bm-5						175		0	336	780	0	0	98	301	345	0
Bm-6						177		576	385	261	104	0	463	119	621	0
h keratinocytes 3/25/02 #11								0	1129	385	0	0	708	195	619	0
Bm-10						227		0	0	14	0	16	0	1516	309	0
HT818								0	180	0	242	0	483	408	1308	0
h fibroblasts 3/21/02 #12								0	362	226	91	46	0	84	1057	0
prostate, h								0	182	86	187	60	180	0	1021	0
MMMG-OS poly A+								82	0	0	493	845	1535	0	833	0
SA-OS poly A+								1046	71	0	572	836	2116	211	808	808
AH poly A+								1194	1814	0	778	1386	2280	288	1231	186
HCT-116-3							wt	0	0	0	2064	180	0	382	615	0
HCT-116-4							wt	0	0	0	0	56	0	1404	189	0
HCT-116-5							wt	0	0	0	377	14	0	754	414	0
HCT-116-6							wt	0	0	0	260	0	0	1034	888	0
A549-6							wt	0	0	0	4348	0	0	343	913	0
HT29-3							mutant	0	0	0	3771	100	0	378	803	0
EKVX-6							mutant	0	0	0	0	0	0	175	386	0
HT29-4							mutant	0	0	0	0	0	0	813	644	0
HT29-5							mutant	0	0	0	1388	298	0	238	711	0
HT29-6							mutant	0	0	0	0	194	0	0	810	0
OVCAR-3-3							wt	0	[illegible]	0	1158	42	[illegible]	880	588	0
OVCAR-4-4							[illegible]	[illegible]	[illegible]	[illegible]	487	[illegible]	[illegible]	0	844	[illegible]
[illegible]							[illegible]	0	[illegible]	0	[illegible]	[illegible]	0	872	[illegible]	[illegible]
OVCAR-4-[illegible]							[illegible]	0	[illegible]	0	522	[illegible]	[illegible]	[illegible]	731	[illegible]
SF539-3							wt	0	0	0	0	131	0	315	862	0
SF539-4							wt	0	0	0	0	98	0	494	624	0
SF539-5							wt	0	0	0	1480	79	0	684	806	0
SF539-6							wt	0	0	0	617	0	0	0	1057	0
OVCAR-8-3							mutant	0	0	0	2313	82	0	278	988	0
OVCAR-8-4							mutant	0	0	0	3086	438	0	72	758	0
OVCAR-8-5							mutant	0	0	0	444	0	0	0	307	0
ADR-RES-5							mutant	0	0	0	802	175	0	0	723	0
MCF-7-6							wt	0	0	0	2112	38	0	843	1131	0
HeLa-6							HPV E6	0	0	0	0	883	0	0	1263	0
H1299-6							mutant	0	0	0	368	1111	0	674	771	0
SW480-3							mutant	0	0	0	228	300	0	388	841	0
SW480-4							mutant	0	0	0	3044	80	0	0	708	0
SW480-5							mutant	0	0	0	0	577	0	379	1149	0
SW480-6							mutant	0	0	0	240	450	0	1271	1267	0
C33A-3							mutant	0	0	0	0	88	0	165	1108	0
C33A-4							mutant	0	0	0	0	0	0	0	821	0
C33A-5							mutant	0	0	0	211	0	0	881	1143	0
C33A-6							mutant	0	0	0	675	313	0	1294	1256	0
Hs68-6							wt	0	0	0	0	807	0	0	618	0
U2OS-3							mutant	0	0	0	86	836	0	201	728	0
U2OS-4							mutant	0	0	0	2742	15	0	146	681	0
U2OS-5							mutant	0	0	0	1376	219	0	622	718	0
U2OS-6							mutant	0	0	0	528	0	0	1087	626	0
WI 38-6							wt	0	0	0	4047	0	0	0	738	0
Hs68-3							wt	0	0	0	4744	204	0	785	808	0
Hs68-4							wt	0	0	0	1334	2368	0	2882	1018	0
SF-268-3							mutant	0	0	0	740	1384	0	0	564	0
SF-268-4							mutant	0	0	0	6402	1398	0	751	721	0
SF-268-5							mutant	0	0	0	1880	898	0	0	954	0
SF-268-6							mutant	0	0	0	1800	0	0	10	780	0
DuPong-13								0	0	0	1829	47	0	1587	1098	0
Mikhail-20								0	0	0	6046	0	0	0	845	0
Mikhail-21								0	0	0	67	78	0	1386	831	0
Mikhail-22								0	0	0	2514	238	0	227	928	0
OVCAR-8-5							mutant	0	0	0	0	95	0	312	741	0
Mikhail-10								0	0	0	15	3	0	86	343	0
Mikhail-11								0	0	0	0	68	0	1	381	0
Mikhail-12								0	0	0	0	248	0	2124	601	0
Mikhail-13								0	0	0	0	1844	0	4881	642	0
Mikhail-14								0	0	0	0	207	0	821	806	0
Mikhail-15								0	0	0	0	887	0	1883	680	0
Mikhail-16								0	0	0	0	2	0	0	376	0
Mikhail-17								0	0	0	0	0	0	0	380	0
Mikhail-18								0	0	0	557	33	0	1234	684	0
Mikhail-19								0	0	0	4	65	0	448	458	0

Table 3 (cont'd)

Tissue	Tumor-cyto	Normal-cyto	Tumor - tis	Tumor cells	Normal	Endos	p53	SEQ [illegible]
adrenal gland - h		1						84
lymph node - h		2						834
bone marrow - h		3						822
mammary gland - h		4						0
brain - h		5						3881
pancreas - h		6						226
cerebellum - h		7						686
pituitary gland - h		8						2327
fetal brain - h		9						2719
placenta - h		10						1203
fetal kidney - h		11						717
prostate - h		12						782
fetal liver - h		13						537
salivary gl. - h		14						848
fetal lung - h		15						419
skeletal muscle - h		16						0
heart - h		17						154
small intestine - h		18						534
kidney - h		19						282
spinal cord - h		20						230
liver - h		21						81
Spleen - h		22						167
lung - h		23						436
stomach - h		24						821
testis - h		[illegible]						8
thymus - h		27						841
HPAEC		28				28		332
thyroid gland - h		29						0
RPTEC		30				30		168
trachea - h		31						3128
HMVEC		32						91
uterus - h		33						198
HCAEC		34						199
Pancreas - h		35						0
lymph node - h		36						179
Skeletal muscle - h		37						71
fetal liver - h		38						1636
Heart - h		39						102
thymus - h		40						146
Duodenum - h		41						123
Fetal brain - h		42						637
Salivary gl. - h		43						140
testis - h		44						0
HT218-normal					395			0
HT213-normal					393			0
HT157-normal					391			0
Ovr-13					389	389		1250
Ovr-12					354	354		1237
cerebellum - h					344			96
brain - h					342			5
RPTEC					334	334		0
lymph node - h					332			136
h adult SMC 10/21/02 #17					330			141
fetal brain - h					328			70
HT299-normal					327			69
thymus - h					326			386
HT149 - normal					321			0
HEPM 3d untreated					320			0
uterus - h					318			148
trachea - h					316			202
thyroid gland - h					314			173
salivary gl. - h					311			0
prostate - h					309			66
pituitary gland - h					307			190
pancreas - h					305			0
mammary gland - h					303			0
bladder - h					302			307
testis - h					299			16
[illegible]					297			80
[illegible]					295			21
[illegible]					294			[illegible]
[illegible]					292			0
skeletal muscle - h					290			0
bone marrow - h					279			267
adrenal gland - h					277			136
HPAEC					276	276		0
HT282-normal					268			0
HT283-normal					266			86
Ovr-11					238	238		331
Ovr-8					235	235		222
HT272-normal					234			0
Ovr-7					233	233		296
Ovr-6					231	231		487
Ovr-2					229	229		82
Ovr-1					227	227		442
bladder - h					222			80
Heart - h					219			0
stomach - h					214			1606
fetal liver - h					213			0
placenta - h					212			123
HCAEC					211	211		0
fetal brain - h					210			0
HMVEC					209			0
Duodenum - h					205			267
Skeletal muscle - h					203			0
Pancreas - h					201			0
testis - h					199			8
Salivary gl. - h					197			0
HEPM 3d TGFB1 [illegible]					195			46
thymus - h					193			8
WI-38 72h					179			8
lymph node - h					81			0
lung - h					59			0
kidney - h					57			6
heart - h					55			0
fetal lung - h					53			6
fetal liver - h					51			28
fetal kidney - h					49			0
HELA-2h-031000				79				0
HELA-4h-031000				81				834
HELA-6h-031000				83				71
HELA-8h-031000				85				834
HELA-[illegible]-031000				86				87
HELA-9h-031000				88				161
HELA-10h-031000				92				0
HELA-11h-031000				94				91
HELA-12h-031000				96				0
NCI-H322M				146				120
NCI-H460				148				7
NCI-H522				150				66
SNB-19				152				294
SNB-75				154				0
SF-268				156				137
SF-295				158				0
CCRF-CEM				160				185
DU-145				162				0
HCT 116				164				0

Table 3 (cont'd)

Tissue	Tumor-syn	Normal-syn	Tumor - tis.	Tumor cells	Normal	Endoc	p53	SEQ_116 S
Caki-1				125				4
786-0				166				0
T-47D				169				0
Km-3				171				72
CRL 1441 RNA 8/30				181				0
781T untreated + DHam				183				186
KB poly A+				184				47
HOS poly A+				185				0
ACHN				196				52
UACC-62				200				0
MCF-7/ADR-RES				202				86
UTOS (bloody) poly a+				204				0
WISH (Collagen) poly A+				206				34
468 medulla mRNA				208				209
CCL137 RNA 3/21/98				216				0
WI-38 72h 0.5%FBS, 24h 10% FBS				219				0
CRL 1441 + TPA (24h) 8/30				220				242
Km-1				221				68
Km-2				223				79
Km-4				225				0
HOP-92				241				0
MOLT-4				242				0
[illegible]				243				0
[illegible]				244				0
[illegible]				245				0
RPMI 8226				246				50
A549/ATCC				247				241
SR				248				0
OVCAR-3				249				86
HCT-15				250				0
OVCAR-4				251				0
UO-31				252				0
OVCAR-5				253				249
SN12C				254				0
OVCAR-8				255				0
LOX IMVI				256				0
IGROV1				257				0
SK-MEL-2				258				182
SK-OV-3				259				0
SK-MEL-5				260				0
SF-539				261				0
SK-MEL-28				262				0
K-562				263				22
UACC-257				264				33
M14				265				0
MCF7				267				48
MDA-MB-435				269				166
HT279				270				0
MDA-N				271				0
Y79 poly A+				274				0
KHOS poly A+				298				26
HTB38 24h TPA RNA 8/23				308				147
HELA-EXP-031698				313				83
HTB38 6h RNA				322				0
HT351				323				0
468 medulla RNA				324				125
NCI-H226				336				0
HOP-62				337				0
MDA-MB-231				338				61
U251				339				0
PT cells poly A+				340				0
PC-3				341				0
HCC-2998				343				0
SW-620				345				0
HT192				346				148
COLO 205				347				0
HT210				348				0
KM-12				349				0
HT151				350				20
[illegible]				[illegible]				0
HT[illegible]				[illegible]				480
HOP_[illegible]				353				0
TK-10				355				363
Malme-3M				357				241
Hs 578T				359				0
HT213			50					312
HT286			52					0
HT139			54					0
HT155			56					0
HT163			58					165
HT170			60					61
HT172			62					137
HT136			63					0
HT176			64					32
HT154			65					10
HT160			66					40
HT168			67					140
HT169			68					0
HT143			69					0
HT159			70					98
HT146			71					130
HT222			72					161
HT302			73					0
HT314			74					0
HT317			76					0
Medulloblastoma 9/25 116			77					0
HT323			78					21
HT327			80					137
HT335			82					0
HT148			85					86
HT348			87					29
HT311			170					18
HT366			185					0
HT140			187					0
HT281			189					205
HT372			191					75
TCGP			207					40
HT180			216					48
HT367			217					82
HT369			224					236
HT379			226					0
HT371			228					114
HT377			230					125
HT382			236					112
[illegible] RNA			281					480
HT338			299					231
HT336			301					0
HT362			316					80
HT384			317					0
HT312			319					0
HT162			325					0
HT386			358					48
HT117			360					13
T-47D	160							83
MDA-N	161							0
MDA-MB-435	158							0
MDA-MB-231	157							36

Table 3 (cont'd)

Tissue	Tumor-syn	Normal-syn	Tumor - fa	Tumor cells	Normal	Zodiac	p53	SEQ 116 E
Hs 578T	155							0
MCF-7/ADR-RES	153							0
MCF7	151							0
M14	149							7
UACC-257	147							22
UACC-62	145							0
SK-MEL-28	144							33
UO-31	143							6
SK-MEL-5	142							91
KM-12	141							4
SK-MEL-2	140							280
HCT-15	139							328
Malme-3M	138							181
COLO 205	137							250
LOX IMVI	136							0
SW-620	135							0
TK-10	134							0
HCT 116	133							0
786-0	132							82
HCC-2998	131							76
ACHN	130							279
PC-3	129							0
RXF 393	128							237
DU-145	127							88
Caki-1	126							276
SR	125							0
A549	124							137
RPMI 8226	123							8
SN12C	122							138
HL-60	121							0
MOLT-4	120							116
OVCAR-5	119							0
K-562	118							38
OVCAR-4	117							842
CCRF-CEM	116							886
OVCAR-3	115							191
SF-539	114							87
HOP-92	113							6
SF-295	112							181
A549/ATCC	111							110
SF-268	110							133
NCI-H522	109							0
U251	108							304
NCI-H460	107							0
SNB-75	106							30
NCI-H322M	105							436
SNB-19	104							78
NCI-H226	103							83
SK-OV-3	102							6
NCI-H23	101							777
IGROV1	100							0
EKVX	99							54
OVCAR-8	98							0
HOP-62	97							43
h fibroblasts 3/31/92 #12	48							148
h adult SMC 10/21/92 #17	47							210
h keratinocytes 2/7/92 #19	46							135
TCGP	26							0
A549 - 1							wt	5
A549 - 3							wt	379
A549 - 4							wt	458
A549 - 5							wt	367
A549 - 7							wt	72
EKVX - 1							mutant	90
EKVX - 4							mutant	290
EKVX - 3							mutant	0
EKVX - 5							mutant	483
EKVX - 7							mutant	877
MCF-7 - 1							wt	0
MCF-7 - 3							wt	667
MCF-7 - 4							wt	[illegible]
MCF-7 - 5							wt	[illegible]
MCF-7 - 7							wt	0
ADR-RES - 1							mutant	3049
ADR-RES - 3							mutant	158
ADR-RES - 4							mutant	79
ADR-RES - 5							mutant	18
ADR-RES - 7							mutant	98
WI 38 - 1							wt	0
WI 38 - 3							wt	383
WI 38 - 4							wt	888
WI 38 - 5							wt	688
WI 38 - 7							wt	0
HeLa - 1							HPV E6	0
HeLa - 3							HPV E6	38
HeLa - 4							HPV E6	185
HeLa - 5							HPV E6	388
HeLa - 7							HPV E6	166
H1299 - 1							mutant	0
H1299 - 3							mutant	0
H1299 - 4							mutant	0
H1299 - 5							mutant	8
H1299 - 7							mutant	1
A549 - 2							wt	153
EKVX - 2							mutant	8
HCT-116 - 1							wt	0
HCT-116 - 2							wt	820
HT29 - 2							mutant	99
SF539 - 1							wt	0
SF539 - 2							wt	8
SF-268-1							mutant	388
SF-268-2							mutant	631
OVCAR-4 - 1							wt	0
OVCAR-4 - 2							wt	0
OVCAR-5 - 1							mutant	823
OVCAR-5 - 2							mutant	288
MCF-7 - 2							wt	88
ADR-RES - 2							mutant	221
HeLa - 2							HPV E6	173
SW480 - 1							mutant	0
SW480 - 2							mutant	191
H1299 - 2							mutant	1863
C33A - 1							mutant	0
C33A - 2							mutant	0
U2OS - 1							mutant	271
U2OS - 2							mutant	857
Hs68 - 1							wt	0
Hs68 - 2							wt	24
WI 38 - 2							wt	228
Mixed - 1								0
Mixed - 2								0
Mixed - 3								0
Mixed - 4								14630
Mixed - 5								552
Mixed - 6								0
Mixed - 8								0
Mixed - 9								0

Table 3 (cont'd)

Tissue	Tumor-sym	Normal-sym	Tumor - 1o	Tumor cells	Normal	Embryo	p53	SEQ 116 S
DuPong-7								1982
DuPong-8								2881
DuPong-9								603
DuPong-11								2503
DuPong-12								518
DuPong-10								368
DuPong-1								474
DuPong-2								0
DuPong-3								222
DuPong-4								0
DuPong-5								0
DuPong-6								0
A549 - 8							wt	0
EKVX - 8							mutant	54
HCT-116 - 7							wt	0
HCT-116 - 8							wt	0
HT29 - 1							mutant	218
HT29 - 7							mutant	69
HT29 - 8							mutant	0
SF539 - 7							wt	155
SF539 - 8							wt	236
SF-268-7							mutant	213
SF-268-8							mutant	603
OVCAR-4 - 7							wt	405
OVCAR-4 - 8							wt	0
OVCAR-5 - 7							mutant	831
OVCAR-5 - 8							mutant	107
MCF-7 - 8							wt	35
ADR-RES - 8							mutant	857
HeLa - 8							HPV E6	0
SW480 - 7							mutant	0
SW480 - 8							mutant	0
H1299 - 8							mutant	0
C33A - 7							mutant	0
C33A - 8							mutant	0
U2OS - 7							mutant	729
U2OS - 8							mutant	37
[illegible] - 7							wt	0
[illegible] - 8							wt	0
WI 38 - 8							wt	0
456 [illegible] RNA								0
CRL 1572 2/17/98								71
[illegible]-4						84		221
HT366								80
HT378								151
HT285								88
HT308								0
[illegible]-3						173		487
[illegible]-6						176		117
[illegible]-8						177		481
h [illegible] 2/25/92 [illegible]								0
[illegible]-10						237		0
HTB16								0
h fibroblasts 3/31/98 #12								0
prostate, h								0
MNNG-OS poly A+								32
SA-OS [illegible] poly A+								0
[illegible] poly A+								0
HCT-116 - 3							wt	284
HCT-116 - 4							wt	0
HCT-116 - 5							wt	0
HCT-116 - 6							wt	0
A549 - 6							wt	0
HT29 - 3							mutant	874
EKVX - 5							mutant	121
HT29 - 4							mutant	840
HT29 - 5							mutant	0
HT29 - 6							mutant	177
OVCAR-4 - 3							wt	37
OVCAR-4 - 4							wt	0
OVCAR-4 - 5							wt	16
OVCAR-4 - 6							wt	0
SF539 - 3							wt	726
SF539 - 4							wt	83
SF539 - 5							wt	0
SF539 - 6							wt	0
OVCAR-5 - 3							mutant	2219
OVCAR-5 - 4							mutant	286
OVCAR-5 - 5							mutant	0
ADR-RES - 6							mutant	0
MCF-7 - 6							wt	279
HeLa - 6							HPV E6	371
H1299 - 6							mutant	0
SW480 - 3							mutant	61
SW480 - 4							mutant	0
SW480 - 5							mutant	293
SW480 - 6							mutant	225
C33A - 3							mutant	173
C33A - 4							mutant	193
C33A - 5							mutant	0
C33A - 6							mutant	55
[illegible] - 6							wt	0
U2OS - 3							mutant	820
U2OS - 4							mutant	991
U2OS - 5							mutant	544
U2OS - 6							mutant	0
WI 38 - 6							wt	0
[illegible] - 3							wt	288
[illegible] - 4							wt	821
SF-268-3							mutant	277
SF-268-4							mutant	0
SF-268-5							mutant	125
SF-268-6							mutant	33
DuPong-13								21
[illegible] - 20								388
[illegible] - 21								0
[illegible] - 22								0
OVCAR-5 - 6							mutant	811
[illegible] - 10								96
[illegible] - 11								299
[illegible] - 12								894
[illegible] - 13								309
[illegible] - 14								180
[illegible] - 15								232
[illegible] - 16								0
[illegible] - 17								129
[illegible] - 18								0
[illegible] - 19								172

Table 4

Gene Name	SP	ID# na	ID# aa	Family	Group	Length_AA	Extra-Catalytic Domains (Amino acid positions)
X89117_h beta_adrene	H	1	122	AGC	GRK	688	Regulator of G protein signaling domain 54-175; PH domain 559-652
AA144574_m	M	2	123	AGC	GRK	378	PH domain 243-337
AA210825_h	H	9	130	AGC	PKC	978	Phorbol esters/diacylglycerol binding domain (C1 domain) 238-287; PH domain 497-577
AA316804_h	H	11	132	AGC	PKC	890	Phorbol esters/diacylglycerol binding domain (C1 domain) 155-204 and 272-321; PH domain 417-532
AA887783_h	H	21	142	AGC	SGK	446	PX domain 13-120
AA021445_h 3	H	32	152	CAMK	EMK	1311	Vitamin K-dependent carboxylation/gamma-carboxyglutamic (GLA) domain 1072-1113
R31237_1_h, AAC3348	H	34	154	CAMK	EMK	729	UBA domain 327-365
408788.5_h	H	36	156	CAMK	EMK	1330	PAS domain 133-186, 247-280, 354-386
Z38720_h	H	41	161	CAMK	MLCK	874	WD domain, G-beta repeat 674-711
SGK088_h	H	42	162	CAMK	Trio	2287	Immunoglobulin domain 1-62, 97-153, 221-277, 518-578, 1617-1678; Fibronectin type III domain 301-390, 1697-1779
R19772_h	H	44	164	CAMK	Trio	1287	RhoGEF domain 235-405; Fibronectin type III domain 870-955; Immunoglobulin domain 786-851; PH domain419-528
17000139801197_h, IRA	H	76	195	Other	IRAK	596	Death domain 26-108
AA088547_h	H	78	197	Other	IRE	922	PQQ enzyme repeat 39-76
AA232253_h	H	82	201	Other	MLK	800	SAM domain (Sterile alpha motif) 337-408
AA599286_h	H	89	208	Other	SLOB	649	PX domain 16-122
AA838348_h	H	113	232	STE	NEK	836	Regulator of chromosome condensation (RCC1) 387-427, 427-480, 483-532, 598-6[illegible]
PAK6_h	H	115	234	STE	STE20-02	719	P21-Rho-binding domain 11-69

FIGURE 1A

SEQ ID NO: 122_X69117_H BARK2_H
MADLEAVLADVSYLMAMEKSKATPAARASKRIVLPEPSIRSVMQKYLAERNEITFDKIFN
QKIGFLLFKDFCLNEINEAVPQVKFYEEIKEYEKLDNEEDRLCRSRQIYDAYIMKELLSC
SHPFSKQAVEHVQSHLSKKQVTSTLFQPYIEEICESLRGDIFQKFMESDKFTRFCQWKNV
ELNIHLTMNEFSVHRIIGRGGFGEVYGCRKADTGKMYAMKCLDKKRIKMKQGETLALNER
IMLSLVSTGDCPFIVCMTYAFHTPDKLCFILDLMNGGDLHYHLSQHGVFSEKEMRFYATE
IILGLEHVHNRFVVYRDLKPANILLDEHGHARISDLGLACDFSKKKPHASVGTHGYMAPE
VLQKGTAYDSSADWFSLGCMLFKLLRGHSPFRQHKTKDKHEIDRMTLTVNVELPDTFSPE
LKSLLEGLLQRDVSKRLGCHGGSQEVKEHSFFKGVDWQHVYLQKYPPPLIPPRGEVNAA
DAFDIGSFDEEDTKGIKLLDCDQELYKNFPLVISERWQQEVTETVYEAVNADTDKIEARK
[illegible]NKQLGHEEDYALGKDCIMHGYMLKLGNPFLTQWQRRYF[illegible]PNR[illegible]RGEGESRQNL
LTMEQILSVEETQIKDKKCILFRIKGGKQFVLQCESDPEFVQWKKELNETFKEAQRLLRR
APKFLNKPRSGTVELPKPSLCHRNSNGL

SEQ ID NO: 123_AA144574_M BARK2_M
CFVVYRDLKPANILLDEYGHVRISDLGLACDFSKKKPHASVGTHGYMAPEVLQKGTCYDS
SADWFSLGCMLFKLLRGHSPFRQHKTKDKHEIDRMTLTVNVQLPDAFSPELRSLLEGLLQ
RDVSQRLGCGGGGARELKEHIFFKGIDWQHVYLRKYPPPLIPPRGEVNAADAFDIGSFDE
EDTKGIKLLDCDQDLYKNFPLVISERWQQEVVETIYDAVNADTDKIEARKKAKNKQLGQE
EDYAMGKDCIMHGYMLKLGNPFLTQWQRRYFYLFPNRLEWRGEGESRQSLLTMEQIMSVE
ETQIKDRKCILLRIKGGKQFVLQCESDPEFAQWLKELTCTFNEAQRLLRRAPKFLNKPRA
AILEFSKPPLCHRNSSGL

SEQ ID NO: 124_AA826850_H
MGSSMSAATARRPVFDDKEDVNFDHFQILRAIGKGSFGKVCIVQKRDTEKMYAMKYMNKQ
QCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVQ
FSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNIATIIKDGERA
[illegible]TALAGTKPY[illegible]IFXSF[illegible]NGGTGYSFEVD[illegible]WSVGVMAYE[illegible]
QLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVLWDHLSEKRVE
PGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQSENDYLQDCLD
AIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCGPICPSAGSG

SEQ ID NO: 125_AA960957_H
MGGNHSHKPPVFDENEEVNFDHFQILRAIGKGSFGKVCIVQKRDTKKMYAMKYMNKQKCI
ERDEVRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVHFTE
GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIATVVKGAERASSM
AGTKPYMAPEVFQVYMDRGPGYSYPVDWWSLGITAYELLRGWRPYEIHSVTPIDEILNMF
KVERVHYSSTWCKGMVALLRKLLTKDPESRVSSLHDIQSVPYLADMNWDAVFKKALMPGF
VPNKGRLNCDPTFELEEMILESKPLHKKKKRLAKNRSRDGTKDSCPLNGHLQHCLETVRE
EFIIFNREKLRRQQGQGSQLLDTDSRGGGQAQSKLQDGCNNNLLTHTCTRGCSS

SEQ ID NO: 126_TBK1_H
MQSTSNHLWLLSDILGQGATANVFRGRHKKTGDLFAIKVFNNISFLRPVDVQMREFEVLK
KLNHKNIVKLFAIEEETTTRHKVLIMEFCPCGSLYTVLEEPSNAYGLPESEFLIVLRDVV
GGMNHLRENGIVHRDIKPGNIMRVIGEDGQSVYKLTDFGAARELEDDEQFVSLYGTEEYL
HPDMYERAVLRKDHQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEVMYKIITG
KPSGAISGVQKAENGPIDWSGDMPVSCSLSRGLQVLLTPVLANILEADQEKCWGFDQFFA
ETSDILHRMVIHVFSLQQMTAHKIYIHSYNTATIFHELVYKQTKIISSNQELIYEGRRLV
LEPGRLAQHFPKTTEENPIFVVSREPLNTIGLIYEKISLPKVHPRYDLDGDASMAKAITG
VVCYACRIASTLLLYQELMRKGIRWLIELIKDDYNETVHKKTEVVITLDFCIRNIEKTVK

FIGURE 1B

VYEKLMKINLEAAELGEISDIHTKLLRLSSSQGTIETSLQDIDSRLSPGGSLADAWAHQE
GTHPKDRNVEKLQVLLNCMTEIYYQFKKDKAERRLAYNEEQIHKFDKQKLYYHATKAMTH
FTDECVKKYEAFLNKSEEWIRKMLHLRKQLLSLTNQCFDIEEEVSKYQEYTNELQETLPQ
KMFTASSGIKHTMTPIYPSSNTLVEMTLGMKKLKEEMEGVVKELAENNHILERFGSLTMD
GGLRNVDCL

SEQ ID NO: 127_AA305176_H
MDPTAGSKKEPGGGAATEEGVNRIAVPKPPSIEEFSIVKPISRGAFGKVYLGQKGGKLYA
VKVVKKADMINKNMTHQVQAERDALALSKSPFIVHLYYSLQSANNVYLVMEYLIGGDVKS
LLHIYGYFDEEMAVKYISEVALALDYLHRHGIIHRDLKPDNMLISNEGHIKLTDFGLSKV
TLNRDINMMDILTTPSMAKPRQDYSRTPGQVLSLISSLGFNTPIAEKNQDPANILSACLS
ETSQLSQGLVCPMSVDQKDTTPYSSKLLKSCLETVASN[illegible]LLQSRKRLATS
SASSQSHTFISSVESECHSSPKWEKDCQV

SEQ ID NO: 128_AA116841_M
TRPIPWPEGEEKLSDNAQSAMDMLLTIDDSKRAGMRELKQHPLFSEVDWENLQHQTMPFV
PQPDDETDTSYFEARNNAQHLTVSGFSL

SEQ ID NO: 129_AA256100_H
MAMTAGTTTTFPMSNHTRERVTVAKLTLENFYSNLILQHEERETRQKKLEVAMEEEGLAD
EEKKLRRSQHARKETEFLRLKRTRLGLDDFESLKVIGRGAFGEVRLVQKKDTGHIYAMKI
LRKSDMLEKEQVAHIRAERDILVEADGAWVVKMFYSFQDKRNLYLIMEFLPGGDMMTLLM
KKDTLTEEETQFYISETVLAIDAIHQLGFIHRDIKPDNLLLDAKGHVKLSDFGLCTGLKK
AHRTEFYRNLTHNPPSDFSFQNMNSKRKAETWKKNRRQLAYSTVGTPDYIAPEVFMQTGY
NKLCDWWSLGVIMYEMLIGYPPFCSETPQETYRKVMNWKETLVFPPEVPISEKAKDLILR
FCIDSENRIGNSGVEEIKGHPFFEGVDWEHIRERPAAIPIEIKSIDDTSNFDDFPESDIL
QPVPNTTEPDYKSKDWVFLNYTYKRFEGLTQRGSIPTYMKAGKL

SEQ ID NO: 130_AA210825_H
DSLLPTPALGTPLPIPWPVGSLRTPLSLESTRSPTQRLLPSTPKDPAILRSPPPARSFLG
SPLSHHLLTRSRGSRTQGPPGPPGGSRVGSRRAVPGLPPWPPPPHYPAGLPGSPGPGSPP
PPGGLELQSPPPLLPQIPAPGSGVSFHIQIGLTREFVLLPAASELAHVKQLACSIVDQKF
PECGFYGLYDKILLFKHDPTSANLLQLVRSSGDIQEGDLVEVVLSASATFEDFQIRPHAL
TVHSYRAPAFCDHCGEMLFGLVRQGLKCDGCGLNYHKRCAFSIPNNCSGARKRRLSSTSL
ASGHSVRLGTSESLPCTAEELSRSTTELLPRRPPSSSSSSSASSYTGRPIELDKMLLSKV
KVPHTFLIHSYTRPTVCQACKKLLKGLFRQGLQCKDCKFNCHKRCATRVPNDCLGEALIN
GDVPMEEATDFSEADKSALMDESEDSGVIPGSHSENALHASEEEEGEGGKAQSSLGYIPL
MRVVQSVRHTTRKSSTTLREGWVVHYSNKDTLRKRHYWRLDCKCITLFQNNTTNRYYKEI
PLSEILTVESAQNFSLVPPGTNPHCFEIVTANATYFVGEMPGGTPGGPSGQGAEAARGLX
ETAIRQALMPVILQDAPSAPGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSG
QFGVVYGGKHRKTGRDVAVKVIDKLRFPTKQESQLRNEVAILQSLRHPGIVNLECMFETP
EKVFVVMEKLHGDMLEMILSSEKGRLPERLTKFLITQILVALRHLHFKNIVHCDLKPENV
LLASADPFPQVKLCDFGFARIIGEKSFRRSVVGTPAYLAPEVLLNQGYNRSLDMWSVGVI
MYVSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAIDLINNLLQVKMRKRYSVDK
SLSHPWLQEYQTWLDLRELEGKMGERYITHESDDARWEQFAAEHPLPGSGLPTDRDLGGA
CPPQDHDMQGLAERISVL

SEQ ID NO: 131_AA127299_H
IQFIIVGAKDLLAMDSNGLSDPYIKITNLSQKTKVIKKTLTPTWNETFFVHFPEKTTLEL
ECWDHDTFSDDFIGKASISLAEIPALAEVDMWIDMKTKKGEFAGK

FIGURE 1C

SEQ ID NO: 132_AA316804_H
MSANNSPPSAQKSVLPTAIPAVLPAASPCSSPKTGLSARLSNGSFSAPSLTNSRGSVHTV
SFLLQIGLTRESVTIEAQELSLSAVKDLVCSIVYQKFPECGFFGMYDKILLFRHDMNSEN
ILQLITSADEIHEGDLVEVVLSALATVEDFQIRPHTLYVHSYKAPTFCDYCGEMLWGLVR
QGLKCEGCGLNYHKRCAFKIPNNCSGVRKRRLSNVSLPGPGLSVPRPLQPEYVALPSEES
HVHQEPSKRIPSWSGRPIWMEKMVMCRVKVPHTFAVHSYTRPTICQYCKRLLKGLFRQGM
QCKDCKFNCHKRCASKVPRDCLGEVTFNGEPSSLGTDTDIPMDIDNNDINSDSSRGLDDT
EEPSPPEDKMFFLDPSDLDVERDEEAVKTISPSTSNNIPLMRVVQSIKHTKRKSSTMVKE
GWMVHYTSRDNLRKRHYWRLDSKCLTLFQNESGSKYYKEIPLSEILRISSPRDFTNISQG
SNPHCFEIITDTMVYFVGENNGDSSHNPVLAATGVGLDVAQSWEKAIRQALMPVTPQASV
CTSPGQGKDHKDLSTSISVSNCQIQENVDISTVYQIFADEVLGSGQFGIVYGGKHRKTGR
DVAIKVIDKMRFPTKQESQLRNEVAILQNLHHPGIVNLECMFETPERVFVVMEKLHGDML
EMILSSEKSRLPERITKFMVTQILVALRNLHFKNIVHCDLKPENVLLASAEPFPQVKLCD
FGFARIIGEKSFRRSVVGTPAYLAPEVLRSKGYNRSLDMWSVGVIIYVSLSGTFPFNEDE
DINDQIQNAAFMYPPNPWREISGEAIDLINNLLQVKMRKRYSVDKSLSHPWLQDYQTWLD
LREFETRIGERYITHESDDARWEIHAYTHNLVYPKHFIMAPNPDDMEEDP

SEQ ID NO: 133_PKNBETA_H
MEEGAPRQPGPSQWPPEDEKEVIRRAIQKELKIKEGVENLRRVATDRRHLGHVQQLLRSS
NRRLEQLHGELRELHARILLPGPGPGPAEPVASGPRPWAEQLRARHLEALRRQLHVELKV
KQGAENMTHTCASGTPKERKLLAAAQQMLRDSQLKVALLRMKISSLEASGSPEPGPELLA
EELQHRLHVEAAVAEGAKNVVKLLSSRRTQDRKALAEAQAQLQESSQKLDLLRLALEQLL
EQLPPAHPLRSRVTRELRAAVPGYPQPSGTPVKPTALTGTLQVRLLGCEQLLTAVPGRSP
AAALASSPSEGWLRTKAKHQRGRGELASEVLAVLKVDNRVVGQTGWGQVAEQSWDQTFVI
PLERARELEIGVHWRDWRQLCGVAFLRLEDFLDNACHQLSLSLVPQGLLFAQVTFCDPVI
ERRPRLQRQERIFSKRRGQDFLRRSQMNLGMAAWGRLVMNLLPPCSSPSTISPPKGCPRT
PTTLREASDPATPSNFLPKKTPLGEEMTPPPKPPRLYLPQEPTSEETPPTKRPHMEPRTP
RGPSPPASPTRKPPRLQDFRCLAVLGRGHFGKVLLVQFKGTGKYYAIKALKKQEVLSRDE
IESLYCEKRILEAVGCTGHPFLLSLLVCFQTSSHARFVTEFVPGGDLMMQIHEDVFPEPQ
ARFYVACVVLGLQFLHEKKIIYRDLKLDNLLLDAQGFLKIADFGLCKEGIGFGDRTSTFC
GTPEFLAPEVLTQEAYTQAVDWWALGVLLYEMLVGECPFPGDTEEEVFDCIVNMDAPYPG
FLSVQGLEFIQKLLQKCPEKRLGAGEQDAEEIKVQPFFRTTNWQALLARTIQPPFVPTLC
GPADLRYFEGEFTGLPPALTPPAPHSLLTARQQAAFRDFDFVSERFLEP

SEQ ID NO: 134_AI021023_M PKNBETA_M
LKWDNLLLDAQGFLKIADFGLCKEGIGFGDRTSTFCGTPEFLAPEVLTQEAYTRAVDWWG
LGVLLYEMLVGECPFPGDTEEEVFDCIVNMDAPYPGFLSVQGLEFIQKLLQKCPEKRLGA
GEQDAEEIKVQPFFRTTNWQALLARTIQPPFVPTLCGPADLRYFEGEFTGLPPALTPPAP
HSLLTARQQAAFRDFDFVSERFLEP

SEQ ID NO: 135_H19102_H
GGNIRGPWARGWKSLWTGLGTIRSDLEELWELRGHHYLHQESLKPAPVLVEKPLPEWPVP
QFINLFLPEFPIRPIRGQQQLKILGLVAKGSFGTVLKVLDCTQKAVFAVKVVPKVKVLQR
DTVRQCKEEVSIQRQINHPFVHSLGDSWQGKRHLFIMCSYCSTDLYSLWSAVGCFPEASI
RLFAAELVLVLCYLHDLGIMHRDVKMENILLDERGHLKLTDFGLSRHVPQGAQAYTICGT
LQYMAPEVLSGGPYNHAADWWSLGVLLFSLATGKFPVAAERDHVAMLASVTHSDSEIPAS
LNQGLSLLLHELLCQNPLHRLRYLHHFQVHPFFRGVAFDPELLQKQPVNFVTETQATQPS
SAETMPFDDFDCDLESFLLYPIPA

FIGURE 1D

SEQ ID NO: 136_AA476563_H
MEFFRIDSKDSASELLGLDFGEKLYSLKSEPLKPFFTLPDGDSASRSFNTSESKVEFKAQ
DTISRGSDDSVPVISFKDAAFDDVSGTDEGRPDLLVNLPGELESTREAAAMGPTKFTQTN
IGIIENKLLEAPDVLCLRLSTEQCQAHEEKGIEELSDPSGPKSYSITEKHYAQEDPRMLF
VAAVDHSSSGDMSLLPSSDPKFQGLGVVESAVTANNTEESLFRICSPLSGANEYIASTDT
LKTEEVLLFTDQTDDLAKEEPTSLFQRDSETKGESGLVLEGDKEIHQIFEDLDKKLALAS
RFYIPEGCIQRWAAEMVVALDALHREGIVCRDLNPNNILLNDRGHIQLTYFSRWSEVEDS
CDSDAIERMYCAPEVGAITEETEACDWWSLGAVLFELLTGKTLVECHPAGINTHTTLNMP
ECVSEEARSLIQQLLQFNPLERLGAGVAGVEDIKSHPFFTPVDWAELMR

SEQ ID NO: 137_AA625690_H
MLPFAPQDEPWDREMEVFSGGGASSGEVNGLKMVDEPMEEGEADSCHDEGVVKEIPITHH
VKEGYEKADPAQFELLKVLGQGSFGKVFLVRKKTGPDAGQLYAMKVLKKASLKVRDRVRT
KMERDILVEVNHPFIVKLHYAFQTEGKLYLILDFLRGGDVFTRLSKEVLFTEEDVKFYLA
ELALALDHLHQLGIVYRDLKPENILLDEIGHIKLTDFGLSKESVDQEKKAYSFCGTVEYM
APEVVNRRGHSQSADWWSYGVLMFEMLTGTLPFQGKDRNETMNMILKAKLGMPQFLSAEA
QSLLRMLFKRNPANRLGSEGVEEIKRHLFFANIDWDKLYKREVQPPFKPASGKPDDTFCF
DPEFTAKTPKDSPGLPASANAHQLFKGFSFVATSIAEEYKITPITSANVLPIVQINGNAA
QFGEVYELKEDIGVGSYSVCKRCIHATTNMEFAVKIIDKSKRDPSEEIEILMRYGQHPNI
ITLKDVFDDGRYVYLVTDLMKGGELLDRILKQKCFSEREASDILYVISKTVDYLHCQGVV
HRDLKPSNILYMDESASADSIRICDFGFAKQLRGENGLLLTPCYTANFVAPEVLMQQGYD
AACDIWSLGVLFYTMLAGYTPFANGPNDTPEEILLRIGNGKFSLSGGNWDNISDGAKDLL
SHMLHMDPHQRYTAEQILKHSWITHRDQLPNDQPKRNDVSHVVKGAMVATYSALTHKTFQ
PVLEPVAASSLAQRRSMKKRTSTGL

SEQ ID NO: 138_AA215680_H
MSLVACECLPSPGLEPEPCSRARSQAHVYLEQIRNRVALGVPDMTKRDYLVDAATQIRLA
LERDVSEDYEAAFNHYQNGVDVLLRGIHVDPNKERREAVTHKITKYLRRAEEIFNCHLQR
PLSSGASPSAGFSSLRLRPIRTLSSAVEQLRGCRVVGVIEKVQLVQDPATGGTFVVKSLP
RCHMVSRERLTIIPHGVPYMTKLLRYFVSEDSIFLHLEHVQGGTLWSHLLSQAHSRHSGL
SSGSTQERMKAQLNPHLNLLTPARLPSGHAPGQDRIALEPPRTSPNLLLAGEAPSTRPQR
EAEGEPTARTSTSGSSDLPKAPGGHLHLQARRAGQNSDAGPPRGLTWVPEGAGPVLGGCG
RGMDQSCLSADGAGRGCGRATWSVREEQVKQWAAEMLVALEALHEQGVLCRDLHPGNLLL
DQAGHIRLTYFGQWSEVEPQCCGEAVDNLYSAPEVGGISELTEACDWWSFGSLLYELLTG
MALSQSHPSGIQAHTQLQLPEWLSRPAASLLTELLQFEPTRRLGMGEGGVSKLKSHPFFS
TIQWSKLVG

SEQ ID NO: 139_SGK_H
MTVKTEAAKGTLTYSRMRGMVAILIAFMKQRRMGLNDFIQKIANNSYACKHPEVQSILKI
SQPQEPELMNANPSPPPSPSQQINLGPSSNPHAKPSDFHFLKVIGKGSFGKVLLARHKAE
EVFYAVKVLQKKAILKKKEEKHIMSERNVLLKNVKHPFLVGLHFSFQTADKLYFVLDYIN
GGELFYHLQRERCFLEPRARFYAAEIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTD
FGLCKENIEHNSTTSTFCGTPEYLAPEVLHKQPYDRTVDWWCLGAVLYEMLYGLPPFYSR
NTAEMYDNILNKPLQLKPNITNSARHLLEGLLQKDRTKRLGAKDDFMEIKSHVFFSLINW
DDLINKKITPPFNPNVSGPNELRHFDPEFTEEPVPNSIGKSPDSVLVTASVKEAAEAFLG
FSYAPPTDSFL

SEQ ID NO: 140_AA107515_M
MTVKAEAARSTLTYSRMRGMVAILIAFMKQRRMGLNDFIQKIASNTYACKHAEVQSILKM
SHPQEPELMNANPSPPPSPSQQINLGPSSNPHAKPSDFHFLKVIGKGSFGKVLLARHKAE

FIGURE 1E

EVFYAVKVLQKKAILKKKEEKHIMSERNVLLKNVKHPFLVGLHFSFQTADKLYFVLDYIN
GGELFYHLQRERCFLEPRARFYAAEIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTD
XFQLRRIEHNGTTSTFCGTPEYLAPEVLHKQPYDRTVDWWCLGAVLYEMLYGLPPFYSRN
TAEMYDNILNKPLQLKPNITNSARHLLEGLLQKDRTKRLGAKDDFMEIKSHIFFSLINWD
DLINKKITPPFNPNVSGPSDLRHFDPEFTEEPVPSSIGRSPDSILVTASVKEAAEAFLGF
SYAPPVDSFL

SEQ ID NO: 141_AA109508_M
HLQRERRFLEPRARFYAAEVASAIGYLHSLNIIYRDLKPENILLDCQGHVVLTDFGLCKE
GVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAVDWWCLGAVLYEMLHGLPPFYSQDVSQMY
ENILHQPLQIPGGRTVAACDLLQSLLHKDQRQRLGSKADFLEIKNHVFFSPINWDDLYHK
RLTPPFNPNVTGPADLKHF[illegible]FTQEAVSA[illegible]IGCTPDTVASSSGASSAFLGFSYAPEDDD
ILDC

SEQ ID NO: 142_AA887783_H
MQRDHTMDYKESCPSVXIPSSDEHREKKKRFTVYKVLVSVGRSEWFVFRRYAEFDKLYNT
LKKQFPAXALKIPAKRIFGDNFDPDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMD
SPKHQSDPSEDEDERSSQKLHSTSQNINLGPSGNPHAKPTDFDFLKVIGKGSFGKVLLAK
RKLDGKFYAVKVLQKKIVLNRKEQKHIMAERNVLLKNVKHPFLVGLHYSFQTTEKLYFVL
DFVNGGEGHVVLTDFGLCKEGIAISDTTTTFCGTPEYLAPEVIRKQPYDNTVDWWCLGAV
LYEMLYGLPPFYCRDVAEMYDNILHKPLSLRPGVSLTAWSILEELLEKDRQNRLGAKEDF
LEIQNHPFFESLSWADLVQKKIPPPFNPNVAGPDDIRNFDTAFTEETVPYSVCVSSDYSI
VNASVLEADDAFVGFSYAPPSEDLFL

SEQ ID NO: 143_R47805_H
MAHQTGIHATEELKEFFAKARAGSVRLIKVVIEDEQLVLGASQEPVGRWDQDYDRAVLPL
LDAQQPCYLLYRLDSQNAQGFEWLFLAWSPDNSPVRLKMLYAATRATVKKEFGGGHIKDE
LFGTVKDDLSFAGYQKHLSSCAAPAPLTSAERE[illegible]SKH[illegible]AF
FLQPEAQRALQQLKQKMVNYIQMKLDLERETIELVITTEPTDVAQLPS[illegible]PRDAARYHFFL
YKHTHEGDPLESVVFIYSMPGYKCSIKERMLYSSCKSRLLDSVEQDFHLEIAKKIEIGDG
AELTAEFLYDEVHPKQHAFKQAFAKPKGPGGKRGHKRLIRGPGENGDDS

SEQ ID NO: 144_H60215_H
MSKLRMKRRASDRGAGETSARAKALGSGISGNNAKRAGPFILGPRLGNSPVPSIVQCLAR
KDGTDDFYQLKILTLEERGDQGIESQEERQGKMLLHTEYSLLSLLHTQDGVVHHHGLFQD
RTCEIVEDTESSRMVKKMKKRICLVLDCLCAHDFSDKTADLINLQHYVIKEKRLSERETV
VIFYDVVRVVEALHQKNIVHRDLKLGNMVLNKRTHRITITNFCLGKHLVSEGDLLKDQRG
SPAYISPDVLSGRPYRGKPSDMWALGVVLFTMLYGQFPFYDSIPQELFRKIKAAEYTIPE
DGRVSENTVCLIRKLLVLDPQQRLAAADVLEALSAIIASWQSLSSLSGPLQVVPDIDDQM
SNADSSQEAKVTEECSQYEFENYMRQQLLLAEEKSSIHDTRSWVPKRQFGSAPPVRRLGH
DAQPMTSLDTAILAQRYLRK

SEQ ID NO: 145_SGK324_H
MASTRSIELEHFEERDKRPRPGSRRGAPSSSGGSSSSGPKGNGLIPSPAHSAHCSFYRTR
TLQALSSEKKAKKARFYRNGDRYFKGLVFAISSDRFRSFDALLIELTRSLSDNVNLPQGV
RTIYTIDGSRKVTSLDELLEGESYVCASNEPFRKVDYTKNINPNWSVNIKGGTSRALAAA
SSVKSEVKESKDFIKPKLVTVIRSGVKPRKAVRILLNKKTAHSFEQVLTDITEAIKXASG
VVKRLCTLDGKQVRVTCVHLPDFFGDDDVFIACGPEKFRYAQDDFVLDHSECRVLKSSYS
RSSAVKYSGSKSPGPSRRSQISAHGRSSSNVNGGPELDRCISPEGVNGNRCSESSTLLEK
YKIGKVIGDGNFAVVKECIDRSTGKEFALKIIDKAKCCGKEHLIENEVSILRRVKHPNII

FIGURE 1F

MLVEEMETATELFLVMELVKGGDLFDAITSSTKYTERDGSAMVYNLANALRYLHGLSIVH
RDIKPENLLVCEYPDGTKSLKLGDFGLATVVEGPLYTVCGTPTYVAPXIIAETGYGLKVD
IWAAGVITYILLCGFPPFRSENNLQEDLFDQILAGKLEFPAPYWDNITDSAKELISQMLQ
VNVEARCTAGQILSHPWVSDDASQENNMQAEVTGKLKQHFNNALPKQNSTTTGVSVIMVS
GRRQVWPDCGAGLEVFELGSRELPSHGSWCLP

SEQ ID NO: 146_W30246_M SGK324_M
TKSSSSSPTSPGSFRGLKISAQGRSSSNVNGGPELDRCLSPEGVNGNRCSESFPLLEKYR
IGKVIGDGNFAVVKECVDRYTGKEFALKIIDKAKCCGKEHLIENEVSILRRVKHPNIIML
VEEMETATDLFLVMELVKGGDLFDAITSSTKYTERDGSAMVYNLANALRYLHSLSIVHRD
IKPENLLVCEYPDGTKSLKLGDFGLATVVEGPLYTVCGTPTYVAPEIIAETGYGLKVDVW
AAGVITYILLCGFPPFRSENNLQEDLFDQILAGKLEFPAPYWDNITDSPCVCFRKCL

SEQ ID NO: 147_AA383293_H
PAAKRVVVYRNGDPFFPGSQLVVTQRRFPTMEAFLCEVTSAVQAPLAVRALYTPCHGHPV
TNLADLKNRGQYVAAGFERFHKLPPYQAFCLSVFRNGDLVSPPFSLKLSQAASQDWETVL
KLLTEKVKLQSGAVRLCTLEGLPLSAGKELVTGHYYVAVGEDEFKDLPYPALSTRGLLAA
GNEAHLRSGVGTVAGSPKPLGRKAKKETCLIVTLTLKYQQSETSRDGQSFPSGVIGVYGA
PHRRKETAGALEVADDEDTQTEEPLDQRAAQIVEQVTCLQDFFGDDDVFIACGPEKFRYA
QDDFVLDHSRRRLLREHQAGFEKLRRTRGEEKEAEKEKKPCMSGGRRMTLRDDQPAKLEK
EPKTRPEENKPERPSGRKPRPMGIIAANVEKHYETGRVIGDGNFAVVKECRHRETRQAYA
MKIIDKSRLKGKEDMVDSEILIIQSLSHPNIVKLHEVYETDMEIYLILEYVQGGDLFDAI
IESVKFPEPDAALMIMDLCKALVHMHDKSIVHRDLKPENLLVQRNEDKSTTLKLADFGLA
KHVVRPIFTVCGTPTYVAPEILSEKGYGLEVDMWAAGVILYILLCGFPPFRSPXXGDQDE
LFNIIQLGHFEFLPPYWDNISDAAKDLVSRLLVVDPKKRYTAHQVLQHPWIETAGKTNTV
KRQKQVSPSSDGHFRSQHKRVVEQVS

SEQ ID NO: 148_AA197883_M
MPTAPVLRPPPPPATPAPPAPSRPAPPIPGHRGPCDHSLKCLSSKISERKLPGPALPAGR
GPLEKPVLGPRGAVMPLFSPQSSLHSVRAEHSPLKPRVVTVVKLGGQPLRKATLLLNRRS
VQTFEQLLSDISEALGFPRWKNDRVRKLFTLKGREVKSVSDFFREGDAFIAMGKEPLTLK
SIQLAMEELYPKNRALALAPHSRVPSPRLRSRLPSKLLKGSHRCGEAGSYSAEMESKAVS
RHQGKTSTVLAPEDKARAQKWVRGKQESEPGGPPSPGAATQEETHASGEKHLGVEIEKTS
GEIVRCEKCKRERELQLGLQREPCPLGTSELDLGRAQKRDSEKLVRTKSCRRPSKAKFTD
GEEGWKGDSHRGSPRDPPQEMRRPNSNSDKKEIRGSESQDSYPQGAPKAQKDFVEGPPAV
EEGPIDMRREDRHTCRSKHAAWLRREQQAEPPQLPRTRGEEKQAEHEKKPGGLGERRAPE
KESKRKLEEKRPERPSGRKPRPKGIISADVEKHYDIGGVIGDGNFATVKECRHRETKQAY
AMKMIDKSQLKGKEDIVDSEILIIQSLSHPNIVKLHEVYETEAEIYLIMEYVQGGDLFDA
IVENVKFPEPEAAVMITDLCKAFVHMHDKNIVHRDVKPENLLVQRNEDKSITLKLADFGL
AKYVVRPIFTVCGTPTYVAPEILSEKGYGLEVDMWAAGVILYILLCGFPPFRSPERDQDE
LFNIIQVGQFEFLSPYWDNISDAAKDLVRNLLEVDPKKRYTAEQVLQHPWIEMVGHTNTG
NSQKEESPNSLGHFQSQHKKVAEQMP

SEQ ID NO: 149_DRAK2_H
MSRRRFDCRSISGLLTTTPQIPIKMENFNNFYILTSKELGRGKFAVVRQCISKSTGQEYA
AKFLKKRRRGQDCRAEILHEIAVLELAKSCPRVINLHEVYENTSEIILILEYAAGGEIFS
LCLPELAEMVSENDVIRLIKQILEGVYYLHQNNIVHLDLKPQNILLSSIYPLGDIKIVDF
GMSRKIGHACELREIMGTPEYLAPEILNYDPITTATDMWNIGIIAYMLLTHTSPFVGEDN
QETYLNISQVNVDYSEETFSSVSQLATDFIQSLLVKNPEKRPTAEICLSHSWLQQWDFEN

FIGURE 1G

LFHPEETSSSSQTQDHSVRSSEDKTSKSSCNGTCGDREDKENIPEDSSMVSKRFRFDDSL
PNPHELVSDLLC

SEQ ID NO: 150_W44160_M DRAK2_M
MSRRRFDCRSVSGLLTTTPQTPIKTENFNNFYTLTPKELGRGKFAVVRQCISKSTGQEYA
AKSLKKRRRGQDCRAEILHEIAVLELARSCPHVINLHEVYENATEIILVLEYAAGGEIFN
LCLPELAEMVSENDVIRLIKQILEGVHYLHQNNIVHLDLKPQNILLSSIYPLGDIKIVDF
GMSRKIGNASELREIMGTPEYLAPEILNYDPITTATDMWNIGIIAYMLLTHTSPFVGEDN
QETYLNISQVNVDYSEEMFSSVSQLATDFIQSLLVKNPEKRPTAESCLSHSWLQQWDFGS
LFHPEETSGSSQIQDLTLRSSEEKTSKSSCNGSCGAREDKENIPEDGSLVSKRFRFDDSL
PSPHELVPDLFC

SEQ ID NO: 151_H01248_H, DRAK1_H
MIPLEKPGSGGSSPGATSGSGRAGRGLSGPCRPPPPPQARGLLTEIRAVVRTEPFQDGYS
LCPGRELGRGKFAVVRKCIKKDSGKEFAAKFMRKRRKGQDCRMEIIHEIAVLELAQDNPW
VINLHEVYETASEMILVLEYAAGGEIFDQCVADREEAFKEKDVQRLMRQILEGVHFLHTR
DVVHLDLKPQNILLTSESPLGDIKIVDFGLSRILKNSEELREIMGTPEYVAPEILSYDPI
SMATDMWSIGVLTYVMLTGISPFLGNDKQETFLNISQMNLSYSEEEFDVLSESAVDFIRT
LLVKKPEDRATAEECLKHPWLTQSSIQEPSFRMEKALEEANALQEGHSVPEINSDTDKSE
TEESIVTEELIVVTSYTLGQCRQSEKEKMEQKAISKRFKFEEPLLQEIPGEFIY

SEQ ID NO: 152_AA021445_H
MPARIGYYEIDRTIGKGNFAVVKRATHLVTKAKVAIKIIDKTQLDEENLKKIFREVQIMK
MLCHPHIIRLYQVMETERMIYLVTEYASGGEIFDHLVAHGRMAEKEARRKFKQIVTAVYF
CHCRNIVHRDLKAENLLLDANLNIKIADFGFSNLFTPGQLLKTWCGSPPYAAPELFEGKE
YDGPKVDIWSLGVVLYVLVCGALPFDGSTLQNLRARVLSGKFRIPFFMSTECEHLIRHML
VLDPNKRLSMEQICKHKWMKLGDADPNFDRLIAECQQLKEERQVDPLNEDVLLAMEDMGL
DKEQTLQSLRSFAYDHYSAIYSLLCDRHKRHKTLRLGALPSMPRALAFQAPVNIQAEQAG
TAMNISVPQVQLINPENQIVEPDGTLNLDSDEGEEPSPEALVRYLSMRRHTVGVADPRTE
VMEDLQKLLPGFPGVNPQAPFLQVAPNVNFMHNLLPMQNLQPTGQLEYKEQSLLQPPTLQ
LLNGMGPLGRRASDGGANIQLHAQQLLKRPRGPSPLVTMTPAVPAVTPVDEESSDGEPDQ
EAVQRYLANRSKRHTLAMTNPTAEIPPDLQRQLGQQPFRSRVWPPHLVPDQHRSTYKDSN
TLHLPTERFSPVRRFSDGAASIQAFKAHLEKMGNNSSIKQLQQECEQLQKMYGGQIDERT
LEKTQQQHMLYQQEQHHQILQQQIQDSICPPQPSPPLQAACENQPALLTHQLQRLRIQPS
SPPPNHPNNHLFRQPSNSPPPMSSAMIQPHGAASSSQFQGLPSRSAIFQQQPENCSSPPN
VALTCLGMQQPAQSQQVTIQVQEPVDMLSNMPGTAAGSSGRGISISPSAGQMQMQHRTNL
MATLSYGHRPLSKQLSADSAEAHSLNVNRFSPANYDQAHLHPHLFSDQSRGSPSSYSPST
GVGFSPTQALKVPPLDQFPTFPPSAHQQPPHYTTSALQQALLSPTPPDYTRHQQVPHILQ
GLLSPRHSLTGHSDIRLPPTEFAQLIKRQQQRQQQQQQQQQQEYQELFRHMNQGDAGSL
APSLGGQSMTERQALSYQNADSYHHHTSPQHLLQIRAQECVSQASSPTPPHGYAHQPALM
HSESMEEDCSCEGAKDGFQDSKSSSTLTKGCHDSPLLLSTGGPGDPESLLGTVSHAQELG
IHPYGHQPTAAFSKNKVPSREPVIGNCMDRSSPGQAVELPDHNGLGYPARPSVHEHHRPR
ALQRHHTIQNSDDAYVQLDNLPGMSLVAGKALSSARMSDAVLSQSSLMGSQQFQDGENEE
CGASLGGHEHPDLSDGSQHLNSSCYPSTCITDILLSYKHPEVSFSMEQAGV

SEQ ID NO: 153_2R22-5-11_H
MTAVYMNGGGLVNPHYARWDRRDSVESGCQTESSKEGEEGQPRQLTPFEKLTQDMSQDEK
VVREITLGKRIGFYRIRGEIGSGNFSQVKLGIHSLTKEKVAIKILDKTKLDQKTQRLLSR
EISSMEKLHHPNIIRLYEVVETLSKLHLVMEYAGGGELFGKISTEGKLSEPESKLIFSQI
VSAVKHMHENQIIHRDLKAENVFYTSNTCVKVGDFGFSTVSKKGEMLNTFCGSPPYAAPE

FIGURE 1H

LFRDEHYIGIYVDIWALGVLLYFMVTGTMPFRAETVAKLKKSILEGTYSVPPHVSEPCHR
LIRGVLQQIPTERYGIDCIMNDEWMQGVPYPTPLEPFQLDPKHLSETSTLKEEENEVKST
LEHLGITEEHIRNNQGRDARSSITGVYRIILHRVQRKKALESVPVMMLPDPKERDLKKGS
RVYRGIRHTSKFCSIL

SEQ ID NO: 154_R31237_1_H, AAC33487
MSTRTPLPTVNERDTENHTSHGDGRQEVTSRTSRSGARCRNSIASCADEQPHIGNYRLLK
TIGKGNFAKVKLARHILTGREVAIKIIDKTQLNPTSLQKLFREVRIMKILNHPNIVKLFE
VIETEKTLYLIMEYASGGEVFDYLVAHGRMKEKEARSKFRQIVSAVQYCHQKRIVHRDLK
AENLLLDADMNIKIADFGFSNEFTVGGKLDTFCGSPPYAAPELFQGKKYDGPEVDVWSLG
VILYTLVSGSLPFDGQNLKELRERVLRGKYRIPFYMSTDCENLLKRFLVLNPIKRGTLEQ
IMKDRWINAGHEEDELKPFVEPELDISDQKRIDIMVGMGYSQEEIQESL[illegible]DEIHAT
YLLLGRKSSELDASDSSSSSNLSLAKVRPSSDLNNSTGQSPHHKVQRSVSSSQKQRRYSD
HAGPAIPSVVAYPKRSQTSTADGDLKEDGISSRKSSGSAVGGKGIAPASPMLGNASNPNK
ADIPERKKSSTVPSSNTASGGMTRRNTYVCSERTTADRHSVIQNGKENSTIPDQRTPVAS
THSISSAATPDRIRFPRGTASRSTFHGQPRERRTATYNGPPASPSLSHEATPLSQTRSRG
STNLFSKLTSKLTRSRNVSAEQKDENKEAKPRSLRFTWSMKTTSSMDPGDMMREIRKVLD
ANNCDYEQRERFLLFCVHGDGHAENLVQWEMEVCKLPRLSLNGVRFKRISGTSIAFKNIA
SKIANELKL

SEQ ID NO: 155_W90839_M
KGPSWSSRSLGARCRNSIASCPEEQPHVGNYRLLRTIGKGNFAKVKLARHILTGREVAIK
IIDKTQLNPSSLQKLFREVRIMKGLNHPNIVKLFEVIETEKTLYLVMEYASAGEVFDYLV
SHGRMKEKEARAKFRQIVSAVHYCHQKNIVHRDLKAENLLLDAEANIKIADFGFSNEFTL
GSKLDTFCGSPPYAAPELFQGKKYDGPEVDIWSLGVILYTLVSGSLPFDGHNLKELRERV
LRGKYRVPFYMSTDCESILRRFLVLNPAKRCTLEQIMKDKWINIGYEGEELKPDTELKEE
RMPGRKASCSAVGSGSRGLPPSSPMVSSAHNPNKAEIPERRKDSTSTPNNLPPSMMTRRN
TYVCTERPGSERPSL[illegible]NGKENSSG[illegible]PPAS[illegible]SLAPPSGERSRLARGSTIRSTFH
GGQVRDRRAGSGSGGGVQNGPPASPTLAHEAAPLPSGRPRPTTNLFTKLTSKLTRRVTDE
PERIGGPEVTSCHLPWDKTETAPRLLRFPWSVKLTSSRPS

SEQ ID NO: 156_406786.5_H
MEVGGLTVFEEDQRCLSQSLPLPVSAEGPAAQTTAEPSRSFSSAHRHLSRRNGLSRLCQS
RTALSEDRWSSYCLSSLAAQNICTSKLHCPAAPEHTDPSEPRGSVSCCSLLRGLSSGWSS
PLLPAPVCNPNKAIFTVDAKTTEILVANDKACGLLGYSSQDLIGQKLTQFFLRSDSDVVE
ALSEEHMEADGHAAVVFGTVVDIITRSGEKIPVSVWMKRMRQERRLCCVVVLEPVERVST
WVAFQSDGTITSCDSLFAHLHGYVSGEDVAGQHITDLIPSVQLPPSGQHIPKNLKIQRSV
GRARDGTTFPLSLKLKSQPSSEEATTGEAAPVSGYRASVWVFCTISGLITLLPDGTIHGI
NHSFALTLFGYGKTELLGKNITFLIPGFYSYMDLAYNSSLQLPDLASCLDVGNESGCGER
TLDPWQGQDPAEGGQDPRINVVLAGGHVVPRDEIRKLMESQDIFTGTQTELIAGGQLLSC
LSPQPAPGVDNVPEGSLPVHGEQALPKDQQITALGREEPVAIESPGQDLLGESRSEPVDV
KPFASCEDSEAPVPAEDGGSDAGMCGLCQKAQLERMGVSGPSGSDLWAGAAVAKPQAKGQ
LAGGSLLMHCPCYGSEWGLWWRSQDLAPSPSGMAGLSFGTPTLDEPWLGVENDREELQTC
LIKEQLSQLSLAGALDVPHAELVPTECQAVTAPVSSCDLGGRDLCGGCTGSSSACYALAT
DLPGGLEAVEAQEVDVNSFSWNLKELFFSDQTDQTSSNCSCATSELRETPSSLAVGSDPD
VGSLQEQGSCVLDDRELLLLTGTCVDLGQGRRFRESCVGHDPTEPLEVCLVSSEHYAASD
RESPGHVPSTLDAGPEDTCPSAEEPRLNVQVTSTPVIVMRGAAGLQREIQEGAYSGSCYH
RDGLRLSIQFEVRRVELQGPTPLFCCWLVKDLLHSQRDSAARTRLFLASLPGSTHSTAAE
LTGPSLVEVLRARPWFEEPPKAVELEGLAACEGEYSQKYSTMSPLGSGAFGFVWTAVDKG
KNKEVVVKFIKKEKVLEDCWIEDPKLGKVTLEIAILSRVEHANIIKVLDIFENQGFFQLV

FIGURE 1I

MEKHGSGLDLFAFIDRHPRLDEPLASYIFRQVRAGQSRLVSAVGYLRLKDIIHRDIKDEN
IVIAEDFTIKLIDFGSAAYLERGKLFYTFCGTIEYCAPEVLMGNPYRGPELEMWSLGVTL
YTLVFEENPFCELEETVEAAIHPPYLVSKELMSLVSGLLQPVPERRTTLEKLVTDPWVTQ
PVNLADYTWEEVFRVNKPESGVLSAASLEMGNRSLSDVAQAQELCGGPVPGEAPNGQGCL
HPGDPRLLTS

SEQ ID NO: 157_AA544838_M 406786_M
TRPHPCLDEPLASFIFRQLVSAVGYLHSQGIIHRDIKDENIVIAEDFTIKLIDFGSAAYL
ERGKLFYTFCGTIEYCAPEVLIGNPYRGPELEMWSLGVTLYTLIFEENPFCEVEETMEAV
IHPPFLVSQELMSLLSGLLQPCPEQRTTLEKLIRDPWVTQPVNLASYTWEEVCRTNQPES
GLLSAASLEIGSPSPSEMAQREGLCGPPAPRETRGDQHCLHLKDPSLPVS

SEQ ID NO: 158_AA785735_H
MVMADGPRHLQRGPVRVGFYDIEGTLGKGNFAVVKLGRHRITKTEVAIKIIDKSQLDAVN
LEKIYREVQIMKMLDHPHIIKLYQVMETKSMLYLVTEYAKNGEIFDYLANHGRLNESEAR
RKFWQILSAVDYCHGRKIVHRDLKAENLLLDNNMNIKIADFGFGNFFKSGELLATWCGSP
PYAAPEVFEGQQYEGPQLDIWSMGVVLYVLVCGALPFDGPTLPILRQRVLEGRFRIPYFM
SEDCEHLIRRMLVLDPSKRLTIAQIKEHKWMLIEVPVQRPVLYPQEQENEPSIGEFNEQV
LRLMHSLGIDQQKXIESLQNKSYNHFAAIYFLLVERLKSHRSSFPVEQRLDGRQRRPSTI
AEQTVAKAQTVGLPVTMHSPNMRLLRSALLPQASNVEAFSFPASGCQAEAAFMEEECVDT
PKVNGCLLDPVPPVLVRKGCQSLPSNMMETSIDEGLETEGEAEEDPAHAFEAFQSTRSGQ
RRHTLSEVTNQLVVMPGAGKIFSMNDSPSLDSVDSEYDMGSVQRDLNFLEDNPSLKDIML
ANQPSPRMTSPFISLRPTNPAMQALSSQKREVHNRSPVSFREGRRASDTSLTQGIVAFRQ
HLQNLARTKGILELNKVQLLYEQIGPEADPNLAPAAPQLQDLASSCPQEEVSQQQESVST
LPASVHPQLSPRQSLETQYLQHRLQKPSLLSKAQNTCQLYCKEPPRSLEQQLQEHRLQQK
RLFLQKQSQLQAYFNQMQIAESSYPQPSQQLPLPRQETPPPSQQAPPFSLTQPLSPVLEP
SSEQMQYSPFLSQYQEMQLQPLPSTSGPRAAPPLPTQLQQQPPPPPPPPPPRQPGAAPA
PLQFSYQTCELPSAASPAPDYPTPCQYPVDGAQQSDL[illegible]GPDCPRSPGLQEAPSSYD[illegible]AL
SELPGLFDCEMLDAVDPQHNGYVLVN

SEQ ID NO: 159_AA207220_H
MESLVFARRSGPTPSAAELARPLAEGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFLETLG
KGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLMHIRREIEIMSSLNHPHIIAIHEVFE
NSSKIVIVMEYASRGDLYDYISERQQLSEREARHFFRQIVSAVHYCHQNRVVHRDLKLEN
ILLDANGNIKIADFGLSNLYHQGKFLQTFCGSPLYASPEIVNGKPYTGPEVDSWSLGVLL
YILVHGTMPFDGHDHKILVKQISNGAYREPPKPSDCLXGLIRWLLMVNPTRRATLEDVAS
HWWVNWGYATRVGEQEAPHEGGHPGSDSARASMADWLRRSSRPLLENGAKVCSFFKQHAP
GGGSTTPGLERQHSLKKSRKENDMAQSLHSDTADDTAHRPGKSNLKLPKGILKKKVSASA
EGVQEDPPELSPIPASPGQAAPLLPKKGILKKPRQRESGYYSSPEPSESGELLDAGDVFV
SGDPKEQKPPQASGLLLHRKGILKLNGKFSQTALELAAPTTFGSLDELAPPRPLARASRP
SGAVSEDSILSSESFDQLDLPERLPEPPLRGCVSVDNLTGLEEPPSEGPGSCLRRWRQDP
LGDSCFSLTDCQEVTATYRQALRVCSKLT

SEQ ID NO: 160_AA426580_H, MAK_V_H
MPAAAGDGLLGEPAAPGGGGGAEDAARPAAACEGSFLPAWVSGVPRERLRDFQHHKRVGN
YLIGSRKLGEGSFAKVREGLHVLTGEKVAIKVIDKKRAKKDTYVTKNLRREGQIQQMIRH
PNITQLLDILETENSYYLVMELCPGGNLMHKIYEKKRLEESEARRYIRQLISAVEHLHRA
GVVHRDLKIENLLLDEDNNIKLIDFGLSNCAGILGYSDPFSTQCGSPAYAAPELLARKKY
GPKIDVWSIGVNMYAMLTGTLPFTVEPFSLRALYQKMVDKEMNPLPTQLSTGAISFLRSL
LEPDPVKRPNIQQALANRWLNENYTGKVPCNVTYPNRISLEDLSPSVVLHMTEKLGYKNS

FIGURE 1J

DVINTVLSNRACHILAIYFLLNKKLERYLSGKSDIQDSLCYKTRLYQIEKYRAPKESYEA
SLDTWTRDLEFHAVQDKKPKEQEKRGDFLHRPFSKKLDKNLPSHKQPSGSLMTQIQNTKA
LLKDRKASKSSFPDKDSFGCRNIFRKTSDSNCVASSSMEFIPVPPPRTPRIVKKPEPHQP
GPGSTGIPHKEDPLMLDMVRSFESVDRDDHVEVLSPSHHYRILNSPVSLARRNSSERTLS
PGLPSGSMSPLHTPLHPTLVSFAHEDKNSPPKEEGLCCPPPVPSNGPMQPLGSPNCVKSR
GRFPMMGIGQMLRKRHQSLQPSADRPLEASLPPLQPLAPVNLAFDMADGVKTQC

SEQ ID NO: 161_Z36720_H
MDTKLNMLNEKVDQLLHFQEDVTEKLQSMCRDMGHLERGLHRLEASRAPGPGGADGVPHI
DTQAGWPEVLELVRAMQQDAAQHGARLEALFRMVAAVDRAIALVGATFQKSKVADFLMQG
RVPWRRGSPGDSPEEWVKEEEVCFMPPVPPAPGAAGQSLQKDKGELSAEQGIWATLMTLV
INVTAANKERVEEEGGKPKIVLSTSGVQSDAREPGEESQKADVLEGTAERLPPIFASGLG
ADPAQAVVSPGQGDGVPGPAQAFPGHLPLPTKVEAKAPETPSENLRTGLELAPAPGRVNV
VSPSLEVAPGAGQGASSSRPDPEPLEEGTRLTPGPGPQCPGPPGLPAQARATHSGGETPP
RAALLKGAVAPGFSRRDLVFPSIFCACLGISIHIQEMDTPGEMLMTGRGSLGPTLTTEAP
AAAQPGKQGPPGTGRCLQAPGTEPGEQTPEGARELSPLQESSSPGGVKAEEEQRAGAEPG
TRPSLARSDDNDHEVGALGLQQGKSPGAGNPEPEQDCAARAPVRAEAVRRMPPGAEAGSV
VLDDSPAPPAPFEHRVVSVKETSISAGYEVCQHEVLGGGRFGQVHRCTEKSTGLPLAAKI
IKVKSAKDREDVKNEINIMNQLSHVNLIQLYDAFESKHSCTLVMEYVDGGELFDRITDEK
YHLTELDVVLFTRQICEGVHYLHQHYILHLDLKPENILCVNQTGHQIKIIDFGLARRYKP
REKLKVNFGTPEFLAPEVVNYEFVSFPTDMWSVGVITYMLLSGLSPFLGETDAETMNFIV
NCSWDFDADTFEGLSEEAKDFVSRLLVKEKSCRMSATQCLKHEWLNNLPAKASRSKTRLK
SQLLLQKYIAQRKWKKHFYVVTAANRLRKFPTSP

SEQ ID NO: 162_SGK088_H
GEMALFECLVAGPTDVEVDWLCRGRLLQPALLKCKMHFDGRKCKLLLTSVHEDDSGVYTC
KLSTAKDELTCSAPLTVRPSLAPLFTRLLEDVEVLEGRAARFDCKISGTPPPVVTWTHFG
CPMEESENLRLRQDGGLHSLHIAHVGSEDEGLYTVSAVNTHGQAHCSAQLYVEEPPTAAS
GPSSKLEKMPSIPEEPEQGELERLSIPDFLRPLQDLEVGLAKEAMLECQVTGLPYPTISW
FHNGHRIQSSDDRRMTQYRDVHRLVFPAVGPQHAGVYKSVIANKLGKAACYAHLYVTDVV
PGPPDGAPQVVAVTGRMVTLTWNPPRSLDMAIDPDSLTYTVQHQVLGSDQWTALVTGLRE
PGWAATGLRKGVQHIFRVLSTTVKSSSKPSPPSEPVQLLEHGPTLEEAPAMLDKPDIVYV
VEGQPASVTVTFNHVEAQVVWRSCRGALLEARAGVYELSQPDDDQYCLRICRVSRRDMGA
LTCTARNRHGTQTCSVTLELAEAPRFESIMEDVEVGAGETARFAVVVEGKPLPDIMWYKD
EVLLTESSHVSFVYEENECSLVVLSTGAQDGGVYTCTAQNLAGEVSCKAELAVHSAQTAM
EVEGVGEDEDHRGRRLSDFYDIHQEIGRGAFSYLRRIVERSSGLEFAAKFIPSQAKPKAS
ARREARLLARLQHDCVLYFHEAFERRRGLVIVTELCTEELLERIARKPTVCESEIRAYMR
QVLEGIHYLHQSHVLHLDVKPENLLVWDGAAGEQQVRICDFGNAQELTPGEPQYCQYGTP
EFVAPEIVNQSPVSGVTDIWPVGVVAFLCLTGISPFVGENDRTTLMNIRNYNVAFEETTF
LSLSREARGFLIKVLVQDRLRPTAEETLEHPWFKTQAKGAEVSTDHLKLFLSRRRWQRSQ
ISYKCHLVLRPIPELLRAPPERVWVTMPRRPPPSGGLSSSSDSEEEELEELPSVPRPLQP
EFSGSRVSLTDIPTEDEALGTPETGAATPMDWQEQGRAPSQDQEAPSPEALPSPGQEPAA
GASPRRGELRRGSSAESALPRAGPRELGRGLHKAASVELPQRRSPGPGATRLARGGLGEG
EYAQRLQALRQRLLRGGPEDGKVSGLRGPLLESLGGRARDPRMARAASSEAAPHHQPPLE
NRGLQKSSSFSQGEAEPRGRHRRAGAPLEIPVARLGARRLQESPSLSALSEAQPSSPARP
SAPKPSTPKSAEPSATTPSDAPQPPAPQPAQDKAPEPRPEPVRASKPAPPPQALQTLALP
LTPYAQIIQSLQLSGHAQGPSQGPAAPPSEPKPHAAVFARVASPPPGAPEKRVPSAGGPP
VLAEKARVPTVPPRPGSSLSSSIENLESEAVFEAKFKRSRESPLSLGLRLLSRSRSEERG
PFRGAEEEDGIYRPSPAGTPLELVRRPERSRSVQDLRAVGEPGLVRRLSLSLSQRLRRTP
PAQRHPAWEARGGDGESSEGGSSARGSPVLAMRRRLSFTLERLSSRLQRSGSSEDSGGAS

FIGURE 1K

GRSTPLFGRLRRATSEGESLRRLGLPHNQLAAQAGATTPSAESLGSEASATSGSSAPGES
RSRLRWGFSRPRKDKGLSPPNLSASVQEELGHQYVRSESDFPPVFHIKLKDQVLLEGEAA
TLLCLPAACPAPHISWMKDKKSLRSEPSVIIVSCKDGRQLLSIPRAGKRHAGLYECSATN
VLGSITSSCTVAVARVPGKLAPPEVTQTYQDTALVLWKPGDSRAPCTYTLERRVDGESVW
HPVSSGIPDCYYNVTHLPVGVTVRFRVACANRAGQGPFSNSSEKVFVRGTQDSSAVPSAA
HQEAPVTSRPARARPPDSPTSLAPPLAPAAPTPPSVTVSPSSPPTPPSQALSSLKAVGPP
PQTPPRRHRGLQAARPAEPTLPSTHVTPSEPKPFVLDTGTPIPASTPQGVKPVSSSTPVY
VVTSFVSAPPAPEPPAPEPPPEPTKVTVQSLSPAKEVVSSPGSSPRSSPRPEGTTLRQGP
PQKPYTFLEEKARGRFGVVRACRENATGRTFVAKIVPYAAEGKPRVLQEYEVLRTLHHER
IMSLHEAYITPRYLVLIAESCGNRELLCGLSDRFRYSEDDVATYMVQLLQGLDYLHGHHV
IHLDIKPDNLLLAPDNALKIVDFGSAQPYNPQALRPLGHRTGTLEFMAPEMVKGEPIGSA
TDIWGAGVLTYIMLSGRSPFYEPDPQETEARIVGGRFDAFQLYPNTSQSATLFLRKVLSV
HPWSRPSLQDCLAHPWLQDAYLMKLRRQTLTFTTNRLKEFLGEQRRRRAEAATRHKVLLR
SYPGGP

SEQ ID NO: 163_AA542015_M SGK088_M
ATDIWGAGVLTYIMLSGYSPFYEPDPQETEARIVGGRFDAFQLYPNTSQSATLFLRKVLS
VHPWSRPSLQDCLAHPWLQDAYLMKLRRQTLTFTTNRLKEFLGEQRRRRAEAATRHKVLL
RSYPGSP

SEQ ID NO: 164_R19772_H
MKGGDRAYTRGPSLGWLFAKCCCCFPCRDAYSHSSSENGGKSESVANLQAQPSLNFIHSS
PGPKRSTNTLKKWLTSPVRRLNSGKADGNIKKQKKVRDGRKSFDLGSPKPGDETTPQGDS
ADESKKGWGEDEPDEESHTPLPPPMKIFDNDPTQDEMSSSLLAARQASTEVPTAADLVNA
IEKLVKNKLSLEGSSYRGSLKDPAGCLNEGMAPPTPPKNPEEEQKAKALRGRMFVLNELV
QTEKDYVKDLGIVVEGFMKRIEEKGVPEDMRGKDKIVFGNIHQIYDWHKDFFLAELEKCI
QEQDRLAQLFIKHERKLHIYVWYCQNKPRSEYIVAEYDAYFEEVKQEINQRLTLSDFLIK
PIQRITKQLLLKDFLHYSEKAGLECSDIEKAVELMCLVPKR[illegible]LT
AQGKLLQQDTFYVIELDAGMQSRTKERRVFLFEQIVIFSELLRKGSLTPGYMFKRSIKMN
YLVLEENVDNDPCKFALMNRETSERVVLQAANADIQQAWVQDINQVLETQRDFLNALQSP
IEYQRKERSTAVMRSQPARLPQASPRPYSSVPAGSEKPPKGSSYNPPLPPLKISTSNGSP
GFEYHQPGDKFEASKNDLGGCNGTSSMAVIKDYYALKENEICVSQGEVVQVLAVNQQNMC
LVYQPASDHSPAAEGWVPGSILAPLTKATAAESSDGSIKKSCSWHTLRMRKRAEVENTGK
NEATGPRKPKDILGNKVSVKETNSSEESECDDLDPNTSMEILNPNFIQEVAPEFLVPLVD
VTCLLGDTVILQCKVCGRPKPTITWKGPDQNILDTDNSSATYTVSSCDSGEITLKICNLM
PQDSGIYTCIATNDHGTTSTSATVKVQGVPAAPNRPIAQERSCTSVILRWLPPSSTGNCT
ISGYTVEYREEGSQIWQQSVASTLDTYLVIEDLSPGCPYQFRVSASNPWGISLPSEPSEF
VRLPEYDAAADGATISWKENFDSAYTELNEIGRGRFSIVKKCIHKATRKDVAVKFVNKKM
KKKEQAAHEAALLQHLQHPQYITLHDTYESPTSYILILELMDDGRLLDYLMNHDELMEEK
VAFYIRDIMEALQYLHNCRVAHLDIKPENLLIDLRIPVPRVKLIDLEDAVQISGHFHIHH
LLGNPEFAAPEVIQGIPVSLGTDIWSIGVLTYVMLSGVSPFLDESKEETCINVCRVDFSF
PHEYFCGVSNAARDFINVILQEDFRRRPTAATCLQHPWLQPHNGSYSKIPLDTSRLACFI
ERRKHQNDVRPIPNVKSYIVNRVNQGT

SEQ ID NO: 165_5R72_8_2_H
MADSGLDKKSTKCPDCSSASQKDVLCVCSSKTRVPPVLVVEMSQTSSIGSAESLISLERK
KEKNINRDITSRKDLPSRTSNVERKASQQQWGRGNFTEGKVPHIRIENGAAIEEIYTFGR
ILGKGSFGIVIEATDKETETKWAIKKVNKEKAGSSAVKLLEREVNILKSVKHEHIIHLEQ
VFETPKKMYLVMELCEDGELKEILDRKGHFSENETRWIIQSLASAIAYLHNNDIVHRDLK
LENIMVKSSLIDDNNEINLNIKVTDFGLAVKKQSRSEAMLQATCGTPIYMAPEVISAHDY

FIGURE 1L

SQQCDIWSIGVVMYMLLRGEPPFLASSEAKLFELIRKGELHFENAVWNSISDCAKSVLKQ
LMKVDPAHRITAKELLDNQWLTGNKLSSVRPTNVLEMMKEWKNNPESVEENTTEEKNKPS
TEEKLKSYQPWGNVPETNYTSDEEEEKQSTAYEKQFPATSKDNFDMCSSSFTSSKLLPAE
IKGEMEKTPVTPSQGTATKYPAKSGALSRTKKKL

SEQ ID NO: 166_SGK309_H
MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENV
ALKVESAQQPKQVLKMEVAVLKKLQGSGLGQGDGKEEMMKPGAKRGKDHVCRFIGCGRNE
KFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGFLHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHD
DLWSLFYMLVEFAVGQLPWRKIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIASLDY
FTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGTDALLSTSTSTPPPAEHPADGSHVWG
GQCDASAWGPAPGEHRGCATGRAPEXPGECTPNSAREALXGAGPQSPPCPPPRGSXGXSL
GGDRCQPEQTPDQHRQSNCRQGEGRGWPFLSPPIPSLVPLPCSSXAPCPPPISLLARPLF
PVPSPALASLCLPSSSSSVSFTLRRPSA

SEQ ID NO: 167_AA234451_H
MSGGGEQLDILSVGILVKERWKVLRKIGGGGFGEIYDALDMLTRENVALKVESAQQPKQV
LKMEVAVLKKLQGKDHVCRFIGCGRNDRFNYVVMQLQGRNLADLRRSQSRGTFTISTTLR
LGRQILESIESIHSVGSXHRDIKPSNFAMGRFPSTCRKCYMLDFGLARQFTNSCGDVRPP
RAVAGFRGTVRYASINAHRNREMGRHDDLWSLFYMLVEFVVGQLPWRKIKDKEQVGSIKE
RYDHRLMLKHLPPEFSIFLDHISSLDYFTKPDYQLLTSVFDNSIKTFGVIESDPFDWEKT
GNDGSLTTTTTSTTPQLHTRLTPAAIGIANATPIPGDLLRENTDEVFPDEQLSDGENGIP
VGVSPDKLPGSLGHPRPQEKDVWEEMDANKNKIKLGICKAATEEENSHGQANGLLNAPSL
GSPIRVRSEITQPDRDIPLVRKLRSIHSFELEKRLTLEPKPDTDKFLETWYKIVYFSF

SEQ ID NO: 168_AA435956_H
TETIFFEEYVPOLEAGESNGGSNLLHDSVSSFQLFMFQLLRGLAYIHHQHVLHRDLKPQN
LLISHLGELKLADFGLARAKSIPSQTYSSEVVTLWYRPPDALLGATEYSSELDIWGAGCI
FIEMFQGQPLFPGVSNILEQLEKIWEVLGVPTEDTWPGVSKLPNYNPEWFPLPTPRSLHV
VWNRLGRVPEAEDLASQMLKGFPRDRVSAQEALVHDYFSALPSQLYQLPDEESLFTVSGV
RLKPEMCDLLASYQKGHHPAQFSKCW

SEQ ID NO: 169_AA626859_H
NGVADGVIKSVLWQTLQALNFCHIHNCIHRDIKPENILITKQGIIKICDFGFAQILIPGD
AYTDYVATRWYRAPELLVGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIR
TLGKLIPRHQSIFKSNGFFHGISIPEPEDMETLEEKFSDVHPVALNFMKGCLKMNPDDRL
TCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQQNQLLPLIPGSHISPTPDGRKQVLQLK
FDHLPNI

SEQ ID NO: 170_AA061797_M
KIALREIRMLKLKHPNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNGVSDGVIKSV
LWQTLQALNFCHKHNCIHRDVKPENILITKQGMIKICDFGFARILIPGDAYTDYVATRWY
RAPELLVGDTKYGSSVDVWAVGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIPRHQS
IFRSNQFFRGISIPEPEDMETLEEKFSNVQPVALSFMKGCLKMNPDERLTCAQLLDSAYF
ESFQEDQMKRKARSEGRSRRRQQNQLLPLIPGSHISPTPDGRKQVVQLKFDHLPNI

SEQ ID NO: 171_AA397553_H
MPNSERHGGKKDGSGGASGTLQPSSGGGSSNSRERHRLVSKHKRHKSKHSKDMGLVTPEA
ASLGTVIKPLVEYDDISSDSDTFSDDMAFKLDRRENDERRGSDRSDRLHKHRHHQHRRSR

FIGURE 1M

DLLKAKQTEKEKSQEVSSKSGSMKDRISGSSKRSNEETDDYGKAQVAKSSSKESRSSKLH
KEKTRKERELKSGHKDRSKSHRKRETPKSYKTVDSPKRRSRSPHRKWSDSSKQDDSPSGA
SYGQDYDLSPSRSHTSSNYDSYKKSPGSTSRRQSVSPPYKEPSAYQSSTRSPSPYSRRQR
SVSPYSRRRSSSYERSGSYSGRSPSPYGRRRSSSPFLSKRSLSRSPLPSRKSMKSRSRSP
AYSRHSSSHSKKKRSSSRSRHSSISPVRLPLNSSLGAELSRKKKERAAAAAAAKMDGKES
KGSPVFLPRKENSSVEAKDSGLESKKLPRSVKLEKSAPDTELVNVTHLNTEVKNSSDTGK
VKLDENSEKHLVKDLKAQGTRDSKPIALKEEIVTPKETETSEKETPPPLPTIASPPPPLP
TTTPPPQTPPLPPLPPIPALPQQPPLPPSQPAFSQVPASSTSTLPPSTHSKTSAVSSQAN
SQPPVQVSVKTQVSVTAAIPHLKTSTLPPLPLPPLLPGGDDMDSPKETLPSKPVKKEKEQ
RTRHLLTDLPLPPELPGGDLSPPDSPEPKAITPPQQPYKKRPKICCPRYGERRQTESDWG
KRCVDKFDIIGIIGEGTYGQVYKARDKDTGELVALKKVRLDNEKEGFPITAIREIKILRQ
LIHRSVVNMKEIVTDKQDALDFKKDKGAFYLVFEYMDHDLMGLLESGLVHFSEDHIKSFM
KQLMEGLEYCHKKNFLHRDIKCSNILLNNSGQIKLADFGLARLYNSEESRPYTNKVITLW
YRPPELLLGEERYTPAIDVWSCGCILGELFTKKPIFQANLELAQLELISRLCGSPCPAVW
PDVIKLPYFNTMKPKKQYRRRLREEFSFIPSAALDLLDHMLTLDPSKRCTAEQTLQSDFL
KDVELSKMAPPDLPHWQDCHELWSKKRRRQRQSGVVVEEPPPSKTSRKETTSGTSTEPVK
NSSPAPPQPAPGKVESGAGDAIGLADITQQLNQSELAVLLNLLQSQTDLSIPQMAQLLNI
HSNPEMQQQLEALNQSISALTEATSQQQDSETMAPEESLKEAPSAPVILPSAEQMTLEAS
STPADMQNILAVLLSQLMKTQEPAGSLEENNSDKNSGPQGPRRTPTMPQEEAAACPPHIL
PPEKRPPEPPGPPPPPPPPPLVEGDLSSAPQELNPAVTAALLQLLSQPEAEPPGHLPHEH
QALRPMEYSTRPRPNRTYGNTDGPETGFSAIDTDERNSGPALTESLVQTLVKNRTFSGSL
SHLGESSSYQGTGSVQFPGDQDLRFARVPLALHPVVGQPFLKAEGSSNSVVHAETKLQNY
GELGPGTTGASSSGAGLHWGGPTQSSAYGKLYRGPTRVPPRGGRGRGVPY

SEQ ID NO: 172_AA789239_H
MEMYETLGKVGEGSYGTVMKCKHKNTGQIVAIKIFYERPEQSVNKIAMREIKFLKQFHHE
NLVNLIEVFRQKKKIHLVFEFIDHTVLDELQHYCHGLESKRLRKYLFQILRAIDYLHSNN
VIIHRDIKPENILVSQSGITFLCDFGFARTLSAPGDIYTDYVATRWYRAPELVLKDTSYG
KYVPVDIWALGCMIIEMATGNPYLPSSSDLDLLHKIVLKVXFMPELKAKLLQEAKVNSLI
KPKESSKENELRKDERKTVYTNTLLSSSVLGKEIEKEKKPKEIKVRVIKVKGGRGDISEP
KKKEYEGGLGQQDANENVHPMSPDTKLVTIEPPNPINPSTNCNGLKENPHCGGSVTMPPI
NLTNSNLMAANLSSNLFHPSVRLTERAKKRRTSSQSIGQVMPNSRQEDPGPIQSQMEKGI
FNERTGHSDQMANENKRKLNFSRSDRKEFHFPELPVTIQSKDTKGMEVKQIKMLKRESKK
TESSKIPTLLNVDQNQEKQEFIPLSLLSACCPIFTNICSQLTIRVEMAIARGRI

SEQ ID NO: 173_AA124976_M
LADIVHACLQIDPAERTSSTDLLRHDYFTRDGFIEKFIPELRAKLLQEAKVNSFIKPKEN
FKENEPVRDEKKSVFTNTLLYGNPSLYGKEVDRDKRAKELKVRVIKAKGGKGDVPDQKKP
EYEGDHRQQGTADDTQPSSLDKKPSVLELTNPLNPSENSDGVKEDPHAGGCMIMPPINLT
SSNLLAANLSSNLSHPNSRLTERTKKRRTSSQTIGQTLSNSRQEDTGPTQVQTEKGAFNE
RTGQNDQISSGNKRKLNFPKCDRKEFHFPELPFTVQAKEMKGMEVKQIKVLKRESKKTDS
SKIPTLLSMDPNQEKQEGGDGDCEGKNLKRNRFFFSR

SEQ ID NO: 174_AA575635_M CCRK_M
SASGQLKIADFGLARVFSPDGGRLYTHQVATRWYRAPELLYGARQYDQGVDLWAVGCIMG
ELLNGSPLFPGENDIEQLCCVLRILGTPSPRVWPEITELPDYNKISFEEQAPVPLEEVLP
DASPQALDLLGQFLLYPPRQRIAASQALLHQYFFTAPLPAHPSELPIPQRPGGPAPKAHP
GPPHVHDFHVDRPIEESLLNPELIRPFIPEG

FIGURE 1N

SEQ ID NO: 175_AA631990_H
MITSISTEKSGHTHYPFMITTLQYYRGRGGKTAVWRHFSAEGPFAFAEMRHSKRTHCPDW
DSRESWGHESYRGSHKRKRRSHSSTQENRHCKPHHQFKESDCHYLEARSLNERDYRDRRY
VDEYRNDYCEGYVPRHYHRDIESGYRIHCSKSSVRSRRSSPKRKRNRHCSSHQSRSXEIV
DTLGEGAFGKVVECIDHGMDGMHVAVKIVKNVGRYREAARSEIQVLEHLNSTDPNSVFRC
VQMLEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQSINFLHHNKL
THTDLKPENILFVKSDYVVKYNSKMKRDERTLKNTDIKVVDFGSATYDDEHHSTLVSTRH
YRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFQTHDSKEHLAMMERILGPIPQHMIQ
KTRKRKYFHHNQLDWDEHSSAGRYVRRRCKPLKEFMLCHDEEHEKLFDLVRRMLEYDPTQ
RITLDEALQHPFFDLLKKK

SEQ ID NO: 176_AA557536_H
MCTVVDPRIVRRYLLRRQLGQGRTFREITLLQVSGLGPPVQSPCPGTDLSRQERNWPSWA
PEHSPSWPSSRLRLSPQEFGDHPNIISLLDVIRAENDRDIYLVFEFMDTDLNAVIRKGGL
LQDVHVRSIFYQLLRATRFLHSGHVVHRDQKPSNVLLDANCTVKLCDFGLARSLGDLPEG
PEDQAVTEYVATRWYRAPEVLLSSHRYTASCPRYTLGVDMWSLGCILGEMLRGRPLFPGT
STLHQLELILETIPPPSEEXRPRQTLDALLPPDTSPEALDLLRRLLVFAPDKRLSATQAL
QHPYVQRFHCPSDEWAREADVRPRAHEGVQLSVPEYRSRVYQMILECGGSSGTSREKGPE
GVSPSQAHLHKPRADPQLPSRTPVQGPRPRPQSSPGHDPAEHESPRAAKNVPRQNSAPLL
QTALLGNGERPPGAKEAPPLTLSLVKPSGRGAAPSLTSQAAAQVANQALIRGDWNRGGGV
RVASVQQVPPRLPPEARPGRRMFSTSALQGAQGGARALLGGYSQAYGTVCHSALGHLPLL
EGHHV

SEQ ID NO: 177_N28606_H, MOK_H
MKNYKAIGKIGEGTFSEVMKMQSLRDGNYYACKQMKQRFESIEQVNNLREIQALRRLNPH
PNILMLHEVVFDRKSGSLALICELMDMNIYELIRGRRYPLSEKKIMHYMYQLCKSLDHIH
RNGIFHRDVKPENILIKQDVLKLGDFGSCRSVYSKQPYTEYISTRWYRAPECLLTDGFYT
YKMDLWSAGCVFYEIASLQPLFPGVNELDQISKIHDVIGTPAQKTLTKFKQSRAMNFDFP
FKKGSGIPLLTTNLSPQCLSLLHAMVAYDPDERIAAHQALQHPYFQEQRKTEKRALGSHR
KAGFPEHPVAPEPLSNSCQISKEGRKQKQSLKQEEDRPKRRGPAYVMELPKLKLSGVVRL
SSYSSPTLQSVLGSGTNGRVPVLRPLKCIPASKKTDPQKDLKPAPQQCRLPTIVRKGGR

SEQ ID NO: 178_AB023153_H, ICK_H
MNRYTTIRQLGDGTYGSVLLGRSIESGELIAIKKMKRKFYSWEECMNQREVKSLKKLNHA
NVVKLKEVIRENDHLYFIFEYMKENLYQLIKERNKLFPESAIRNIMYQILQGLAFIHKLG
FFHRDLKPENLLCMGPELVKIADFGLAREIRSKPPYTDYVSTRWYRAPEVLLRSTNYSSP
IDVWAVGCIMAEVYTLRPLFPGASEIDTIFKICQVLGTPKKTDWPEGYQLSSAMNFRWPQ
CVPNNLKTLIPNASSEAVQLLRDMLQWDPKKRPTASQALRYPYFQVGHPLGSTTQNLQDS
EKPQKGILERAGPPPYIKPVPPAQPPAKPHTRISSRQHQASQPPLHLTYPYKAEVSRTDH
PSHLQEDKPSPLLFPSLHNKHPQSKITAGLEHKNGEIKPKSRRRWGLISRSTKDSDDWAD
LDDLDFSPSLSRIDLKNKKRQSDDTLCRFESVLDLKPSEPVGTGNSAPTQTSYQRRDTPT
LRSAAKQHYLKHSRYLPGISIRNGILSNPGKEFIPPNPWSSSGLSGKSSGTMSVISKVNS
VGSSSTSSSGLTGNYVPSFLKKEIGSAMQRVHLAPIPDPSPGYSSLKAMRPHPGRPFLDT
QPRSTPGLIPRPPAAQPVHGRTDWASKYPSRR

SEQ ID NO: 179_AA839940_M
SSNNGGMSAEEEIGPGAEPMRGPSLATRDWRDETVGTTDLQQGIDPGAVSPEPGKDHAAQ
GPGRTEAGRVSSAAEAAIVVLDDSAAPPAPFEHRVVSIKDTLISAGYTVSQHEVLGGGRF
GQVHRCTERSTGLALAAKIIKVKNVKDREDVKNEVNIMNQLSHVNLIQLYDAFESKNSFT
LIMEYVDGGELFDRITDEKYHLTELDVVLFTRQICEGVHYLHQHYILHLDLKPENILCVS

FIGURE 10

QTGHQIKIIDFGLARRYKPREKLKVNFGTPEFLAPEVVNYEFVSFPTDMWSVGVITYMLL
SGLSPFLGETDAETMNFIVNCSWDFDADTFKGLSEEAKDFVSRLLVKEKSCRMSATQCLK
HEWLNHLPAKASGSNVRLRSQQLLQKYMAQSKWKKHFHVVAAVNRLRKFPTCP

SEQ ID NO: 180_AA460132_H
MAAARATTPADGEEPAPEAEALAAARERSSRFLSGLELVKQGAEARVFRGRFQGRAAVIK
HRFPKGYRHPALEARLGRRRTVQEARALLRCRRAGISAPVVFFVDYASNCLYMEEIEGSV
TVRDYIQSTMETEKTPQGLSNLAKTIGQVLARMHDEDLIHGDLTTSNMLLKPPLEQLNIV
LIDFGLSFISALPEDKGVDLYVLEKAFLSTHPNTETVFEAFLKSYSTSSKKARPVLKKLD
EVRLRGRKRSMVG

SEQ ID NO: 181_SGK034_H
QREKVNQGNMPGLQSTFLAMDTEEGVEVVWNELHFGDRKAFAAHEEKIQTVFEQLVLVDH
PNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLKKTKKNHKAMNARAWKRWCTQILS
ALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWHRIFSNALPDDLRSPIRAEREELR
NLHFFPPEYGEVADGTAVDIFSFGMCALEMAVLEIQTNGDTRVTEEAIARARHSLSDPNM
REFILCCLARDPARRPSAHSLLFHRVLFEVHSLKLLAAHCFIQHQYLMPENVVEEKTKAM
DLHAVLAELPRPRRPPLQWRYSEVSFMELDKFLEDVRNGIYPLMNFAATRPLGLPRVLAP
PPEEVQKAKTPTPEPFDSETRKVIQMQCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLL
PTDSAQDLASELVHYGFLHEDDRMKLAAFLESTFLKYRGTQA

SEQ ID NO: 182_AA103218_M SGK034_M
HASAPEYGEVNDGTGFVDIFSFGMCALEMAVLEIQANGDTRVTEEAIARARHSLSDPNMR
EFILSCLARDPARRPSAHNLLFHRVLFEVHSLKLLAAHCFIQHQYLMPENVVEEKTKAMD
LHAVLAEMPQPHGPPMQWRYSEVSFLELDKFLEDVRNGIYPLMNFAAARPLGLPRVLAPP
PEEAQKAKTPTPEPFDSETRKVVQMQCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLLP
TDSAQDLAAELVHYGFLHEDDRTKLAAFLETTFLKYRGTQA

SEQ ID NO: 183_NEK7_H, N34132_H
MSGGAAEKQSSTPGSLFLSPPAPAPKNGSSSDSSVGEKLGAAAADAVTGRTEEYRRRRHT
MDKDSRGAAATTTTTEHRFFRRSVICDSNATALELPGLPLSLPQPSIPAAVPQSAPPEPH
REETVTATATSQVAQQPPAAAAPGEQAVAGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPP
ARSGSGGGSAKEPQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVYKGLD
TETTVEVAWCELQDRKLTKSERQRFKEEAEMLKGLQHPNIVRFYDSWESTVKGKKCIVLV
TELMTSGTLKTYLKRFKVMKIKVLRSWCRQILKGLQFLHTRTPLIIHRDLKCDNIFITGP
TGSVKIGDLGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCMLEMATSEY
PYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEIIEGCIRQNKDERYSIKDLLNHAFFQ
EETGVRVELAEEDDGEKIAIKLWLRIEDIKKLKGKYKDNEAIEFCFDLERDVPEDVAQEM
VESGYVCEGDHKTMAKAIKDRVSLIKRKREQRQLVREEQENKKQEESSLKQQVEQSSASQ
TGIKQLPSASTGIPTASTTSASVSTQVEPEEPEADQHQQLQYQQPSISVLSDGTVDSGQG
SSVFTESRVSSQQTVSYGFPXHEQAHSTGTVPGHIPSTVQAQSQPHGVYPPSSVQQGIQQ
TAPPQQTVQYSLSQTSTSSEATTAQPVSQPQAPQVLPQVSAGKQSTQGVSQVAPAEPVAV
AQPQATQPTTLASSVDSAHSDVASGMSDGNENVPSSSGRHEGRTTKRHYRKSVRSRSRHE
KTSRPKLRILNVSNKGDRVVECQLETHNRKMVTFKFDLDGDNPEEIATIMVNNDFILAIE
RESFVDQVREIIEKADEMLSEDVSVEPEGDQGLESLQGKDDYGFSGSQKLEGEFKQPIPA
SSMPQQIGIPTSSLTQVVHSAGRRFIVSPVPESRLRESKVFPSEITDTVAASTAQSPGMN
LSHSASSLSLQQAFSELRRAQMTEGPNTAPPNFSHTGPTFPVVPPFLSSIAGVPTTAAAT
APVPATSSPPNDISTSVIQSEVTVPTEEGIAGVATSTGVVTSGGLPIPPVSESPVLSSVV
SSITIPAVVSISTTSPSLQVPTSTSEIVVSSTALYPSVTVSATSASAGGSTATPGPKPPA
VVSQQAAGSTTVGATLTSVSTTTSFPSTASQLSIQLSSSTSTPTLAETVVVSAHSLDKTS

FIGURE 1P

HSSTTGLAFSLSAPSSSSSPGAGVSSYISQPGGLHPLVIPSVIASTPILPQAAGPTSTPL
LPQVPSIPPLVQPVANVPAVQQTLIHSQPQPALLPNQPHTHCPEVDSDTQPKAPGIDDIK
TLEEKLRSLFSEHSSSGAQHASVSLETSLVIESTVTPGIPTTAVAPSKLLTSTTSTCLPP
TNLPLGTVALPVTPVVTPGQVSTPVSTTTSGVKPGTAPSKPPLTKAPVLPVGTELPAGTL
PSEQLPPFPGPSLTQSQQPLEDLDAQLRRTLSPEMITVTSAVGPVSMAAPTAITEAGTQP
QKGVSQVKEGPVLATSSGAGVFKMGRFQVSVAADGAQKEGKNKSEDAKSVHFESSTSESS
VLSSSSPESTLVKPEPNGITIPGISSDVPESAHKTTASEAKSDTGQPTKVGRFQVTTTAN
KVGRFSVSKTEDKITDTKKEGPVASPPFMDLEQAVLPAVIPKKEKPELSEPSHLNGPSSD
PEAAFLSRDVDDGSGSPHSPHQLSSKSLPSQNLSQSLSNSFNSSYMSSDNESDIEDEDLK
LELRRLRDKHLKEIQDLQSRQKHEIESLYTKLGKVPPAVIIPPAAPLSGRRRRPTKSKGS
KSSRSSSLGNKSPQLSGNLSGQSAASVLHPQQTLHPPGNIPESGQNQLLQPLKPSPSSDN
LYSAPTSDGAISVPSLSAPGQGNKATIIVQKQ

SEQ ID NO: 184_BCON3_H
MSEGESQTVLSSGSDPKVESSSSAPGLTSVSPPVTSTTSAASPEEEEESEDESEILEESP
CGRWQKRREEVNQRNVPGIDSAYLAMDTEEGVEVVWNEVQFSERKNYKLQEEKVRAVFDN
LIQLEHLNIVKFHKYWADIKENKARVIFITEYMSSGSLKQFLKKTKKNHKTMNEKAWKRW
CTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIKIGSVAPDTINNHVKTCREEQKNL
HFFAPEYGEVTNVTTAVDIYSFGMCALEMAVLEIQGNGESSYVPQEAISSAIQLLEDPLQ
REFIQKCLQSEPARRPTARELLFHPALFEVPSLKLLAAHCIVGHQHMIPENALEEITKNM
DTSAVLAEIPAGPGREPVQTLYSQSPALELDKFLEDVRNGIYPLTAFGLPRPQQPQQEEV
TSPVVPPSVKTPTPEPAEVETRKVVLMQCNIESVEEGVKHHLTLLLKLEDKLNRHLSCDL
MPNENIPELAAELVQLGFISEADQSRLTSLLEETLNKFNFARNSTLNSAAVTVSS

SEQ ID NO: 185_AA711829_M
LKQFLKKTKKNHKTMNEKAWKRWCTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIK
IGSVAPDTINNHVKTCREEQKNLHFFAPEYGEVTNVTTAVDIYSFGMCALEMAVLEIQGN
GESSYVPQEAISSAIQLLEDSLQREFIQKCLQSEPARRPTARELLFHPALFEVPSLKLLA
AHCIVGHQHMIPENALEEITKNMDTSAVLAEIPAGPGREPVQTLYSQSPALELDKFLEDV
RNGIYPLTAFGLPRPQQPQQEEVTSPVVPPSVKTPTPEPAEVETRKVVLMQCNIESVEEG
VKHHLTLLLKLEDKLNRHLSCDLMPNESIPDLAAELVQLGFISEADQSRLTSLLEETLNK
FNFTRNSTLNTATVTVSS

SEQ ID NO: 186_AA099102_H
MSSCVSSQPSSNRAAPQDELGGRGSSSSESQKPCEALRGLSSLSIHLGMESFIVVTECEP
GCAVDLGLARDRPLEADGQEVPLDTSGSQARPHLSGRKLSLQERSQGGLAAGGSLDMNGR
CICPSLPYSPVSSPQSSPRLPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVK
LAYNENDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIQPRGPIEQVYQEIAIL
KKLDHPNVVKLVEVLDDPNEDHLYMVFELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGI
EYLHYQKIIHRDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNYVGTPAFMAPESLS
ETRKIFSGKAKDVWAMGVTLYCFVFGQCPFMDERIMCLHSKIKSQALEFPDQPDIAEDLK
DLITRMLDKNPESRIVVPEIKLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPS
LATVILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESLSELKEARQRRQP
PGHRPAPRGGGGSALVRGSPCVESCWAPAPGSPARMHPLRPEEAMEPE

SEQ ID NO: 187_5R69_17_2_H
MQEIPQEQIKEIKKEQLSGSPWILLRENEVSTLYKGEYHRAPVAIKVFKKLQAGSIAIVR
QTFNKEIKTMKKFESPNILRIFGICIDETVTPPQFSIVMEYCELGTLRELLDREKDLTLG

FIGURE 1Q

KRMVLVLGAARGLYRLHHSEAPELHGKIRSSNFLVTQGYQVKLAGFELRKTQTSMSLGTT
REKTDRVKSTAYLSPQELEDVFYQYDVKSEIYSFGIVLWEIATGDIPFQGEECEDWLSQW
L

SEQ ID NO: 188_H85811_H
MAPVYEGMASHVQVFSPHTLQSSAFCSVKKLKIEPSSNWDMTGYGSHSKVYSQSKNIPLS
QPATTTVSTSLPVPNPSLPYEQTIVFPGSTGHIVVTSASSTSVTGQVLGGPHNLMRRSTV
SLLDTYQKCGLKRKSEEIENTSSVQIIEEHPPMIQNNASGATVATATTSTATSKNSGSNS
EGDYQLVQHEVLCSMTNTYEVLEFLGRGTFGQVVKCWKRGTNEIVAIKILKNHPSYARQG
QIEVSILARLSTESADDYNFVRAYECFQHKNHTCLVFEMLEQNLYDFLKQNKFSPLPLKY
IRPVLQQVATALMKLKSLGLIHADLKPENIMLVDPSRQPYRVKVIDFGSASHVSKAVCST
YLQSRYYRAPEIILGLPFCEAIDMWSLGCVIAELFLGWPLYPCDSEYDQIRYISQTQGLP
AEYLLSAGTKTTRFFNRDTDSPYPLWRLKTPDDHEAETGIKSKEARKYIFNCLDDMAQVN
MTTDLEGSDMLVEKADRREFIDLLKKMLTIDADKRITPIETLNHPFVTMTHLLDFPHSTH
VKSCFQNMEICKRRVNMYDTVNQSKTPFITHVAPSTSTNLTMTFNNQLTTVHNQPSAASM
AAVAQRSMPLQTGTAQICARPDPFQQALIVCPPGFQGLQASPSKHAGYSVRMENAVPIVT
QAPGAQPLQIQPGLLAQQAWPSGTQQILLPPAWQQLTGVATHTSVQHATVIPETMAGTQQ
LADWRNTHAHGSHYNPIMQQPALLTGHVTLPAAQPLNVGVAHVMRQQPTSTTSSRKSKQH
QSSVRNVSTCEVSSSQAISSPQRSKRVKENTPPRCAMVHSSPACSTSVTCGWGDVASSTT
RERQRQTIVIPDTPSPTVSVITISSDTDEEEEQKHAPTSTVSKQRKNVISCVTVHDSPYS
DSSSNTSPYSVQQRAGHNNANAFDTKGSLENHCTGNPRTIIVPPLKTQASEVLVECDSLV
PVNTSHHSSSYKSKSSSNVTSTSGHSSGSSSGAITYRQQRPGPHFQQQQPLNLSQAQQHI
TTDRTGSHRRQQAYITPTMAQAPYSFPHNSPSHGTVHPHLAAAAAAAHLPTQPHLYTYTA
PAALGSTGTVAHLVASQGSARHTVQHTAYPASIVHQVPVSMGPRVLPSPTIHPSQYPAQF
AHQTYISASPASTVYTGYPLSPAKVNQYPYI

SEQ ID NO: 189_DYRK3_H
MMIDEPKCPPCSNVLCNPSEPEPPRRLNMTTEQFTGDHTQHFLDGGEMKVEQLFQEFGNR
KSNTIQSDGISDSEKCSPTVSQGKSSDCLNTVKSNSSSKAPKVVPLTPEQALKQYKHHLT
AYEKLEIINYPEIYFVGPNAKKRHGVIGGPNNGGYDDADGAYIHVPRDHLAYRYEVLKII
GKGSFGQVARVYDHKLRQYVALKMVRNEKRFHRQAAEEIRILEHLKKQDKTGSMNVIHML
ESFTFRNHVCMAFELLSIDLYELIKKNKFQGFSVQLVRKFAQSILQSLDALHKNKIIHCD
LKPENILLKHHGRSSTKVIDFGSSCFEYQKLYTYIQSRFYRAPEIILGSRYSTPIDIWSF
RCILAELLTGQPLFPGEDEGDQLACMMELLGMPPPKLLEQSKRAKYFINSKGIPRYCSVT
TQADGRVVLVGGRSRRGKKRGPPGSKDWGTALKGCDDYLFIEFLKRCLHWDPSARLTPAQ
ALRHPWISKSVPRPLTTIDKVSGKRVVNPASAFQGLGSKLPPVVGIANKLKANLMSETNG
SIPLCSVLPKLIS

SEQ ID NO: 190_AA589241_M DYRK3_M
TRPELLGMPPQKLLEQSKRAKYFINSKGLPRYCSVSTQTDGRVVLLGGRSRRGKKRGPPG
SKDWATALKGCGDYLFIEFLKRCLQWDPSARLTPAQALRHPWISKSTPKPLTMDKVPGKR
VVNPTNAFQGLGSKLPPVVGIASKLKANLMSETSGSIPLCSVLPKLIS

SEQ ID NO: 191_5R72_16_2_H
MAGGRGAPGRGRDEPPESYPQRQDHELQALEAIYGADFQDLRPDACGPVKEPPEINLVLY
PQGLTGEEVYVKVDLRVKCPPTYPDVVPEIELKNAKGLSNESVNLLKSRLEELAKKHCGE
VMIFELAYHVQSFLSEHNKPPPKSFHEEMLERRAQEEQQRLLEAKRKEEQEQREILHEIQ
RRKEEIKEEKKRKEMAKQERLEIASLSNQDHTSKKDPGGHRTAAILHGGSPDFVGNGKHR
ANSSGRSRRERQYSVCNSEDSPGSCEILYFNMGSPDQLMVHKGKCIGSDEQLGKLVYNAL
ETATGGFVLLYEWVLQWQKKMGPFLTSQEKEKIDKCKKQIQGTETEFNSLVKLSHPNVVR

FIGURE 1R

YLAMNLKEQDDSIVVDILVEHISGVSLAAHLSHSGPIPVHQLRRYTAQLLSGLDYLHSNS
VVHKVLSASNVLVDAEGTVKITDYSISKRLADICKEDVFEQTRVRFSDNALPYKTGKKGD
VWRLGLLLLSLSQGQECGEYPVTIPSDLPADFQDFLKKCVCLDDKERWSPQQLLKHSFIN
PQPKMPLVEQSPEDSGGQDYVETVIPSNRLPSAAFFSETQRQFSRYFIEFEELQLLGKGA
FGAVIKVQNKLDGCCYAVKRIPINPASRQFRRIKGEVTLLSRLHHENIVRYYNAWIERHE
RPAGPGTPPPDSGPLAKDDRAARGQPASDTDGLDSVEAAAPPPILSSSVEWSTSGERSAS
ARFPATGPGSSDDEDDDEDEHGGVFSQSFLPASDSESDIIFDNEDENSKSQNQDEDCNEK
NGCHESEPSVTTEAVHYLYIQMEYCEKSTLRDTIDQGLYRDTVRLWRLFREILDGLAYIH
EKGMIHRDLKPVNIFLDSDDHVKIGDFGLATDHLAFSADSKQDDQTGDLIKSDPSGHLTG
MVGTALYVSPEVQGSTKSAYNQKVDLFSLGIIFFEMSYHPMVTASERIFVLNQLRDPTSP
KFPEDFDDGEHAKQKSVISWLLNHDPAKRPTATELLKSELLPPPQMEESELHEVLHHTLT
NVDGKAYRTMMAQIFSQRISPAIDYTYDSDILKGNFSIRTAKMQQHVCETIIKIFKRHGA
VQLCTPLLLPRNRQIYEHNEAALFMDHSGMLVMLPFDLRIPFARYVARNNILNLKRYCIE
RVFRPRKLDRFHPKELLECAFDIVTSTTNSFLPTAEIIYTIYEIIQEFPALQERNYSIYL
NHTMLLKAILLHCGIPEDKLSQVYIILYDAVTEKLTRREVEAKFCNLSLSSNSLCRLYKF
IEQKGDLQDLMPTINSLIKQKTGIAQLVKYGLKDLEEVVGLLKKLGIKLQVLINLGLVYK
VQQHNGIIFQFVAFIKRRQRAVPEILAAGGRYDLLIPQFRGPQALGPVPTAIGVSIAIDK
ISAAVLNMEESVTISSCDLLVVSVGQMSMSRAINLTQKLWTAGITAEIMYDWSQSQEELQ
EYCRHHEITYVALVSDKEGSHVKVKSFEKERQTEKRVLETELVDHVLQKLRTKVTDERNG
REASDNLAVQNLKGSFSNASGLFEIHGATVVPIVSVLAPEKLSASTRRRYETQVQTRLQT
SLANLHQKSSEIEILAVDLPKETILQFLSLEWDADEQAFNTTVKQLLSRLPKQRYLKLVC
DEIYNIKVEKKVSVLFLYSYRDDYYRILF

SEQ ID NO: 192_R43524_H, HRI_H
MLGGNSGVRKREEEGDGAGAVAAPPAIDFPAEGPDPEYDESDVPAEIQVLKEPLQQPTFP
FAVANQLLLVSLLEHLSHVHEPNPLRSRQVFKLLCQTFIKMGLLSSFTCSDEFSSLRLHH
NRAITHLMRSAKERVRQDPCEDISRIQKIRSREVALEAQTSRYLNEFEELVILGKGGYGR
VVKVRNKLDGQYYAIKKIHIKGATKKVCMKVLREVKVLAGLQHPNIVGYHTAWIEHVHVI
QPRADRAAIELPSLEVLSDQEEDREQCGVKNDESSSSSIIFAEPTPEKEKRFGESDTENQ
NNKSVKYTTNLVIRESGELESTLELQENGLAGLSASSIVEQQLPLRRNSHLEESFTSTEE
SSEENVNFLGQTEAQYHLMLHIQMQLCELSLWDWIVERNKRGREYVDESACPYVMANVAT
KIFQELVEGVFYIHNMGIVHRDLKPRNIFLHGPDQQVKIGDFGLACTDILQKNTDWTNRN
GKRTPTHTSRVGTCLYASPEQLEGSEYDAKSDMYSLGVVLLELFQPFGTEMERAEVLTGL
RTGQLPESLRKRCPVQAKYIQHLTRRNSSQRPSAIQLLQSELFQNSGNVNLTLQMKIIEQ
EKEIAELKKQLNLLSQDKGVRDDGKDGGVG

SEQ ID NO: 193_17000057519457_H
MAAARATTPADGEEPAPEAEALAAARERSSRFLSGLELVKQGAEARVFRGRFQGRAAVIK
HRFPKGYRHPALEARLGRRRTVQEARALLRCRRAGISAPVVFFVDYASNCLYMEEIEGSV
TVRDYIQSTMETEKTPQGLSNLAKTIGQVLARMHDEDLIHGDLTTSNMLLKPPLEQLNIV
LIDFGLSFISALPEDKGVDLYVLEKAFLSTHPNTETVFEAFLKSYSTSSKKARPVLKKLD
EVRLRGRKRSMVG

SEQ ID NO: 194_AA013524_M
LVQQGAEARVFRGRFQGRAAVVKHRFPKSYRHPELEARLGRRRTVQEARALLRCRRAGIA
APVVFFVDYASNCLYMEEIEDSVTVRDYIQSTMETEKDPQCLLDLARRMGQVLAGMHDQD
LIHGDLTTSNMLLRRPLAQLHIVLIDFGLSFVSGLPEDKGVDLYVLEKAFLSTHPHTETA
FEAFLKSYGASSKKSSPVLKKLDEVRLRGRKRSMVG

FIGURE 1S

SEQ ID NO: 195_17000139801197_H, IRAKM_H
MAGNCGARGALSAHTLLFDLPPALLGELCAVLDSCDGALGWRGLAERLSSSWLDVRHIEK
YVDQGKSGTRELLWSWAQKNKTIGDLLQVLQEMGHRRAIHLITNYGAVLSPSEKSYQEGG
FPNILFKETANVTVDNVLIPEHNEKGVLLKSSISFQNIIEGTRNFHKDFLIGEGEIFEVY
RVEIQNLTYAVKLFKQEKKMQCKKHWKRFLSELEVLLLFHHPNILELAAYFTETEKFCLI
YPYMRNGTLFDRLQCVGDTAPLPWHIRIGILIGISKAIHYLHNVQPCSVICGSISSANIL
LDDQFQPKLTDFAMAHFRSHLEHQSCTINMTSSSSKHLWYMPEEYIRQGKLSIKTDVYSF
GIVIMEVLTGCRVVLDDPKHIQLRDLLRELMEKRGLDSCLSFLDKKVPPCPRNFSAKLFC
LAGRCAATRAKLRPSMDEVLNTLESTQASLYFAEDPPTSLKSFRCPSPLFLENVPSIPVE
DDESQNNNLLPSDEGLRIDRMTQKTPFECSQSEVMFLSLDKKPESKRNEEACNMPSSSCE
ESWEPKYIVPSQDLRPYKVNIDPSSEAPGHSCRSRPVESSCSSKFSWDEYEQYKKE

SEQ ID NO: 196_AA340598_M IRAKM_M
MWKRFLSELEVLLLFRHPHILELAAYFTETEKLCLVYPYMSNGTLFDRLQCTNGTTPLSW
HVRISVLIGIAKAIQYLHNTQPCAVICGNVSSANILLDDQLQPKLTDFAAAHFRPNLEQQ
SSTINMTGGGRKHLWYMPEEYIRQGRLSVKTDVYSFGIVIMEVLTGCKVVLDDPKHVQLR
DLLMELMEKRGLDSCLSFLDRKIPPCPRNFSAKLFSLAGRCVATKAKLRPTMDEVLSSLE
STQPSLYFAEDPPTSLKSFRCPSPLFLDNVPSIPVEDDENQNNHSVPPKEVLGTDRVTQK
TPFECSQSEVTFLGLDRNRGNRGSEADCNVPSSSHEECWSPELVAPSQDLSPTVISLGSS
WEVPGHSYGSKPMEKRCSSGLFCSEHEQSKKQ

SEQ ID NO: 197_AA088547_H
MASAVRGSRPWPRLGLQLQFAALLLGTLSPQVHTLRPENLLLVSTLDGSLHALSKQTGDL
KWTLRDDPVIEGPMYVTEMAFLSDPADGSLYILGTQKQQGLMKLPFTIPELVHASPCRSS
DGVFYTGRKQDAWFVVDPESGETQMTLTTEGPSTPRLYIGRTQYTVTMHDPRAPALRWNT
TYRRYSAPPMDGSPGKYMSHLASCGMGLLLTVDPGSGTVLWTQDLGVPVMGVYTWHQDGL
RQLPHLTLARDTLHFLALRWGHIRLPASGPRDTATLFSTLDTQLLMTLYVGKDETGFYVS
RLLVHTGVALYPRGLTEAPADGPTTDEVTLQVSGEREGSPSTAVRYPSGSVALPSC[illegible]
GHHELPPVLHTTMLRVHPTLGSGTAETRPPENTQAPAFFLELLSLSREKLWDSELHPEEK
TPDSYLGLGPQDLLAASLTAVLLGGWILFVMRQVVEKQQETPLAPADFAHISQDAQSLHS
GASRRSQKRLQSPSKQAQPLDDPEAEQLTVVGKISFNPKDVLGRGAGGTFVFRGQFEGRA
VAVKRLLRECFGLVRREVQLLQESDRHPNVLRYFCTERGPQFHYIALELCRASLQEYVEN
PDLDRGGLEPEVVLQQLMSGLAHLHSLHIVHRDLKPGNILITGPDSQGLGRVVLSDFGLC
KKLPAGRCSFSLHSGIPGTEGWMAPELLQLLPPDSPTSAVDIFSAGCVFYYVLSGGSHPF
GDSLYRQANILTGAPCLAHLEEEVHDKVVARDLVGAMLSPLPQPRPSAPQVLAHPFFWSR
AKQLQFFQDVSDWLEKESEQEPLVRALEAGGCAVVRDNWHEHISMPLQTDLRKFRSYKGT
SVRDLLRAVRNKKHHYRELPVEVRQALGQVPDGFVQYFTNRFPRLLLHTHRAMRSCASES
LFLPYYPPDSEARRPCPGATGR

SEQ ID NO: 198_HGP_6644466
MEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFMQKLGFGTGVNVYLMKRSPRGLSHSP
WAVKKINPICNDHYRSVYQKRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGE
KSLNDLIEERYKASQDPFPAAIILKVALNMARGLKYLHQEKKLLHGDIKSSNVVIKGDFE
TIKICDVGVSLPLDENMTVTDPEACYIGTEPWKPKEAVEENGVITDKADIFAFGLTLWEM
MTLSIPHINLSNDDDDEDKTFDESDFDDEAYYAALGTRPPINMEELDESYQKVIELFSVC
TNEDPKDRPSAAHIVEALETDV

SEQ ID NO: 199_AA449542_M
SPRGLSHSPWAVKKISLLCDDHYRTVYQKRLTDEAKILKNLNHPNIIGYRAFTEASDGSL
CLAMEYGGEKSLNDLIEERNKDSGSPFPAAVILRVALHMARGLKYLHQEKKLLHGDIKSS

FIGURE 1T

NVVIKGDFETIKICDVGVSLPLDENMTVTDPEACYIGTEPWKPKEALEENGIITDKADVF
AFGLTLWEMMTLCIPHVNLPDDDVDEDATFDESDFDDEAYYAALGTRPSINMELDDSYQK
AIELFCVCTNEDPKDRPSAAHIVEALELDGQCCGLSESKH

SEQ ID NO: 200_5R57_10_2_M TESK2_M
LLDSDLYLPWTVRVKLAYGIAVGLSYLHFKGIFHRDLTSKV

SEQ ID NO: 201_AA232253_H
MSSLGASFVQIKFDDLQFFENCGGGSFGSVYRAKWISQDKEVAVKKLLKIEKEAEILSVL
SHRNIIQFYGVILEPPNYGIVTEYASLGSLYDYINSNRSEEMDMDHIMTWATDVAKGMHY
LHMEAPVKVIHRDLKSRNVVIAADGVLKICDFGASRFHNHTTHMSLVGTFPWMAPEVIQS
LPVSETCDIYSYGVVLWEMLTREVPFKGLEGLQVAWLVVEKNERLTIPSSCPRSFAELLH
QCWEADAKKRPSFKQIISILESMSNDTSLPDKCNSFLHNKAEWRCEIEATLERLKKLERD
LSFKEQELKERERRLKMWEQKLTEQSNTPLLPSFEIGAWTEDDVYCWVQQLVRKGDSSAE
MSVYASLFKENNITGKRLLLLEEEDLKDMGIVSKGHIIHFKSAIEKLTHDYINLFHFPPL
IKDSGGEPEENEEKIVNLELVFGFHLKPGTGPQDCKWKMYMEMDGDEIAITYIKDVTFNT
NLPDAEILKMTKPPFVMEKWIVGIAKSQTVECTVTYESDVRTPKSTKHVHLIQWSRTKPQ
DEVKAVQLAIQTLFTNSDGNPGSRSDSSADCQWLDTLRMRQIASNTSLQRSQSNPILGSP
FFSHFDGQDSYAAAVRRPQVPIKYQQITPVNQSRSSSPTQYGLTKNFSSLHLNSRDSGFS
SGNTDTSSERGRYSDRSRNKYGRGSISLNSSPRGRYSGKSQHSTPSRGRYPGKFYRVSQS
ALNPHQSPDFKRSPRDLHQPNTIPGMPLHPETDSRASEEDSKVSEGGWTKVEYRKKPHRP
SPAKTNKERARGDHRGWRNF

SEQ ID NO: 202_AI375137_H
MGNYKSRPTQTCTDEWKKKVSESYVITIERLEDDLQIKEKELTELRNIFGSDEAFSKVNL
NYRTENGLSLLHLCCICGGKKSHIRTLMLKGLRPSRLTRNGFTALHLAVYKDNAELITSL
LHSGADIQQVGYGGLTALHIATIAGHLEAADVLLQHGANVNIQDAVFFTPLHIAAYYGHE
QVTRLLLKFGADVNVSGEVGDRPLHLASAKGFLNIAKLLMEEGSKADVNAQDNEDHVPLH
FCSRFGHHDIVKYLLQSDLEVQPHVVNIYGDTPLHLACYNGKFEVAKEIIQISGTESLTK
ENIFSETAFHSACTYGKSIDLVKFLLDQNVININHQGRDGHTGLHSACYHGHIRLVQFLL
DNGADMNLVACDPSRSSGEKDEQTCLMWAYEKGHDAIVTLLKHYKRPQDELPCNEYSQPG
GDGSYVSVPSPLGKIKSMTKEKADILLLRAGLPSHFHLQLSEIEFHEIIGSGSFGKVYKG
RCRNKIVAIKRYRANTYCSKSDVDMFCREVSILCQLNHPCVIQFVGACLNDPSQFAIVTQ
YISGGSLFSLLHEQKRILDLQSKLIIAVDVAKGMEYLHNLTQPIIHRDLNSHNILLYEDG
HAVVADFGESRFLQSLDEDNMTKQPGNLRWMAPEVFTQCTRYTIKADVFSYALCLWEILT
GEIPFAHLKPAAAAADMAYHHIRPPIGYSIPKPISSLLIRGWNACPEGRPEFSEVVMKLE
ECLCNIELMSPASSNSSGSLSPSSSSDCLVNRGGPGRSHVAALRSRFELEYALNARSYAA
LSQSAGQYSSQGLSLEEMKRSLQYTPIDKYGYVSDPMSSMHFHSCRNSSSFEDSS

SEQ ID NO: 203_H97685_H
MESERSPLYRQLIDLGYLSSSHWNCGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRL
VDAAKALNLVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESLMNIANRKQEE
MKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEPVGTREIKCCIRQIQELIISRLNQA
VANKLISSVDYLRESFVGTLERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTFHSGS
SVTRMLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAKSICSQFRTRLNS
SHEAFAASLRQLEAGHSGRLEKTEDLWLRVRKDHAPRLARLSLESRSLQDVLLHRKPKLG
QELGRGQYGVVYLCDNWGGHFPCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLHG
SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIALDVVEGIRFLHSQGLVH
RDIKLKNVLLDKQNRAKITDLGFCKPEAMMSGSIVGTPIHMAPELFTGKYDNSVDVYAFG

FIGURE 1U

ILFWYICSGSVKLPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDGDPLK
RPLLGIVQPMLQGIMNRLCKSNSEQPNRGLDDST

SEQ ID NO: 204_W20810_M
DVNLKASKASDVYSFGILVWAVLAGREAELVDKTSLIRETVCDRQSRPPLTELPPGSPET
PGLEKLKELMIHCWGSQSENRPSFQDCEPKTNEVYNLVKDKVDAAVSEVKHYLSQHRSSG
RNLSAREPSQRGTEMDCPRETMVSKMLDRLHLEEPSGPVPGKCPERQAQDTSVGPATPAR
TSSDPVAGTPQIPHTLPFRGTTPGPVFTETPGHPQRNQGDGRHGTPWYPWTPPNPMTGP
PALVFNNCSEVQIGNYNSLVAPPRTTASSSAKYDQAQFGRGRGWQPFHK

SEQ ID NO: 205_AA744236_H
MGSENSALKSYTLREPPPFTLPSGLAVYPAVLQDGKPASVFVYKRENEDKVNKAAKHLKTL
RHPCLLRFLSCTVEADGIHLVTERVQPLEVALETLSSAEVCAGIYDILLALIFLHDRGHL
THNNVCLSSVFVSEDGHWKLGGMETVCKVSQATPEFLRSIQSIRDPASIPPEEMSPEFTT
LPECHGHARDAFSFGTLVESLLTILNEQVSADVLSSFQQTLHSTLLNPIPKCRPALCTLL
SHDFFRNDFLEVVNFLKSLTLKSEEEKTEFFKFLLDRVSCLSEELIASRLVPLLLNQLVF
AEPVAVKSFLPYLLGPKKDHAQGETPCLLSPALFQSRVIPVLLQLFEVHEEHVRMVLLSH
IEAYVEHFTQEQLKKVILPQVLLGLRDTSDSIVAITLHSLAVLVSLLGPEVVVGGERTKI
FKRTAPSFTKNTDLSLEGDPFSQPIKFPINGLSDVKNTSEDSENFPSSSKKSEEWPDWSE
PEEPENQTVNIQIWPREPCDDVKSQCTTLDVEESSWDDCEPSSLDTKVNPGGGITATKPV
TSGEQKPIPALLSLTEESMPWKSSLPQKISLVQRGDDADQIEPPKVSSQERPLKVPSELG
LGEEFTIQVKKKPVKDPEMDWFADMIPEIKPSAAFLILPELRTEMVPKKDDVSPVMQFSS
KFAAAEITEGEAEGWEEEGELNWEDNNW

SEQ ID NO: 206_AI052250_H
MESMLNKLKSTVTKVTADVTSAVMGIPVTREFDVGRHIASGCNGLAWKIFNGTKKSTKQE
VAVFVFDKKLIDKYQKFEKDQIIDSLKRGVQQLTRLRHPRLLTVQHPLEESRDCLAFCTE
PVFASLANVLGNWENLPSPISPDIKDYKLYDVETKYGLLQVS[illegible]
PENIILNKSGAWKIMGFDFCVSSTNPSEQEPKFPCKEWDPNLPSLCLPNPEYLAPEYILS
VSCETASDMYSLGTVMYAVFNKGKPIFEVNKQDIYKSFSRQLDQLSRLGSSSLTNIPEEV
REHVKLLLNVTPTVRPDADQMTKIPFFDDVGAVTLQYFDTLFQRDNLQKSQFFKGLPKVL
PKLPKRVIVQRILPCLTSEFVNPDMVPFVLPNVLLIAEECTKEEYVKLILPELGPVFKQQ
EPIQILLIFLQKMDLLLTKTPPDEIKNSVLPMVYRALEAPSIQIQELCLNIIPTFANLID
YPSMKNALIPRIKNACYKHLPLRFV

SEQ ID NO: 207_AA278842_H
MWFFARDPVRDFPFELIPEPPEGGLPGPWALHRGRKKATGSPVSIFVYDVKPGAEEQTQV
AKAAFKRFKTLRHPNILAYIDGLETEKCLHVVTEAVTPLGIYLKARVEAGGLKELEISWG
LHQIVKALSFLVNDCSLIHNNVCMAAVFVDRAGEWKLGGLDYMYSAQGNGGGPPRKGIPE
LEQYDPPELADSSGRVVREKWSADMWRLGCLIWEVFNGPLPRAAALRNPGKIPKTLVPHY
CELVGANPKVRPNPARFLQNCRAPGGFMSNRFVETNLFLEEIQIKEPAEKQKFFQELSKS
LDAFPEDFCRHKVLPQLLTAFEFGNAGAVVLTPLFKVGKFLSAEEYQQKIIPVVVKMFSS
TDRAMRIRLLQQMEQFIQYLDEPTVNTQIFPHVVHGFLDTNPAIREQTVKSMLLLAPKLN
EANLNVELMKHFARLQAKDEQGPIRCNTTVCLGKIGSYLSASTRHRVLTSAFSRATRDPF
APSRVAGVLGFAATHNLYSMNDCAQKILPVLCGLTVDPEKSVRDQAFKAIRSFLSKLESV
SEDPTQLEEVEKDVHAASSPGMGGAAASWAGWAVTGVSSLTSKLIRSHPTTAPTETNIPQ
RPTPEGVPAPAPTPVPATPTTSGHWETQEEDKDTAEDSSTADRWDDEDWGSLEQEAESVL
AQQDDWSTGGQVSRASQVSNSDHKSSKSPESDWSSWEAEGSWEQGWQEPSSQEPPPDGTR
LASEYNWGGPESSDKGDPFATLSARPSTQPRPDSWGEDNWEGLETDSRQVKAELARKKRE
ERRREMEAKRAERKVAKGPMKLGARKLD

FIGURE 1V

SEQ ID NO: 208_AA599286_H
MAFMEKPPAGKVLLDDTVPLTAAIEASQSLQSHTEYIIRVQGGISVENSWQIVRRYSDFD
LLNNSLQIAGLSLPLPPKKLIGNMDREFIAERQKGLQNYLNVITTNHILSNCELVKKFLD
PNNYSANYTEIALQQVSMFFRSEPKWEVVEPLKDIGWRIRKKYFLMKIKNQPKERLVLSW
ADLGPDKYLSDKDFQCLIKLLPSCLHPYIYRVTFATANESSALLIRMFNEKGTLKDLIYK
AKPKDPFLKKYCNPKKIQGLELQQIKTYGRQILEVLKFLHDKGFPYGHLHASNVMLDGDT
CRLLDLENSLLGLPSFYRSYFSQFRKINTLESVDVHCFGHLLYEMTYGRPPDSVPVDSFP
PAPSMAVVAVLESTLSCEACKNGMPTISRLLQMPLFSDVLLTTSEKPQFKIPTKLKEALR
IAKECIEKRLIEEQKQIHQHRRLTRAQSHHGSEEERKKRKILARKKSKRSALENSEEHSA
KYSNSNNSAGSGASSPLTSPSSPTPPSTSGISALPPPPPPPPPPAAPLPPASTEAPAQLS
SQAVNGMSKGALLSSIQNFQKGTLRKAKPVITVLRRSAEASCLHIEGKVLFYSY[illegible]PPR
YPLPGKVIAEPVQPQTVLFCRCSCKQLFERNNSLSRIKLGWHAKKKKKK

SEQ ID NO: 209_AA425725_H
MSASTGGGGDSGGSGGSSSSSQASCGPESSGSELALATPVPQMLQGLLGSDDEEQEDPKD
YCKGGYHPVKIGDVFNGRYHVVRKLGWGHFSTVWLCWDIQRKRFVALKVVKSAGHYTETA
VDEIKLLKCVRDSDPSDPKRETIVQLIDDFRISGVNGVHVCMVLEVLGHQLLKWIIKSNY
QGLPVPCVKSIVRQVLHGLDYLHTKCKIIHTDIKPENILLCVGDAYIRRLAAEATEWQQA
GAPPPSRSIVSTAPQEVLTGKLSKNKRKKMRRKRKQQKRLLEERLRDLQRLEAMEAATQA
EDSGLRLDGGSGSTSSSGFSGSLFSPASCSILSGSSNQRETGGLLSPSTPFGASNLLVNP
LEPQNADKIKIKIADLGNACWVHKHFTEDIQTRQYRAVEVLIGAEYGPPADIWSTACMAF
ELATGDYLFEPHSGEDYSRDEDHIAHIVELLGDIPPAFALSGRYSREFFNRRGELRHIHN
LKHWGLYEVLMEKYEWPLEQATQFSAFLLPMMEYIPEKRASAADCLQHPWLNP

SEQ ID NO: 210_SGK022_H
MEDFLLSNGYQLGKTIGEGTYSKVKEAFSKKHQRKVAIKVIDKMGGPSEFIQRFLPRELQ
IVRTLDHKNIIQVYEMLESADGKIYLVMELAEGGDVFDCVLNGGPLPESRAKALFRQMVE
AIRYCHGCGVAHRDLKCENALLQGFNLKLTDFGFAKVLPKSHRELSQTFCGSTAYAAPEV
LQGIPHDSKKGDVWSMGVVLYVMLCASLPFDDTDIPKMLWQQQKGVSFPTHLSISADCQD
LLKRLLEPDMILRPSIEEVSWHPWLAST

SEQ ID NO: 211_AA060026_M SGK022_M
MEDFLLSNGYQLGKTIGEGTYSKVKEAFSKKHQRKVAIKIIDKMGGPEEFIQRFLPRELQ
IVRTLDHKNIIQVYEMLESADGKIYLVMELAEGGDVFDCVLNGGPLPESRAKALFRQMVE
AIRYCHGCGVAHRDLKCENALLQGFNLKLTDFGFAKVLPKSRRELSQTFCGSTAYAAPEV
LQGIPHDSKKGDVWSMGVVLYVMLCASLPFDDTDIPKMLWQQQKGVSFPTHLGISTECQD
LLKRLLEPDMILRPSIEEVSWHPWLAST

SEQ ID NO: 212_AA399669_H
MGKGDVLEAAPTTTAYHSLMDEYGYEVGKAIGHGSYGSVYEAFYTKQKVMVAVKIISKKK
ASDDYLNKFLPREIQQVMKVLRHKYLINFYRAIESTSRVYIILELAQGGDVLEWIQRYGA
CSEPLAGKWFSQLTLGIAYLHSKSIVHRDLKLENLLLDKWENVKISDFGFAKMVPSNQPV
GCSPXYRQVNCFSHLSQTYCGSFAYACPEILRGLPYNPFLSDTWSMGVILYTLVVAHLPF
DDTNLKKLLRETQKEVTFPANHTISQECKVQLLIACVAQWRKTQARPLSPLL

SEQ ID NO: 213_AA758539_H
MDDATVLRKKGYIVGINLGKGSYAKVKSAYSERLKFNVAVKIIDRRKTPTDFVERFLPRE
MDILATVNHGSIIKTYEIFETSDGRIYIIMELGVQGDLLEFIKCQGALHEDVARKMFRQL
SSAVKYCHDLDIVHRDLKCENLLLDKDFNIKLSDFGFSKRCLRDSNGRIILSKTFCGSAA

FIGURE 1W

YAAPEVLQSIPYQPKVYDIWSLGVILYIMVCGSMPYDDSDIRKMLRIQKEHRVDFPRSKN
LTCECKDLIYRMLQPDVSQRLHIDEILSHSWLQPPKPKATSSASFKREGEGKYRAECKLD
TKTGLRPDHRPDHKLGAKTQHRLLVVPENENRMEDRLAETSRAKDHHISGAEVGKAST

SEQ ID NO: 214_AA883975_H
MSGDKLLSELGYKLGRTIGEGSYSKVKVATSKKYKGTVAIKVVDRRRAPPDFVNKFLPRE
LSILRGVRHPHIVHVFEFIEVCNGKLYIVMEAAATDLLQAVQRNGRIPGVQARDLFAQIA
GAVRYLHDHHLVHRDLKCENVLLSPDERRVKLTDFGFGRQAHGYPDLSTTYCGSAAYASP
EVLLGIPYDPKKYDVWSMGVVLYVMVTGCMPFDDSDIAGLPRRQKRGVLYPEGLELSERC
KALIAELLQFSPSARPSAGQVARNCWLRAGDSG

SEQ ID NO: 215_AA[illegible]05[illegible]46[illegible]_H
VGRQETGVRRWAFLICQPISPPLTSSEFIQRFLPRELQIVRTLDHKNIIQVYEMLESADG
KICLVMELAEGGDVFDCVLNGGPLPESRAKALFRQMVEAIRYCHGCGVAHRDLKCENALL
QGFNLKLTDFGFAKVLPKSHRELSQTFCGSTAYAAPEVLQGIPXKMLWQQQKGVSFPTHL
SISADCQDLLKRLLEPDMILRPSIEEVSWHPWLAST

SEQ ID NO: 216_H29974_H
YSLLAEIGRGSYGVVYEAVAGRSGARVAVKKIRCDAPENVELALAEFWALTSLKRRHQNV
VQFEECVLQRNGLAQRMSHGNKSSQLYLRLVETSLKGERILGYAEEPCYLWFVMEFCEGG
DLNQYVLSRRPDPATNKSFMLQLTSAIAFLHKNHIVHRDLKPDNILITERSGTPILKVAD
FGLSKVCAGLAPRGKEGNQDNKNVNVNKYWLSSACGSDFYMAPEVWEGHYTAKADIFALG
IIIWAMIERITFIDSETKKELLGTYIKQGTEIVPVGEALLENPKMELHIPQKRRTSMSEG
IKQLLKDMLAANPQDRPDAFELETRMDQVTCAA

SEQ ID NO: 217_AA498104_M H29974_M
PLLLPPPPAAMETGKENGARRGTKSPERKRRSPVQRVLCEKLRPAAQAMDPAGAEVPGEA
FLARRRPLAG[illegible]DVPARPR[illegible]LAEIGRGSYGVVYEAVAGRSGARVAVKK[illegible]
LALAEFWALTSLKRRHQNIVQFEECVLQRNGLAQRMSHGNKNSQLYLRLVETSLKGERIL
GYAEEPCYLWFVMEYCEGGDLNQYVLSRRPDPATNKSFMLQLTSAIAFLHKNHIVHRDLK
PDNILITERSGTPILKVADFGLSKVCAGLAPRGKEGNQDNKNVNVNKYWLSSACGSDFYM
APEVWEGHYTAKADIFALGIIIWAMIERITFIDSETKKELLGTYIKQGTEIVPVGEALLE
NPKMELHIPQKRRTSMSEGVKQLLKDMLAANPQDRPDAFELETRMDQVTCAA

SEQ ID NO: 218_AA215311_H
MVSSQPKYDLIREVGRGSYGVVYEAVIRKTSARVAVKKIRCHAPENVELALREFWALSSI
KSQHPNVIHLEECILQKDGMVQKMSHGSNSSLYLQLVETSLKGEIAFDPRSAYYLWFVMD
FCDGGDMNEYLLSRKPNRKTNTSFMLQLSSALAFLHKNQIIHRDLKPDNILISQTRLDTS
DLEPTLKVADFGLSKVCSASGQNPEEPVSVNKCFLSTACGTDFYMAPEVWEGHYTAKADI
FALGIIIWAMLERITFIDTETKKELLGSYVKQGTEIVPVGEALLENPKMELLIPVKKKSM
NGRMKQLIKEMLAANPQDRPDAFELELRLVQIAFKDSSWET

SEQ ID NO: 219_AA018361_H
MRAAFPAGGAGGSVEPPSARPAPQPAGTAARSEEAPARAQAAGMAGPGWGPPRLDGFILT
ERLGSGTYATVYKAYAKKDTREVVAIKCVAKKSLNKASVENLLTEIEILKGIRHPHIVQL
KDFQWDSDNIYLIMEFCAGGDLSRFIHTRRILPEKVARVFMQQLASALQFLHERNISHLD
LKPQNILLSSLEKPHLKLADFGFAQHMSPWDEKHVLRGSPLYMAPEMVCQRQYDARVDLW
SMGVILYEALFGQPPFASRSFSELEEKIRSNRVIELPLRPLLSRDCRDLLQRLLERDPSR
RISFQDFFAHPWVDLEHMPSGESLGRATALVVQAVKKDQEGDSAAALSLYCKALDFFVPA

FIGURE 1X

LHYEVDAQRKEAIKAKVGQYVSRAEELKAIVSSSNQALLRQGTSARDLLREMARDKPRLL
AALEVASAAMAKEEAAGGEQDALDLYQHSLGELLLLLRSPRAGGGSCFTLRFRTSWPELN
T

SEQ ID NO: 220_AA311714_H
MENFILYEEIGRGSKTVVYKGRRKGTINFVAILCTDKCRRPEITNWVRLTREIKHKNIVT
FHEWYETSNHLWLVXENLPEDVVREFGIDLISGLHHLHKLGILFCDISPRKILLEGPGTL
KFSNFCLAKVEGENLEEFFALVAAEEGGGDNGENVLKKSMKSRVKGSPVYTAPEVVRGAD
FSISSDLWSLGCLLYEMFSGKPPFFSESVSELTEKILCEDPLPPIPKDSSRPKASSDFIN
LLDGLLQRDPQKRLTWTRLLQHSFWKKAFAGADQESSVEDLSLSRNTMECSGPQDSKELL
QNSQSHQAHGHKSGQPLGHSFRLENPTEFRPKSTLEGQLNESMFLLSSRPT[illegible]V
SPGEDMTHCSPQKTSPLTKITSGHLSQQDLESQMRELIYTDSDLVVTPIIDNPKIMKQPP
VKFDAKILHLPTYSVDKLLFLKDQDWNDFLQQVCSQIDSTEKSMGASRAKLNLLCYLCVV
AGHQEVATRLLHSPLFQLLIQHLRIAPNWDIRAKVAHVIGLLASHTTELQENTPVVETTS
SIGIGILNCLVQHSTPVPRQCLVYV

SEQ ID NO: 221_SGK384_H
SLAHVLRARQILTEPEVRDYLRGLVSGLRYLHQRCILHR

SEQ ID NO: 222_AA210451_M SGK384_M
MGQQHGTRNGLTHRELPRGVGLLLAMALMNVALYLCLDQLFISPGRSTADSRRCPPGYFR
MGRMRNCSRWLSCEELRTEVRQLKRVGEGAVKRVFLSEWKEHKVALSRLTRLEMKEDFLH
GLQMLKSLQSEHVVTLVGYCEEDGTILTEYHPLGSLSNLEETLNLSKYQDVNTWQHRLQL
AMEYVSIINYLHHSPLGTRVMCDSNDLPKTLSQYLLTSNFSIVANDLDALPLVDHDSGVL
IKCGHRELHGDFVAPEQLWPYGEDTPFQDDLMPSYNEKVDIWKIPDVSSFLLGHVEGSDM
VRFHLFDIHKACKSQIPAERPTAQNVLDAYQRVFHSLRDTVMSQTKEMI

SEQ ID NO: 223_SGK071_2_H
EVVAVQMMVECMDDHYASQALEELMPLLKLRHAHISVYQELFITWNGEISSLYLCLVMEF
NELSFQEVIEDKRKAKKIIDSEWMQNVLGQVLDALEYLHHLDIIHRNLKPSNIILISSDH
CKLQDLSSNVLMTDKAKWNIRAEEDPFRKSWMAPEALNFSFSQKSDIWSLGCIILDMTSC
SFMDGTEAMHLRKSLRQSPGSLKAVLKTMEEKQIPDVETFRNLLPLMLQIDPSDRITIKD
VVHITFLRGSFKSSCVSLTLHRQMVPASITDMLLEGNVASILGDAGDTKGERALKLLSMA
LASYCLVPEGSLFMPLALLHMHDQWLSCDQDRVPGKRDFASLGKLGKLLGPIPKGLPWPP
ELVEVVVTTMELHDRVLDVQLCACSLLLHLLGQALVHHPEAKAPCNQAITSTLLSALQSH
PEEEPLLVMVYSLLAITTTQESESLSEELQNAGLLEHILEHLNSSLESRDVCASGLGLLW
ALLLDDPILALQRPRKKRAPNHGKPGKPKNPASTQSIIVNKAPLEKVPDLISQVLATYPA
DGEMAEASCGVFWLLSLLGCIKEQQFEQVVALLLQSIRLCQDRALLVNNAYRGLASLVKV
SELAAFKVVVQEEGGSGLSLIKETYQLHRDDPEVVENVGMLLVHLASYEEILPELVSSSM
KALLQEIKERFTSSLVSDSSAFSKPGLPPGGSPQLGCTTSGGLE

SEQ ID NO: 224_AA118352_M SGK071_M
EEDPCQKSWMAPEALKFSFSTKSDIWSLGCIILDMATCSFLNDTEAMQLRKAIRHHPGSL
KPILKTMEEKQIPGTDVYYLLLPFMLHINPSDRLAIKDVMQVTFMSNSFKSSSVALNMQR
QKVPIFITDVLLEGNMANILGSWLCASFVNDSRHCDSGIGSQRLGFDFQSVSWTEHPLKD
VMQNFSSRPEVQLRAINKLLTMPEDQLGLPWPTELLEEVISIIKQHGRILDILLSTCSLL
LRVLGQALAKDPEAEIPRSSLIISFLMDTLRSHPNSERLVNVVYNVLAIISSQGQISEEL
EEEGLFQLAQENLEHFQEDRDICLSILSLLWSLLVDVVTVDKEPLEQLSGMVTWVLATHP
EDVEIAEAGCAVLWLLSLLGCIKESQFEQVVVLLLRSIQLCPGRVLLVNNAFRGLASLAK

FIGURE 1Y

VSELVAFRIVVLEEGSSGLHLIQDIYKLYKDDPEVVENLCMLLAHLTSYKEILPEMESGG
IKDLVQVIRGRFTSSLELISYADEILQVLEANAQPGLQEDQLEPPAGQEAPLQGEPLFRP

SEQ ID NO: 225_018653.9_H
GRGRGAGHARGLGRGPAGRRAEPPRSLSRPGPGPGSRAGPAGRGEGSDAAPAGGSGRGFL
RLLPAGLRPQRALRSGSEPPRPGQSPEPSPAPGAGRRGGRGELARQIRARYEEVQRYSRG
GPGPGAGRPERRRLMDLAPGGPGLPRPRPPWARPLSDGAPGWPPAPGPGSPGPGPRLGCA
ALRNVSGAQYMGSGYTKAVYRVRLPGGAAVALKAVDFSGHDLGSCVREFGVRRGCYRLAA
HKLLKEMVLLERLRHPNVLQLYGYCYQDSEDIPDTLTTITELGAPVEMIQLLQTSWEDRF
RICLSLGRLLHHLAHSPLGSVTLLDFRPRQFVLVDGELKVTDLDDARVEETPCAGSTDCI
LEFPARN[illegible]TLPCSAQGWCEGMNEKRNLYNAYRFFFTYLLPHSAPPSLRPLLDSI[illegible]TGE
LAWGVDETLAQLEKVLHFYRSGQYLQNSTASSSTE[illegible]PDSTIPQEDYRCWPSYHHGSC
LLSVFNLAEAVDVCESHAQCRAFVVTNQTTWTGRQLVFFKTGWSQVVPDPNKTTYVKASG

SEQ ID NO: 226_AA396601_M
TRPGCAALRNVSGAQYVGSGYTKAVYRVRLPGGAAVALKAVDFSGHDLGSCVREFGARRG
CYRLAAHKLLKEMVLLERLRHPNVLQLYGYCYQDSEGIPDTLTTITELGAPVEMIQLLQT
SWEDRFRICLSLGRLLHHLAHSPLGSVTLLDFRPRQFVLVNGELKVTDLDDARVEETPCT
SSADCTLEFPARNFSLPCSAQGWCEGMNEKRNLYNAYRFFFTYLLPHSAPPSLRPLLDSI
VNATGELAWGVDETLAQLETALHLFRSGQYLQNSTSSRAEYQRIPDSAITQEDYRCWPSY
HHGGCLLSVFNLAEAIDVCESHAQCRAFVVTNQTTWTGRKLVFFKTGWNQVVPDAGKTTY
VKAPG

SEQ ID NO: 227_VRK3_H
MISFCPDCGKSIQAAFKFCPYCGNSLPVEEHVGSQTFVNPHVSSFQGSKRGLNSSFETSP
KKVKWSSTVTSPRLSLFSDGDSSESEDTLSSSERSKGSGSRPPTPKSSPQKTRKSPQVTR
GSPQKTSCSPQKTRQSPQTLKRSRVTTSLEALPTGTVLTDKSGRQWKLKSFQTRDNQGIL
YEA[illegible]TCDSSPQKQKFSLRLDAKDGRLFNEQNFFQRAAKPLQVNK[illegible]
IPTCMGFGVHQDKYRFLVLPSLGRSLQSALDVSPKHVLSERSVLQVACRLLDALEFLHEN
EYVHGNVTAENIFVDPEDQSQVTLAGYGFAFRYCPSGKHVAYVEGSRSPHEGDLEFISMD
LHKGCGPSRRSDLQSLGYCMLKWLYGFLPWTNCLPNTEDIMKQKQKFVDKPGPFVGPCGH
WIRPSETLQKYLKVVMALTYEEKPPYAMLRNNLEALLQDLRVSPYDPIGLPMVP

SEQ ID NO: 228_S71575_M VRK3_M
IPTCIGFGIHQDKYRFLVFPSLGRSLQSALDDNPKHVVSERCVLQVACRLLDALEYLHEN
EYVHGNLTAENVFVNPEDLSQVTLVGYGFTYRYCPGGKHVAYKEGSRSPHDGDLEFISMD
LHKGCGPSRRSDLQTLGYCMLKWLYGSLPWTNCLPNTEKITRQKQKYLDSPERLVGLCGR
WNKASETLREYLKVVMALNYEEKPPYATLRNSLEALLQDMRVSPYDPLDLQMVP

SEQ ID NO: 229_AA45427_H
MGHALCVCSRGTVIIDNKRYLFIQKLGEGGFSYVDLVEGLHDGHFYALKRILCHEQQDRE
EAQREADMHRLFNHPNILRLVAYCLRERGAKHEAWLLLPFFKRGTLWNEIERLKDKGNFL
TEDQILWLLLGICRGLEAIHAKGYAHRDLKPTNILLGDEGQPVLMDLGSMNQACIHVEGS
RQALTLQDWAAQRCTISYRAPELFSVQSHCVIDERTDVWSLGCVLYAMMFGEGPYDMVFQ
KGDSVALAVQNQLSIPQSPRHSSALRQLLNSMMTVDPHQRPHIPLLLSQLEALQPPAPGQ
HTTQI

SEQ ID NO: 230_H05721_H
MAVRQALGRGLQLGRALLLRFTGKPGRAYGLGRPGPAAGCVRGERPGWAAGPGAEPRRVG
LGLPNRLRFFRQSVAGLAARLQRQFVVRAWGCAGPCGRAVFLAFGLGLGLIEEKQAESRR

FIGURE 1Z

AVSACQEIQAIFTQKSKPGPDPLDTRRLQGFRLEEYLIGQSIGKGCSAAVYEATMPTLPQ
NLEVTKSTGLLPGRGPGTSAPGEGQERAPGAPAFPLAIKMMWNISAGSSSEAILNTMSQE
LVPASRVALAGEYGAVTYRKSKRGPKQLAPHPNIIRVLRAFTSSVPLLPGALVDYPDVLP
SRLHPEGLGHGRTLFLVMKNYPCTLRQYLCVNTPSPRLAAMMLLQLLEGVDHLVQQGIAH
RDLKSDNILVELDPDGCPWLVIADFGCCLADESIGLQLPFSSWYVDRGGNGCLMAPEVST
ARPGPRAVIDYSKADAWAVGAIAYEIFGLVNPFYGQGKAHLESRSYQEAQLPALPESVPP
DVRQLVRALLQREASKRPSARVAANVLHLSLWGEHILALKNLKLDKMVGWLLQQSAATLL
ANRLTEKCCVETKMKMLFLANLECETLCQAALLLCSWRAAL

SEQ ID NO: 231_AI086865_H
MEKYERIRVVGRGAFGIVHLCLRKADQKLVIIKQIPVEQMTKEERQAAQNECQVLKLLNH
PNVIEYYENFLEDKALMIAMEYAPGGTLAEFIQKRCNSLLEEETILHFFVQILLALHHVH
THLILHRDLKTQNILLDKHRMVVKIGDFGISKILSSKSTPCYISPELCEGKPYNQKSDIW
ALGCVLYELASLKRAFEAANLPALVLKIMSGTFAPISDRYSPELRQLVLSLLSLEPAQRP
PLSHIMAQPLCIRALLNLHTDGREVRGPQQHREQDHQCPLQRGIIMTFGSGSNGCLGHGS
LTDISQPTIVEALLGYEMVQQVEEALSFTLLGSAPLDQEPLLSIDLGTAHSAAVTGEEDL
GSGDVNRLPSWERGHLLAGVASSTDVSTFSEGDCKEPDKCCWRHKQCTGHIIYPFASDCV
RHSLHLHSVNHCNCNSRLKDSSEDSSSSRGAGPTCSHVIESPCFELTPEEEHVERFRYGW
CKSYRPVSVAVIHHPLYHECGADDLNXKKRKRRRRKSKPPIPTQVGPATASPDLGTSMAT
GTPDSTAPITIWRSESPTGKGQGSKVIKKVKKKKEKEKDKEEMDEKAKLKKKAKKGQLTK
KKSPVKLEPSPPDVSRSLSARQLARMSESSPESREELESEDSYNGRGQGELSSEDIVESS
SPRKRENTVQAKKTGAKPSQARKVNKRKSPPGSNPNLS

SEQ ID NO: 232_AA836348_H
MSVLGEYERHCDSINSDFGSESGGCGDSSPGPSASQGPRAGGGAAEQEELHYIPIRVLGR
GAFGEATLYRRTEDDSLVVWKEVDLTRLSEKERRDALNEIVILALLQHDNIIAYYNHFMD
NTTLLIELEYCNGGNLYDKILRQKDKLFEEEMVVWYLFQIVSAVSCIHKAGILHRDIKTL
NIFLTKANIIKLGDYGLAKKLNSEYSMAETLVGTPYYMSPELCQGVKYNFKSDIWAVGCV
IFELLTLKRTFDATNPLNLCVKIVQGIRAMEVDSSQYSLELIQMVHSCLDQDPEQRPTAD
ELLDRPLLRKRRRSSTVTEAPIAVVTSRTSEVYVWGGGKSTPQKLDVIKSGCSARQVCAG
NTHFAVVTVEKELYTWVNMQGGTKLHGQLGHGDKASYRQPKHVEKLQGKAIRQVSCGDDF
TVCVTDEGQLYAFGSDYYGCMGVDKVAGPEVLEPMQLNFFLSNPVEQVSCGDNHVVVLTR
NKEVYSWGCGEYGRLGLDSEEDYYTPQKVDVPKALIIVAVQCGCDGTFLLTQSGKVLACG
LNEFNKLGLNQCMSGIINHEAYHEVPYTTSFTLAKQLSFYKIRTIAPGKTHTAAIDERGR
LLTFGCNKCGQLGVGNYKKRLGINLLGGPLGGKQVIRVSCGDEFTIAATDEKVLNSKTIR
SNSSGLSIGTVFQSSSPGGGGGGGGEEEDSQQESETPDPSGGFRGTMEADRGMEGLISP
TEAMGNSNGASSSCPGWLRKELENAEFIPMPDSPSPLSAAFSESEKDTLPYEELQGLKVA
SEAPLEHKPQVEASVTELFAFESQLVTSAESCSNLCWEGNTTDSSCVCVQLSAGGG

SEQ ID NO: 233_R86668_H, MKK6_H
MNLLLSYRDVQDYSAIIELVETLQALPTCDVAEQHNVCFHYTFALNRRNRPGDRAKALSV
LLPLVQLEGSVAPDLYCMCGRIYKDMFFSSGFQDAGHREQAYHWYRKAFDVEPSLHSGIN
AAVLLIAAGQHFEDSKELRLIGMKLGCLLARKGCVEKMQYYWDVGFYLGAQILANDPTQV
VLAAEQLYKLNAPIWYLVSVMETFLLYQHFRPTPEPPGGPPRRAHFWLHFLLQSCQPFKT
ACAQGDQCLVLVLEMNKVLLPAKLEVRGTDPVSTVTLSLLEPETQDIPSSWTFPVASICG
VSASKRDERCCFLYALPPAQDVQLCFPSVGHCQWFCGLIQAWVTNPDSTAPAEEAEGAGE
MLEFDYEYTETGERLVLGKGTYGVVYAGRDRHTRVRIAIKEIPERDSRFSQPLHEEIALH
RRLRHKNIVRYLGSASQGGYLKIFMEEVPGGSLSSLLRSVWGPLKDNESTISFYTRQILQ
GLGYLHDNHIVHRDIKGDNVLINTFSGLLKISDFGTSKRLAGITPCTETFTGTLQYMAPE
IIDQGPRGYGKAADIWSLGCTVIEMATGRPPFHELGSPQAAMFQVGMYKVHPPMPSSLSA

FIGURE 1AA

EAQAFLLRTFEPDPRLRASAQTLLGDPFLQPGKRSRSPSSPRHAPRPSDAPSASPTPSAN
STTQSQTFPCPQAPSQHPPSPPKRCLSYGGTSQLRVPEEPAAEEPASPEESSGLSLLHQE
SKRRAMLAAVLEQELPALAENLHQEQKQEQGARLGRNHVEELLRCLGAHIHTPNRRQLAQ
ELRALQGRLRAQGLGPALLHRPLFAFPDAVKQILRKRQIRPHWMFVLDSLLSRAVRAALG
VLGPEVEKEAVSPRSEELSNEGDSQQSPGQQSPLPVEPEQGPAPLMVQLSLLRAETDRLR
EILAGKEREYQALVQRALQRLNEEARTYVLAPEPPTALSTDQGLVQWLQELNVDSGTIQM
LLNHSFTLHTLLTYATRDDLIYTRIRGGMVCRIWRAILAQRAGSTPVTSGP

SEQ ID NO: 234_PAK6_H
MFGKKKKKIEISGPSNFEHRVHTGFDPQEQKFTGLPQQWHSLLADTANRPKPMVDPSCIT
PIQLAPMKTIVRGNKPCKETSINGLLEDFDNISVTRSNSLRKESPPTPDQGASSHGPGHA
EENGFITFSQYSSESDTTADYTTEKYREKSLYGDDLDPYYRGSHAAKQNGHVMKMKHGEA
YYSEVKPLKSDFARFSADYHSHLDSLSKPSEYSDLKWEYQRASSSSPLDYSFQFTPSRTA
GTSGCSKESLAYSESEWGPSLDDYDRRPKSSYLNQTSPQPTMRQRSRSGSGLQEPMMPFG
ASAFKTHPQGHSYNSYTYPRLSEPTMCIPKVDYDRAQMVLSPPLSGSDTYPRGPAKLPQS
QSKSGYSSSSHQYPSGYHKATLYHHPSLQSSSQYISTASYLSSLSLSSSTYPPPSWGSSS
DQQPSRVSHEQFRAALQLVVSPGDPREYLANFIKIGEGSTGIVCIATEKHTGKQVAVKKM
DLRKQQRRELLFNEVVIMRDYHHDNVVDMYSSYLVGDELWVVMEFLEGGALTDIVTHTRM
NEEQIATVCLSVLRALSYLHNQGVIHRDIKSDSILLTSDGRIKLSDFGFCAQVSKEVPKR
KSLVGTPYWMAPEVISRLPYGTEVDIWSLGIMVIEMIDGEPPYFNEPPLQAMRRIRDSLP
PRVKDLHKVSSVLRGFLDLMLVREPSQRATAQELLGHPFLKLAGPPSCIVPLMRQYRHH

SEQ ID NO: 235_SURTK106_H
MNDRNEIQMEAKLQSLTIIAQEILCRFFITLRRHARFLLTKLGRQGMARSGITHSCAVCI
LCGPSREGDSPVAMGMTRMLLECSLSDKLCVIQEKQYEVIIVPTLLVTIFLILLGVILWL
FIREQRTQQQRSGPQGIAPVPPPRDLSWEAGHGGNVALPLKETSVENFLGATTPALAKLQ
VPREQLSEVLEQICSGSCGPIFRANMNTGDPSKPKSVILKALKEPAGLHEVQDFLGRIQF
HQYLSKHKQILVQLEGCCTEKPLYMVLEDVAQGDLLGFLWTCRRDVMTMDGLLYDLTEKQ
VYHIGKQVLLALEFLQEKHLFHGDVAARNILMQSDLTAKLCGLGLAYEVYTRGAISSTQT
IPLKWLAPERLLLRPASIRADVWSFGILLYEMVTLGAPPYPEVPPTSILEHLQRRKIMKR
PSSCTHTMYSIMKSCWRWREADRPSPRELRLRLEAAIKTADDEAVLQVPELVVPELYAAV
AGIRVESLFYNYSML

SEQ ID NO: 236_AA098024_M
LQEKHLFHGDVAARNILIQSDLTPKLCHLGLAYEVHAHGAISSARSSTIPLKWLAPERLL
LRPASIRGDIWSFGILLYEMVTLGAPPYPEVPPTSILQYLQRKKIMKRPSSCSHAMYNIM
KCCWRWSEDSRPLLVQLLQRLEAASRSADDKAVLQVPELVVPELYADVAGIRAESISYSF
SVL

SEQ ID NO: 237_SGK2ALPHA_H
MNSSPAGTPSPQPSRANGNINLGPSANPNAQPTDFDFLKVIGKGNYGKVLLAKRKSDGAF
YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDYVNGGE
LFFHLQRERRFLEPRARFYAAEVASAIGYLHSLNIIYRDLKPENILLDCQGHVVLTDFGL
CKEGVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAVDWWCLGAVLYEMLHGLPPFYSQDVS
QMYENILHQPLQIPGGRTVAACDLLQSLLHKDQRQRLGSKADFLEIKNHVFFSPINWDDL
YHKRLTPPFNPNVTGPADLKHFDPEFTQEAVSKSIGCTPDTVASSSGASSAFLGFSYAPE
DDDILDC

FIGURE 1BB

SEQ ID NO: 238_CCRK_H
MDQYCILGRIGEGAHGIVFKAKHVETGEIIALKKVALRRLEDGFPNQALREIKALQEMED
NQYVVQLKAVFPHGGGFVLAFEFMLSDLAEVVRHAQRPLAQAQVKSYLQMLLKGVAFCHA
NNIVHRDLKPANLLISASGQLKIADFGLARVFSPDGSRLYTHQVATRSVGCIMGELLNGS
PLFPGKNDIEQLCYVLRILGTPNPQVWPELTELPDYNKISFKEQVPMPLEEVLPDVSPQA
LDLLGQFLLYPPHQRIAASKALLHQYFFTAPLPAHPSELPIPQRLGGPAPKAHPGPPHIH
DFHVDRPLEGVAVEPRADSALHPGGVRSWPWSRLPAPQDHSVHLFLCHLPGFTLQGLPMA
TVGPHHTLPLSPCEGWSRGRGHVPSQEYENIQSSRGDSWPVLGEPYLLCATDVPIRTVSS
AASQGLHMQNDDACLGAASPECCLLVKEKCRE

SEQ ID NO: 239_TESK2_H
MDRSKRNSIAGFPPRVERLEEFEGGGGGEGNVSQVGRVWPSSYRALISAFSRLTRLDDFT
CEKIGSGFFSEVFKVRHRASGQVMALKMNTLSSNRANMLKEVQLMNRLSHPNILRYINSG
NLEQLLDSNLHLPWTVRVKLAYDIAVGLSYLHFKGIFHRDLTSKNCLIKRDENGYSAVVA
DFGLAEKIPDVSMGSEKLAVVGSPFWMAPEVLRDEPYNEKADVFSYGIILCEIIARIQAD
PDYLPRTENFGLDYDAFQHMVGDCPPDFLQLTFNCCNMDPKLRPSFVEIGKTLEEILSRL
QEEEQERDRKLQPTARGLLEKAPGVKRLSSLDDKIPHKSPCPRRTIWLSRSQSDIFSRKP
PRTVSVLDPYYRPRDGAARTPKVNPFSARQDLMGGKIKFFDLPSKSVISLVFDLDAPGPG
TMPLADWQEPLAPPIRRWRSLPGSPEFLHQEACPFVGREESLSDGPPPRLSSLKYRVKEI
PPFRASALPAAQAHEAMDCSILQEENGFGSRPQGTSPCPAGASEEMEVEERPAGSTPATF
STSGIGLQTQGKQDG

FIGURE 2A

SEQ ID NO: 1_X69117_H BARK2_H
ATGGCGGACCTGGAGGCCGTGCTGGCCGATGTCAGTTACCTGATGGCCATGGAGAAGAGC
AAGGCGACCCCGGCCGCCCGCGCCAGCAAGAGGATCGTCCTGCCGGAGCCCAGTATCCGG
AGTGTGATGCAGAAGTACCTTGCAGAGAGAAATGAAATAACCTTTGACAAGATTTTCAAT
CAGAAAATTGGTTTCTTGCTATTTAAAGATTTTTGTTTGAATGAAATTAATGAAGCTGTA
CCTCAGGTGAAGTTTTATGAAGAGATAAAGGAATATGAAAAACTTGATAATGAGGAAGAC
CGCCTTTGCAGAAGTCGACAAATTTATGATGCCTACATCATGAAGGAACTTCTTTCCTGT
TCACATCCTTTCTCAAAGCAAGCTGTAGAACACGTACAAAGTCATTTATCCAAGAAACAA
GTGACATCAACTCTTTTTCAGCCATACATAGAAGAAATTTGTGAAAGCCTTCGAGGTGAC
ATTTTTCAAAAATTTATGGAAAGTGACAAGTTCACTAGATTTTGTCAGTGGAAAAACGTT
GAATTAAATATCCATTTGACCATGAATGAGTTCAGTGTGCATAGGATTATTGGACGAGGA
GGATTCGGGGAAGTTTATCG[illegible]TGCAGGAAAGCAGACACTGGAAAAATGTA[illegible]GCAA[illegible]GAAA
TGCTTAGATAAGAAGAGGATCAAAATGAAACAAGGAGAAACATTAGCTTTAAATGAAAGA
ATCATGTTGTCTCTTGTCAGCACAGGAGACTGTCCTTTCATTGTATGTATGACCTATGCC
TTCCATACCCCAGATAAACTCTGCTTCATCCTGGATCTGATGAACGGGGGCGATTTGCAC
TACCACCTTTCACAACACGGTGTGTTCTCTGAGAAGGAGATGCGGTTTTATGCCACTGAA
ATCATTCTGGGTCTGGAACACGTGCACAATCGGTTTGTTGTCTACAGAGATTTGAAGCCA
GCAAATATTCTCTTGGATGAACATGGACACGCAAGAATATCAGATCTTGGTCTTGCCTGC
GATTTTTCCAAAAAGAAGCCTCATGCGAGTGTTGGCACCCATGGGTACATGGCTCCCGAG
GTGCTGCAGAAGGGGACGGCCTATGACAGCAGTGCCGACTGGTTCTCCCTGGGCTGCATG
CTTTTCAAACTTCTGAGAGGTCACAGCCCTTTCAGACAACATAAAACCAAAGACAAGCAT
GAAATTGACCGAATGACACTCACCGTGAATGTGGAACTTCCAGACACCTTCTCTCCTGAA
CTGAAGTCCCTTTTGGAGGGCTTGCTTCAGCGAGACGTTAGCAAGCGGCTGGGCTGTCAC
GGAGGCGGCTCACAGGAAGTAAAAGAGCACAGCTTTTTCAAAGGTGTTGACTGGCAGCAT
GTCTACTTACAAAAGTACCCACCACCCTTGATTCCTCCCCGGGGAGAAGTCAATGCTGCT
GATGCCTTTGATATTGGCTCATTTGATGAAGAGGATACCAAAGGGATTAAGCTACTTGAT
TGCGACCAAGAACTCTACAAGAACTTCCCTTTGGTCATCTCTGAACGCTGGCAGCAAGAA
GTAACGGAAACAGTTTATGAAGCAGTAAATGCAGA[illegible]ACAGATA[illegible]GAC[illegible]AG
AGAGCTAAAAATAAGCAACTTGGCCACGAAGAAGATTACGCTCTGGGGAAGGACTGTATT
ATGCACGGGTACATGCTGAAACTGGGAAACCCATTTCTGACTCAGTGGCAGCGTCGCTAT
TTTTACCTCTTTCCAAATAGACTTGAATGGAGAGGAGAGGGAGAGTCCCGGCAAAATTTA
CTGACAATGGAACAGATTCTCTCTGTGGAAGAAACTCAAATTAAAGACAAAAAATGCATT
TTGTTCAGAATAAAAGGAGGGAAACAATTTGTCTTGCAATGTGAGAGTGATCCAGAGTTT
GTGCAGTGGAAGAAAGAGTTGAACGAAACCTTCAAGGAGGCCCAGCGGCTATTGCGTCGT
GCCCCGAAGTTCCTCAACAAACCTCGGTCAGGTACTGTGGAGCTCCCAAAGCCATCCCTC
TGTCACAGGAACAGCAACGGCCTCTGA

SEQ ID NO: 2_AA144574_M BARK2_M
CTGCTTCGTAGTCTACAGAGACCTGAAGCCTGCGAACATCCTCCTAGATGAATATGGGCA
CGTGAGGATATCGGATCTCGGCCTTGCCTGTGATTTCTCCAAAAAGAAGCCTCATGCCAG
CGTGGGCACCCATGGGTACATGGCTCCCGAGGTGTTGCAGAAGGGAACGTGCTATGACAG
CAGCGCCGACTGGTTCTCCCTGGGCTGTATGCTCTTCAAACTTCTGCGGGGCCACAGCCC
CTTCAGGCAGCATAAAACCAAAGACAAGCATGAGATAGACCGAATGACCCTGACCGTGAA
CGTGCAGCTTCCAGATGCCTTCTCCCCTGAGCTGAGGTCCCTCTTAGAGGGTTTGCTCCA
GCGGGACGTGAGCCAGCGGCTGGGCTGCGGAGGAGGAGGGGCACGAGAGTTGAAGGAGCA
CATCTTCTTCAAGGGCATTGACTGGCAGCATGTGTACTTACGGAAGTACCCGCCACCCCT
AATCCCTCCTCGGGGAGAGGTCAACGCTGCAGATGCCTTCGATATCGGCTCCTTCGATGA
GGAAGACACCAAAGGCATTAAGCTGTTGGACTGTGACCAGGACCTCTATAAGAACTTCCC
ACTGGTGATCTCCGAGCGCTGGCAGCAAGAAGTGGTGGAGACCATCTATGACGCCGTCAA
TGCTGATACTGATAAAATCGAGGCCAGGAAGAAGGCTAAAAATAAGCAACTTGGTCAAGA

FIGURE 2B

GGAAGATTACGCTATGGGGAAGGACTGCATCATGCACGGGTACATGCTGAAGCTGGGGAA
CCCCTTTCTCACACAGTGGCAAAGACGCTATTTTTACCTGTTCCCCAACAGACTGGAGTG
GAGAGGAGAGGGCGAGTCTCGGCAAAGTCTACTGACCATGGAACAGATCATGTCTGTGGA
GGAGACCCAGATTAAAGACAGAAAGTGCATCTTACTCAGGATAAAGGGAGGGAAGCAATT
TGTCTTGCAATGTGAGAGTGACCCCGAGTTTGCACAGTGGCTGAAGGAGCTGACCTGCAC
CTTCAATGAGGCCCAGAGACTGCTGCGCCGTGCCCCCAAATTCCTCAACAAACCACGGGC
CGCCATCCTGGAGTTCTCCAAGCCACCACTGTGTCACAGAAATAGCAGCGGCCTCTGAAC
CACAGAGCAGCGGGGCCTGAAGGAGGGGCCCCAGCTCTTCAGCCCAGGAGTGGAACGAAG
CCACGGGGAACCGTGTGGGGCTAAGACACAGTGTTTCTGAGCACTGACGGGGCTGCTCCA
AGCCGAGGAGGCTCAGGACACCAGGGCGGCCTTCTGGGAGCTGGGACATCCTCGGGGCTG
TCCTATCCACACTCGAAATTACTGAAGAAGCAGAGGCATTCTGCTGTG

SEQ ID NO: 3_AA826850_H
GAAGAGGATGGGCTCGTCCATGTCGGCGGCCACCGCGCGGAGGCCGGTGTTTGACGACAA
GGAGGACGTGAACTTCGACCACTTCCAGATCCTTCGGGCCATTGGGAAGGGCAGCTTTGG
CAAGGTGTGCATTGTGCAGAAGCGGGACACGGAGAAGATGTACGCCATGAAGTACATGAA
CAAGCAGCAGTGCATCGAGCGCGACGAGGTCCGCAACGTCTTCCGGGAGCTGGAGATCCT
GCAGGAGATCGAGCACGTCTTCCTGGTGAACCTCTGGTACTCCTTCCAGGACGAGGAGGA
CATGTTCATGGTCGTGGACCTGCTACTGGGCGGGGACCTGCGCTACCACCTGCAGCAGAA
CGTGCAGTTCTCCGAGGACACGGTGAGGCTGTACATCTGCGAGATGGCACTGGCTCTGGA
CTACCTGCGCGGCCAGCACATCATCCACAGAGATGTCAAGCCTGACAACATTCTCCTGGA
TGAGAGAGGACATGCACACCTGACCGACTTCAACATTGCCACCATCATCAAGGACGGGGA
GCGGGCGACGGCATTAGCAGGCACCAAGCCGTACATGGCTCCGGAGATCTTCCAXTCTTT
TGTCAACGGCGGGACCGGCTACTCCTTCGAGGTGGACTGGTGGTCGGTGGGGGTGATGGC
CTATGAGCTGCTGCGAGGATGGAGGCCCTATGACATCCACTCCAGCAACGCCGTGGAGTC
CCTGGTGCAGCTGTTCAGCACCGTGAGCGTCCAGTATGTCCCCACGTGGTCCAAGGAGAT
GGTGGCCTTGCTGCGGAAGCTCCTCACTGTGAACCCCGAGCACCGGCTCTCCAGCCTCCA
GGACGTCCAGGCAGCCCGGGAGCTGGCTGCCTGCTCCTGGGACCACCTGACCGAGAAGAG
GGTGGAGCCGGGCTTCGTGCCCAACAAAGGCCGTCTGCACTGCGACCCCACCTTTGAGCT
GGAGGAGATGATCCTGGAGTCCAGGCCCCTGCACAAGAAGAAGAAGCGCCTGGCCAAGAA
CAAGTCCCGGGACAACAGCAGGGACAGCTCCCAGTCCGAGAATGACTATCTTCAAGACTG
CCTCGATGCCATCCAGCAAGACTTCGTGATTTTTAACAGAGAAAAGCTGAAGAGGAGCCA
GGACCTCCCGAGGGAGCCTCTCCCCGCCCCTGAGTCCAGGGATGCTGCGGAGCCTGTGGA
GGACGAGGCGGAACGCTCCGCCCTGCCCATGTGCGGCCCCATTTGCCCCTCGGCCGGGAG
CGGCTAGGCCGGGATGCCCGTGGTCCTCACCCCTTGAGCTGCTTTGGAGACTCGGCTGCC
AGAGGGAGGGCCATGGGCCGAGGCCTGGCATTCACGTTCCCACCCAGCCTGGCTGGCGGT
GCCCACAGTGCCCCGGACACATTTCACACCTCAGGCTCGTGGTGGTGCAGGGGACAAGAG
GCTGTGGGTGCAGGGGACACCTGTGGAGGGCATTTCCCGTGGCCCCCGAGACCCGCCTA
GATGGAGGAAGCGCTGCTGGGCGCCCTCTTACCGCTCACGGGGAGCTGGGGCCATGGATG
GGACAGGAGTCTTTGTCCCTGCTCAGCCCGGAGGCTGTGCACGGCCCTCGTCACAAGGTG
ACCCTTGCAGCACAGGCCGCGGGTGCCCCAGGCTCGGCTCAGTTCTTGGAGGTCAAGGGC
ATGGGTTGGGGTAGTGGGTGGGGAGGTGAATGTTTTCTAGAGATTCAAACTGCTCCAGCA
ATTTCTGTATAGTTTTCACCTCTGAGAATTACAATGTGAGAACCGCTC

SEQ ID NO: 4_AA960957_H
GTCCCACATCCCGCATCCGGCATCCCAGCGGCCGGGCATGTAGCAGCGGCAGCAACGGCG
GAATATGGGCGGGAACCACTCCCACAAGCCCCCCGTGTTTGACGAGAATGAGGAAGTCAA
CTTTGACCATTTTCAGATTCTGCGGGCCATTGGTAAAGGGAGTTTTGGAAAGGTATGCAT
CGTGCAGAAGCGAGACACTAAGAAAATGTATGCAATGAAGTACATGAACAAGCAGAAGTG
CATCGAGAGGGATGAGGTTCGGAATGTTTTCCGGGAGCTGCAGATCATGCAAGGGCTGGA

FIGURE 2C

GCACCCCTTCCTGGTCAATCTGTGGTACTCCTTCCAGGATGAGGAGGACATGTTCATGGT
GGTGGACCTGCTCCTGGGAGGCGACCTGCGCTACCATCTGCAGCAGAATGTGCATTTCAC
AGAGGGGACTGTGAAACTCTACATCTGTGAGCTGGCACTGGCCCTGGAGTATCTTCAGAG
GTACCACATCATCCACAGAGACATCAAGCCAGACAATATCCTGCTGGATGAACACGGACA
TGTTCACATTACAGACTTCAACATAGCGACGGTAGTGAAAGGAGCAGAAAGGGCTTCCTC
CATGGCTGGCACCAAGCCCTACATGGCTCCAGAAGTATTCCAGGTGTACATGGACAGAGG
CCCCGGATACTCGTACCCTGTCGACTGGTGGTCCCTGGGCATCACAGCCTATGAGCTGCT
GCGGGGCTGGAGGCCGTACGAAATCCACTCGGTCACGCCCATCGATGAAATCCTCAACAT
GTTCAAGGTGGAGCGTGTCCACTACTCCTCCACGTGGTGCAAGGGGATGGTGGCCCTGCT
GAGGAAGCTCCTGACCAAGGATCCTGAGAGCCGCGTGTCCAGCCTTCATGACATACAGAG
[illegible]TACTTGGC[illegible]GACATGAACTGGACGCGGTGTTCAAGAAGG[illegible]CTCATGCCCGG
CTTTGTGCCCAATA[illegible]AGCCAGGT[illegible]AACTGCGA[illegible]CCACATTTGAGCTTGAAGAGATGA[illegible]
TCTAGAATCCAAGCCACTTCACAAAAAGAAGAAGCGATTGGCAAAGAACAGATCCAGGGA
TGGCACAAAGGACAGCTGCCCGCTGAATGGACACCTGCAGCACTGTTTGGAGACTGTCCG
GGAGGAATTCATCATATTCAACAGAGAGAAGCTCAGGAGGCAGCAGGGACAGGGCAGCCA
GCTCTTGGACACCGACAGCCGAGGGGGAGGCCAGGCCCAAAGCAAGCTCCAGGACGGGTG
CAACAACAACCTCCTCACCCACACCTGCACCCGTGGCTGCAGCAGCTGAGCCCACACTTG
TTGCTGCTCAACAGGACTGCACTCGTCTCTGCCCTGCCCACCCAGAGCCCCTCTTTGTGC
CCTGATGGTCCCTGTCTCACCCCTGAAAACATCAGATGCAGAAAAAGCCCTGGACTTGGA
GCTGGGAAGCCTGGGTTCTGGTCCCATCTCCATGACTGATTCACGTGTGACCTCAGACAA
GTCACGCCCTCTCTGTGCCTCCGTTTTCTGCATCTGCCAAAGGGGTTAAACACTTCTGCC
CCACTTCAAATTACAAGATTATGGGGAGAACCCAATTAGGTAGGAAACATGAAAAACCTT
TGATATTTATAAAATCATTTTTACGTGCAAAATATAACCTTAATATTTGAAGTGACCCCC
ATTCCCCAAAGCAATCAAACCGTCATGACTTTGCAATTTGGCACATCCTAGCTTGTTAGA
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CTATGGAAACAACGCTGCCAAATCCTGGAGCAAAACCTGAAGTGTCTTCATGTGCATTCT
CTGGCAGGCCACAGTCCTGAGCTTGTAAGATGGTGCAGCATGCAGACCAGACTTGTCCCC
[illegible]CAGG[illegible]CTCCCCTCAT[illegible]TAAGAAGACT[illegible]
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ATCCAACTGGCCCGAAAGCCCAGACCTGCAGCAGAACTCTCCAACTCTCTATCAGCTTTC
AGGGTTTTCTCTCCTGGGAAGGGTGTAAAATCAGCTTGTCAGATTCTTCTTACAGAGAGT
ATCCAATCGGTATTGGTGGAGCGGCTCCCTATTTATACAATAGGAAGCATGGGTGCTTAG
AAAGTTTATTTCAGGAGGAAAATGGGTTCACACAAAAAGCAAACTACATTCTGATCTGCT
CAGGGAGAAGCTTGCCTTTGAACTGGAAGATGTTGGGATGAGCAGGGAAAGCTTAGACTT
TGGAGTCAGGTTTGTGTTCAGAATCCAGCCCTGCTGGCTACTAACTAACTGGGAGACCTT
AGGCAAAGCATGCAATCGCTCTGAATGGCAGTTTCCTCATTTTTAAACAGGGATAATAAA
ACTAATATTGCAGGGGAGTTACAGGGTTAAATAAGATCCTGTGTGTAACCCCAAGCATTG
GATGACTCATAGAATGGCCTTTTTTGTCAGCATAATCGTCATCATTATTTAGATACTTTC
TTCCTTCACTCACCCAGCAGGTCAGTTTTCTGTGCAAACAAACCTGTTTAGGATTCTTCC
AAATGTTCTTCCTGGGGTCTTTGATATTTGTTTGTTACATCCTGCTGAAGTTCGACTGTG
TTTTTATTTTTTCATCCAACTTCCATTTTTCACTTTTTACATGATTACTCAATCCTTGGG
GCTGTCCATGTCATCTCTTAGATTTCTTAAAAGACATTTTAATGTATGGTTAGGTTTTAT
ATTTTTATTTTTTAAAAAAGAAATAGTCAGTGTTTTCCTCCTTTCAACCGAGACTATTTC
TGGATTGTGTGCTCCTCGTCAGTTGACTTGTTTTGCACACTTTTCTTTACTTCATGTCCC
CATCAACAACCGTCCTGCTCCCCACCTCCCCCAGGAAATAAGGGGCCTGCTCCTCTCCCT
ACTGTGACCCTGGAGGCTCTTAAGATGATGATGGTTTTTTTATTGGGCTGAGTTCACGA
ATTAGGGGCAGGAGCTGGAAGTCGCCCTAGGAACACCAGATTTCCTGGTTCTGTTCAAGT
TGGCATTTCTTGTTTGGAATAAACTATTTCTTGGACATTCCTTC

FIGURE 2D

SEQ ID NO: 5_TBK1_H

TCCTGAGTCTCGAGGAGGCCGCGGGAGCCCGCCGGCGGTGGCGCGGCGGAGACCCGGCTG
GTATAACAAGAGGATTGCCTGATCCAGCCAAGATGCAGAGCACTTCTAATCATCTGTGGC
TTTTATCTGATATTTTAGGCCAAGGAGCTACTGCAAATGTCTTTCGTGGAAGACATAAGA
AAACTGGTGATTTATTTGCTATCAAAGTATTTAATAACATAAGCTTCCTTCGTCCAGTGG
ATGTTCAAATGAGAGAATTTGAAGTGTTGAAAAAACTCAATCACAAAAATATTGTCAAAT
TATTTGCTATTGAAGAGGAGACAACAACAAGACATAAAGTACTTATTATGGAATTTTGTC
CATGTGGGAGTTTATACACTGTTTTAGAAGAACCTTCTAATGCCTATGGACTACCAGAAT
CTGAATTCTTAATTGTTTTGCGAGATGTGGTGGGTGGAATGAATCATCTACGAGAGAATG
GTATAGTGCACCGTGATATCAAGCCAGGAAATATCATGCGTGTTATAGGGGAAGATGGAC
AGTCTGTGTACAAACTCACAGATTTTGGTGCAGCTAGAGAATTAGAAGATGATGAGCAGT
TTGTTTCTCTGTATGGCACAGAAGAATATTTGCACCCTGATATGTATGAGAGAGCAGTGC
TAAGAAAAGATCATCAGAAGAAATATGGAGCAACAGTTGATCTTTGGAGCATTGGGGTAA
CATTTTACCATGCAGCTACTGGATCACTGCCATTTAGACCCTTTGAAGGGCCTCGTAGGA
ATAAAGAAGTGATGTATAAAATAATTACAGGAAAGCCTTCTGGTGCAATATCTGGAGTAC
AGAAAGCAGAAAATGGACCAATTGACTGGAGTGGAGACATGCCTGTTTCTTGCAGTCTTT
CTCGGGGTCTTCAGGTTCTACTTACCCCTGTTCTTGCAAACATCCTTGAAGCAGATCAGG
AAAAGTGTTGGGGTTTTGACCAGTTTTTTGCAGAAACTAGTGATATACTTCACCGAATGG
TAATTCATGTTTTTTCGCTACAACAAATGACAGCTCATAAGATTTATATTCATAGCTATA
ATACTGCTACTATATTTCATGAACTGGTATATAAACAAACCAAAATTATTTCTTCAAATC
AAGAACTTATCTACGAAGGGCGACGCTTAGTCTTAGAACCTGGAAGGCTGGCACAACATT
TCCCTAAAACTACTGAGGAAAACCCTATATTTGTAGTAAGCCGGGAACCTCTGAATACCA
TAGGATTAATATATGAAAAAATTTCCCTCCCTAAAGTACATCCACGTTATGATTTAGACG
GGGATGCTAGCATGGCTAAGGCAATAACAGGGGTTGTGTGTTATGCCTGCAGAATTGCCA
GTACCTTACTGCTTTATCAGGAATTAATGCGAAAGGGGATACGATGGCTGATTGAATTAA
TTAAAGATGATTACAATGAAACTGTTCACAAAAAGACAGAAGTTGTGATCACATTGGATT
TCTGTATCAGAAACATTGAAAAAACTGTGAAAGTATATGAAAAGTTGATGAAGATCAACC
TGGAAGCGGCAGAGTTAGGTGAAATTTCAGAC[illegible]CA
GTTCTCAGGGAACAATAGAAACCAGTCTTCAGGATATCGACAGCAGATTATCTCCAGGTG
GATCACTGGCAGACGCATGGGCACATCAAGAAGGCACTCATCCGAAAGACAGAAATGTAG
AAAAACTACAAGTCCTGTTAAATTGCATGACAGAGATTTACTATCAGTTCAAAAAAGACA
AAGCAGAACGTAGATTAGCTTATAATGAAGAACAAATCCACAAATTTGATAAGCAAAAAC
TGTATTACCATGCCACAAAAGCTATGACGCACTTTACAGATGAATGTGTTAAAAAGTATG
AGGCATTTTTGAATAAGTCAGAAGAATGGATAAGAAAGATGCTTCATCTTAGGAAACAGT
TATTATCGCTGACTAATCAGTGTTTTGATATTGAAGAAGAAGTATCAAAATATCAAGAAT
ATACTAATGAGTTACAAGAAACTCTGCCTCAGAAAATGTTTACAGCTTCCAGTGGAATCA
AACATACCATGACCCCAATTTATCCAAGTTCTAACACATTAGTAGAAATGACTCTTGGTA
TGAAGAAATTAAAGGAAGAGATGGAAGGGGTGGTTAAAGAACTTGCTGAAAATAACCACA
TTTTAGAAAGGTTTGGCTCTTTAACCATGGATGGTGGCCTTCGCAACGTTGACTGTCTTT
AGCTTTCTAATAGAAGTTTAAGAAAAGTTTCCGTTTGCACAAGAAAATAACGCTTGGGCA
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TGTAAATATGTACAATATTGTAAATACATAAAAAATATACAAATTTTTGGCTGCTGTGAA
GATGTAATTTTATCTTTTAACATTTATAATTATATGAGGAAATTTGACCTCAGTGATCAC
GAGAAGAAAGCCATGACCGACCAATATGTTGACATACTGATCCTCTACTCTGAGTGGGGC
TAAATAAGTTATTTTCTCTGACCGCCTACTGGAAATATTTTTAAGTGGAACCAAAATAGG
CATCCTTACAAATCAGGAAGACTGACTTGACACGTTTGTAAATGGTAGAACGGTGGCTAC
TGTGAGTGGGGAGCAGAACCGCACCACTGTTATACTGGGATAACAATTTTTTTGAGAAGG
ATAAAGTGGCATTATTTTATTTTACAAGGTGCCCAGATCCCAGTTATCCTTGTATCCATG
TAATTTCAGATGAATTATTAAGCAAACATTTTAAAGTGAATTCATTATTAAAAACTATTC
ATTTTTTTCCTTTGGCCATAAATGTGTAATTGTCATTAAAATTCTAAGGTCATTTCAACT

FIGURE 2E

GTTTTAAGCTGTATATTTCTTTAATTCTGCTTACTATTTCATGGAAAAAAATAAATTTCT
CAATTTTAAAAAA

SEQ ID NO: 6_AA305176_H
TGGCTGCTCGCGGAGGGGCAGTGTACGCGGGGCCGCTGTAGGCTGTCCAGCGATGGATCC
CACCGCGGGAAGCAAGAAGGAGCCTGGAGGAGGCGCGGCGACTGAGGAGGGCGTGAATAG
GATCGCAGTGCCAAAACCGCCCTCCATTGAGGAATTCAGCATAGTGAAGCCCATTAGCCG
GGGCGCCTTCGGGAAAGTGTATCTGGGGCAGAAAGGCGGCAAATTGTATGCAGTAAAGGT
TGTTAAAAAAGCAGACATGATCAACAAAAATATGACTCATCAGGTCCAAGCTGAGAGAGA
TGCACTGGCACTAAGCAAAAGCCCATTCATTGTCCATTTGTATTATTCACTGCAGTCTGC
AAACAATGTCTACTTGGTAATGGAATATCTTATTGGGGGAGATGTCAAGTCTCTCCTACA
TATATATGGTTATTTTGATGAAGAGATGGCTGTGAAATATATTTCTGAAGTAGCACTGGC
TCTAGACTACCTTCACAGACATGGAATCATCCACAGGGACTTGAAACCGGACAATATGCT
TATTTCTAATGAGGGTCATATTAAACTGACGGATTTTGGCCTTTCAAAAGTTACTTTGAA
TAGAGATATTAATATGATGGATATCCTTACAACACCATCAATGGCAAAACCTAGACAAGA
TTATTCAAGAACCCCAGGACAAGTGTTATCGCTTATCAGCTCGTTGGGATTTAACACACC
AATTGCAGAAAAAAATCAAGACCCTGCAAACATCCTTTCAGCCTGTCTGTCTGAAACATC
ACAGCTTTCTCAAGGACTCGTATGCCCTATGTCTGTAGATCAAAAGGACACTACGCCTTA
TTCTAGCAAATTACTAAAATCATGTCTTGAAACAGTTGCCTCCAACCCAGGAATGCCTGT
GAAGTGTCTAACTTCTAATTTACTCCAGTCTAGGAAAAGGCTGGCCACATCCAGTGCCAG
TAGTCAATCCCACACCTTCATATCCAGTGTGGAATCAGAATGCCACAGCAGTCCCAAATG
GGAAAAAGATTGCCAGGTTTGAGGGACATTTATCTTAATGAAAATCAATTATGTATGTCA
AATGAATGTGAGAAATATTATACCTTTTCATATAAATTCCATAAAGAAATGAAATTGTTA
CATGAATGGCAGTCATAGTATTAATCAGAAATTCATTTTCCTGCACATTCTGTCAAATTC
TTTTGAAATATTTCATTTCTCATTCAATTGTGACATTGTTCTTACTTGATTATATAATGA
GATTCTTGCAGTAAATTGATAATAAATGCTTGGCTTCTGTGTATCTAGGTGGACCTCACT
TGTTTTTAGAAGTCCTTCCCATGATACAGACATTGGCTTGTTGGTTTTGTTTTATTTTGT
TTTTAACATATGTCATTTAAAAGTCATATTTATCTCCTTT

SEQ ID NO: 7_AA116841_M
CCACGCGTCCGATCCCATGGCCAGAAGGCGAAGAAAAGCTATCTGATAATGCTCAAAGTG
CAATGGACATGCTTTTAACCATTGATGATTCAAAGAGAGCTGGAATGAGAGAACTAAAAC
AGCATCCTCTCTTCAGTGAAGTGGACTGGGAAAATCTGCAGCATCAGACTATGCCTTTCG
TACCCCAACCAGACGACGAAACAGATACATCCTATTTTGAAGCCAGAAATAATGCTCAAC
ATCTGACCGTATCTGGGTTTAGTCTGTAGCACATGCGTGTCATTTTTATCTAACTTGTGA
TATAGAATTAAGTTTTACAGTAATATGCTACTTAATACTAGATTGGTCTAAATGGGATAA
AAGTCATTATTTTACCCAGACTGAACAGCTTTTAATTACTAAGTACAACAGTTTTTACAG
AATTAAAATACTATAAGCAATATAATCAGTAATTAATCTTTACCTTAGAACTGTATATAA
GCCATAATAGCTTTTTTCATCTTATTTATTCACTGCACTTTATGAAGAGCAAAGTATCAA
TAAACTAAAACACTACCACTCTAAATAGAGGGAGTGAGCCGT

SEQ ID NO: 8_AA256100_H
AGGGAGCTGACGGGCGCCCGGCCGGCTGCGGTCCGTGCGGAGGCTGAGCCGGCCGCGGGC
GCGACCGGAGGCAGTTTCCGTTACTATGGCAATGACGGCAGGGACTACAACAACCTTTCC
TATGAGCAACCATACCCGGGAAAGAGTGACTGTAGCCAAGCTCACATTGGAGAATTTTTA
TAGCAACCTAATTTTACAGCATGAAGAGAGAGAAACCAGGCAGAAGAAATTAGAAGTGGC
CATGGAAGAAGAAGGATTAGCAGATGAAGAGAAAAAGTTACGTCGATCACAACACGCTCG
CAAAGAAACAGAGTTCTTACGGCTCAAAAGGACCAGACTTGGCTTGGATGACTTTGAGTC
TCTGAAAGTTATAGGAAGAGGAGCTTTTGGAGAGGTGCGGTTGGTCCAGAAGAAAGATAC
AGGCCATATCTATGCAATGAAGATATTGAGAAAGTCTGATATGCTTGAAAAAGAGCAGGT

FIGURE 2F

GGCCCATATCCGAGCAGAAAGAGATATTTTGGTAGAAGCAGATGGTGCCTGGGTGGTGAA
GATGTTTTACAGTTTTCAGGATAAGAGGAATCTTTATCTAATCATGGAATTTCTCCCTGG
AGGTGACATGATGACATTGCTAATGAAGAAAGACACCTTGACAGAAGAGGAAACACAGTT
CTACATTTCAGAGACTGTTCTGGCAATAGATGCGATCCACCAGTTGGGTTTCATCCATCG
GGATATTAAGCCAGACAACCTTTTATTGGATGCCAAGGGTCATGTAAAATTATCTGATTT
TGGTTTATGTACGGGATTAAAGAAAGCTCACAGGACTGAATTTTATAGAAATCTCACACA
CAACCCACCAAGTGACTTCTCATTTCAGAACATGAACTCAAAGAGGAAAGCAGAAACTTG
GAAGAAGAACAGGAGACAACTGGCATATTCCACAGTTGGGACACCAGATTACATTGCTCC
AGAAGTATTCATGCAGACTGGTTACAACAAATTGTGTGACTGGTGGTCTTTGGGAGTGAT
TATGTATGAAATGCTAATAGGATATCCACCTTTCTGCTCTGAAACACCTCAAGAAACATA
GAGAAAACTGATGAACTGGAAAGAAACTCTGGTATTTCCTCCAGAGGTACCTATATCTGA
GAAAGCCAAGGACTTAATTCTCAGTTTTTGTATTGATTCTGAAAACAGAATTGGAAATAC
TGGAGTAGAAGAAATAAAAGGTCATCCCTTTTTTGAAGGTGTCGACTGGGAGCACATAAG
GGAAAGGCCAGCAGCAATCCCTATAGAAATCAAAAGCATTGATGATACTTCAAATTTTGA
TGACTTCCCTGAATCTGATATTTTACAACCAGTGCCAAATACCACAGAACCGGACTACAA
ATCCAAAGACTGGGTTTTTCTCAATTATACCTATAAAAGGTTTGAAGGGTTGACTCAACG
TGGCTCTATCCCCACCTACATGAAAGCTGGGAAGTTATGAATGAAGATAACATTCACCCA
TAACCAAGAGAACTCAGGTAGCTGCATCACCAGGCTTGCTTGGCGTAGATAACAATACAC
TGAAATACTCCTGAAGATGGTGGTGCTTATTGACTACAAGAGGAAATTCTACAGGATTAG
GATTTCTAAGACTACTATAGGAATTGGTTGGCAGTGCCAGCTGGCTCTTTTTTTTAATAT
TTTATTATTTTTGTTAACTTTATTATATGAAGGTACTGGAATAAAAGGAACAGACATCCC
TTTCTAACTGCACTGCCTACATGCGTATTAAGGTCCATTCTGCCTGTGTGTGCTGTGGCT
TTGAACTGTAACACCTCTAATCAATTCAGGAGAAACACATATCATTTAAAGCAACATAGG
CTAACCTGTAGGTAACACTGCAGTATTGATGTTTTACTGCAAATCTTATGGGTCTAGATA
ATCAGTAAAAGCCATCTTCCATAGTTGGTGTTAGAACATTGCCCTATTGGTTTGGACATC
TGTAGAATATATATGAAGACAATTTCTGTAATGGTTTTAAGAGATTTAAAAAGAAATTCA
CTGGTTCTTTACAAAATAGAATTTATCATCAAGTTATTACACAAACTTCACAGTAAGGAG
TGACAAGTTTAAAATAAGGAAGACAAAGTTTAACACCTTCACTCAAGCACTCCAGTAATG
TATTTACGTTGCATTCAGAAATACTGATGACCTTCATATACGTAGTCTGTATACTCATAG
GGAGATGTACTGTATTATATAACATGTAAAGTTGATTTTCTTGTGACAAGAGAACTTCTT
TTTTTAACAAGAGGACATGGCATTATTTTAATTTGATTATGGTGAGTTGAATTTAAGACA
TGACCATGAAGGCTGCTTGTAGAATTAGTGTATTTTTATTAAACTATTTTTTTAAATGTC
AAACTTCTATCATGTAAATGGACTTATAGAGAACAAAAAGCTATTTACTTTGGTTTTCTA
GAAAGTTGTTACATATCATGGCTGGTTAACTTTTATTTCTTTTGATGAAAATTTTTCCTT
TGATAGTACTTGTATTATTGTGCCATTATTTTCTTATGCTCCAAATGTACCAAAGATCTT
GAACAGAGTGGATGTTCACAACTGAGTAGAATTTTCCTTTCCTGTGGGCATGCTGTATTC
AGACCTGACAGATCTTTGATAGAGGTCAGCTTATTAAAGGGCAATATTGTTCTTGTTTAG
CTACATCACTGTGGTGAATATAGATGGAATTAAGGAAGTAAATGCAGGCCAGGGGGTTGT
GATGAGAGGATAGGGGAGATAATATCAGCATCAAATTCTTTGGGTATCTCTCTAAGAATT
AAATAATCTTTTCTAGCTTAATATTTTAATTCTAATTCAAACAACTCTGAGGTTTTGGTT
TCATTAGTAATAGTTGAGGAATAATATACTAGCAAAGAATGGCCTAATGTTTGTCATAAC
TGTTAATGGATGAAATTTTTTAAAGATACAACCATGATAACCATTATAAATGATCTATGA
TCAAAATCTAAAGTGATGAATTATTTGTAGGAATGTCTTCCTAATGGGGAAGAATTGCAT
AGGAGCATTATGCAAATCTACACAAGCTTTTATAAATGTTGCTGCTGGGTAGCTCCACAG
TGTTTCATAAGGCCATCCTGTTTCCCCCAACTCCCCCATTTTTGGTTTGTTTCTTTTTAA
ATATTTGTTGAGTACTTACGTGTTTATCTAACAGTTCACTTCCATTTTTCTAGTCTGGAT
TTTTTGAGTATTTAGGAAAGAGAGCTATTAAAAACTCTGGGGATTTCTCAATGTGACTAA
CTCTAATTTTTCTAATTATAACTGCCTTTAATTAACATAATATTAACTTTTGCTGAGGTT
TATGAGATTTTCTCACCCCACATCGCTCCCCTTTTTTTAAAAAGGACTGTTTTGCTAGTG
TGATAATGAATAGGTAAGATATGAGATAATTGCAACATTGTCCTAGTTCTAGTATGGTAA

FIGURE 2G

CTATTCTTGAAATGGTATTGAAAAATACCGTTAATTCAAATTGACAGAGATTGATAAAAA
GAAACTGATTTACCTAAGTTTACTTTTAATTGCATAATAGAGCATTTTTTGTTTTGAGT
TCCCTCATTCTTATTACCAGAAAGAGCTTGCAAATAGTTTTACTTTCTTGGCACTGGAAG
GGTAGTTCTGGAAAGCTACTTTGTTGAGAGTCTCATTCTTCCCTGGAGTTAATAGAGTGA
TTCACAATCTTTGGGGTTTTCTCCTCATCAAAAGCATTTCTTAAGTGCCTATCTAAAAGC
AATTAAAGACTGTGTCTGCCCTTTAGAAGCTAAGAATTTGATTCATGATGCAAATTAACT
AGATAATTTGCAAAGTACCCTTGAGATTGAATTTTCTCTATTATATATTTCCCATATTTC
AGGTGAATAATTTAATTTAAATGACAAAACCCTATCTAGTCAACTGGGCATAATGACATT
TTCTTTAAATTAGACTCTATTTTGAATTAAAAGAGTTTTATTATAAACCGTGTGTTTTTG
GTTTTTCTAAGTATATAGAAAGCTTGTATAATTCAGATTTATCAATTTCCTGATTTAATG
TAGACTTTGACTTTTTTATTAAAAACCTTTGTATTAAAGCAAGTTATGTTATTTTTCTTT
TATGCATTTATTACTAACATAGCTTTAAATCTTTAAATGTATTGAAGCATTGTGCTGTCT
GAAAATAAGGAATTGCTTATAAACCAGCCACTTCTGAATACAATATGTAGCTGATTTAAT
AAGCTAGTTAGTGAATGGAAAATAAGTGTGGAGTATTAAAAATGTTCTTTGGTTGGTAAG
GCCTAAGATAGGGTTTCATTTATTTCTATACTTTTTCTGTTTTTTAAACACCTGCATATT
TTTATGTAAATCTCTAAATTTAAAATATTTTAAGTACATTTATTTTTGGTGTTTTATTGT
ATAAAACCTTAGACAATCAATCAGTCAGTCTTTACTGACAGGAGCAGCAGCTATCTGTCT
TTTGCTGATCTACAAATAAATGAATTGAGAATTTAGTCCATAGAGGTCCCTGGCTACCAA
ACACATTCTCCTTTGAATTGTTAAAATTCAGAACATTCAAAATAACTGTTTTGCTACAAC
CCATGATTATTTTCCTGTTGTGTTTATTTAAATTTACTTTCTCTTTAGAAGTGCACTTAT
TTCTGAAAAATCTTAATGAAACAAACGCTTAGAACAAATATAAATATGAGACACTTGGGA
CTACTAGAGATATTTTAGATTTTTATGAAAAAAATGTGAGGGGATATTGCTGCTTTAAAA
AGGAATAAAGTAATAAAAATATATCTCAGCTATTTTTTTAAAGCAATATAATTCAGCAAT
TGTCTAGAAAAGTAATCATGAGGCTACTGAGTTTGGTGTTCAGTTACTGAGTTTCAAAAA
TGTTTTGGTGGCATGAGGACAAAATTTCATTGAAGGTAAGATAAGAATAAAAACTATGTT
TAC

SEQ ID NO: 9_AA210825_H
CACGAGGGCTACTGGCGCCTGGCGACCCTCCCTGCCCCCCACCCAACCCCGCTCCGGCAA
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CCCTTCTACCCACTCCGGCCCTCGGGACCCCTCTGCCCATCCCCTGGCCGGTCGGGTCCC
TGCGAACCCCTTTATCTCTGGAATCCACTCGGTCCCCGACTCAGAGACTCCTGCCCTCCA
CCCCCAAGGACCCCGCCATCCTCAGGTCCCCTCCGCCTGCCAGATCTTTTCTCGGATCCC
CGCTCTCCCACCACCTGCTCACGAGATCCCGCGGATCTAGAACCCAGGGTCCCCCGGGGC
CCCCCGGCGGGTCCCGGGTGGGCTCCAGGCGGGCGGTCCCCGGCCTCCCCCCATGGCCAC
CGCCCCCTCATTATCCCGCCGGGCTCCCTGGCTCTCCCGGGCCGGGGTCTCCTCCGCCCC
CCGGCGGCCTAGAGCTGCAGTCGCCGCCACCGCTACTGCCCCAGATCCCGGCCCCGGGTT
CCGGGGTCTCCTTTCACATCCAGATCGGGCTGACCCGCGAGTTCGTGCTGTTGCCCGCCG
CCTCCGAGCTGGCTCATGTGAAGCAGCTGGCCTGTTCCATCGTGGACCAGAAGTTCCCTG
AGTGTGGCTTCTACGGCCTTTACGACAAGATCCTGCTTTTCAAACATGACCCCACGTCGG
CCAACCTCCTGCAGCTGGTGCGCTCGTCCGGAGACATCCAGGAGGGCGACCTGGTGGAGG
TGGTGCTGTCGGCCTCGGCCACCTTCGAGGACTTCCAGATCCGCCCGCACGCCCTCACGG
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TGCGCCAGGGCCTCAAGTGCGATGGCTGCGGGCTGAACTACCACAAGCGCTGTGCCTTCA
GCATCCCCAACAACTGTAGTGGGGCCCGCAAACGGCGCCTGTCATCCACGTCTCTGGCCA
GTGGCCACTCGGTGCGCCTCGGCACCTCCGAGTCCCTGCCCTGCACGGCTGAAGAGCTGA
GCCGTAGCACCACCGAACTCCTGCCTCGCCGTCCCCCGTCATCCTCTTCCTCCTCTTCTG
CCTCATCGTATACGGGCCGCCCCATTGAGCTGGACAAGATGCTGCTCTCCAAGGTCAAGG
TGCCGCACACCTTCCTCATCCACAGCTATACACGGCCCACCGTTTGCCAGGCTTGCAAGA
AACTCCTCAAGGGCCTCTTCCGGCAGGGCCTGCAATGCAAAGACTGCAAGTTTAACTGTC

FIGURE 2H

ACAAACGCTGCGCCACCCGCGTCCCTAATGACTGCCTGGGGAGGCCCTTATCAATGGAG
ATGTGCCGATGGAGGAGGCCACCGATTTCAGCGAGGCTGACAAGAGCGCCCTCATGGATG
AGTCAGAGGACTCCGGTGTCATCCCTGGCTCCCACTCAGAGAATGCGCTCCACGCCAGTG
AGGAGGAGGAAGGCGAGGGAGGCAAGGCCCAGAGCTCCCTGGGGTACATCCCCCTAATGA
GGGTGGTGCAATCGGTGCGACACACGACGCGGAAATCCAGCACCACGCTGCGGGAGGGTT
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GCAAGTGTATCACGCTCTTCCAGAACAACACGACCAACAGATACTATAAGGAAATTCCGC
TGTCAGAAATCCTCACGGTGGAGTCCGCCCAGAACTTCAGCCTTGTGCCGCCGGGCACCA
ACCCACACTGCTTTGAGATCGTCACTGCCAATGCCACCTACTTCGTGGGCGAGATGCCTG
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CAGCCATCCGCCAGGCCCTGATGCCCGTCATCCTTCAGGACGCACCCAGCGCCCCAGGCC
ACGCGCCCCACAGACAAGCTTCTCTGAGCATCTCTGTGTCCAACAGTCAGATCCAAGAGA
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TTGACAAACTGCGCTTCCCTACCAAGCAGGAGAGCCAGCTCCGGAATGAAGTGGCCATTC
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AAGTGTTTGTGGTGATGGAGAAGCTGCATGGGGACATGTTGGAGATGATCCTGTCCAGTG
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TGAGACACCTTCACTTCAAGAACATTGTCCACTGTGACTTGAAACCAGAAAACGTGTTGC
TGGCATCAGCAGACCCATTTCCTCAGGTGAAGCTGTGTGACTTTGGCTTTGCTCGCATCA
TCGGCGAGAAGTCGTTCCGCCGCTCAGTGGTGGGCACGCCGGCCTACCTGGCACCCGAGG
TGCTGCTCAACCAGGGCTACAACCGCTCGCTGGACATGTGGTCAGTGGGCGTGATCATGT
ACGTCAGCCTCAGCGGCACCTTCCCTTTCAACGAGGATGAGGACATCAATGACCAGATCC
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TCAGCCACCCCTGGTTACAGGAGTACCAGACGTGGCTGGACCTCCGAGAGCTGGAGGGGA
AGATGGGAGAGCGATACATCACGCATGAGAGTGACGACGCGCGCTGGGAGCAGTTTGCAG
CAGAGCATCCGCTGCCTGGGTCTGGGCTGGCCCTGGACAGGGATCTCGGTGGCGCCTGTC
CACCACAGGACCACGACATGCAGGGGCTGGCGGAGCGCATCAGTGTTCTCTGAGGTCCTG
TGCCCTCGTCCAGCTGCTGCCCTCCACAGCGGTTCTTCACAGGATCCCAGCAATGAACTG
TTCTAGGGAAAGTGGCTTCCTGCCCAAACTGGATGGGACACGTGGGGAGTGGGGTGGGGG
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CCATGGCCTTGATCTCAGCAAAA

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GAATGTTGGGACCACGATACTTTTTCAGATGATTTTATTGGCAAGGCTTCCATTTCTTTG
GCAGAGATTCCAGCTTTGGCAGAAGTTGATATGTGGATAGATATGAAAACGAAAAAAGGA
GAATTTGCAGGAAAA

SEQ ID NO: 11_AA316804_H
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TCTAATGGAAGCTTCAGTGCACCATCACTCACCAACTCCAGAGGCTCAGTGCATACAGTT
TCATTTCTACTGCAAATTGGCCTCACACGGGAGAGTGTTACCATTGAAGCCCAGGAACTG
TCTTTATCTGCTGTCAAGGATCTTGTGTGCTCCATAGTTTATCAAAAGTTTCCAGAGTGT
GGATTCTTTGGCATGTATGACAAAATTCTTCTCTTTCGCCATGACATGAACTCAGAAAAC
ATTTTGCAGCTGATTACCTCAGCAGATGAAATACATGAAGGAGACCTAGTGGAAGTGGTT

FIGURE 2I

CTTTCAGCTTTAGCCACAGTAGAAGACTTCCAGATTCGTCCACATACTCTCTATGTACAT
TCTTACAAAGCTCCTACTTTCTGTGATTACTGTGGTGAGATGCTGTGGGGATTGGTACGT
CAAGGACTGAAATGTGAAGGCTGTGGATTAAATTACCATAAACGATGTGCCTTCAAGATT
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GAAAAGATGGTAATGTGCAGAGTGAAAGTTCCACACACATTTGCTGTTCACTCTTACACC
CGTCCCACGATATGTCAGTACTGCAAGCGGTTACTGAAAGGCCTCTTTCGCCAAGGAATG
CAGTGTAAAGATTGCAAATTCAACTGCCATAAACGCTGTGCATCAAAAGTACCAAGAGAC
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CCAATGGATATTGACAATAATGACATAAATAGTGATAGTAGTCGGGGTTTGGATGACACA
GAAGAGCCATCACCCCCACAAAGATAAGATGTTCTTCTTGGATCCATCTGATCTCGATGTC
GAAAGAGATGAAGAAGCCGTTAAAACAATCAGTCCATCAACAAGCAATAATATTCCGCTA
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GAAATGATTCTATCCAGTGAGAAAAGTCGGCTTCCAGAACGAATTACTAAATTCATGGTC
ACACAGAA[illegible]CTTGTTCC[illegible]TTGAGGAATCTGCATTTTAAGAATATTGTGC[illegible]CATTT[illegible]
AAGCCAGAAAATGTGCTGCTTGCATCAGCAGAGCCATTTCCTCAGGTGAAGCTGTGTGAC
TTTGGATTTGCACGCATCATTGGTGAAAAGTCATTCAGGAGATCTGTGGTAGGAACTCCA
GCATACTTAGCCCCTGAAGTTCTCCGGAGCAAAGGTTACAACCGTTCCCTAGATATGTGG
TCAGTGGGAGTTATCATCTATGTGAGCCTCAGTGGCACATTTCCTTTTAATGAGGATGAA
GATATAAATGACCAAATCCAAAATGCTGCATTTATGTACCCACCAAATCCATGGAGAGAA
ATTTCTGGTGAAGCAATTGATCTGATAAACAATCTGCTTCAAGTGAAGATGAGAAAACGT
TACAGTGTTGACAAATCTCTTAGTCATCCCTGGCTACAGGACTATCAGACTTGGCTTGAC
CTTAGAGAATTTGAAACTCGCATTGGAGAACGTTACATTACACATGAAAGTGATGATGCT
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CCTAATCCAGATGATATGGAAGAAGATCCTTAA

SEQ ID NO: 12_PKNBETA_H
ATGGAGGAGGGGGCGCCGCGGCAGCCTGGGCCGAGCCAGTGGCCCCCAGAGGATGAGAAG
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CCCGGCCCTGGGCCTGGCCCAGCTGAGCCTGTGGCCTCAGGACCCCGGCCGTGGGCAGAG
CAGCTCAGGGCTCGGCACCTAGAGGCTCTCCGGAGGCAGCTGCATGTGGAGCTGAAGGTG
AAACAGGGGGCTGAGAACATGACCCACACGTGCGCCAGTGGCACCCCCAAGGAGAGGAAG
CTCCTTGCAGCTGCCCAGCAGATGCTGCGGGACAGCCAGCTGAAGGTGGCCCTGCTGCGG
ATGAAGATCAGCAGCCTGGAGGCCAGTGGGTCCCCGGAGCCAGGGCCTGAGCTACTGGCG
GAGGAGCTACAGCATCGACTGCACGTTGAGGCAGCGGTGGCTGAGGGCGCCAAGAACGTG

FIGURE 2J

GTGAAACTGCTTAGTAGCCGGAGAACACAGGACCGCAAGGCACTGGCTGAGGCCCAGGCC
CAGCTACAGGAGTCCTCTCAGAAACTGGACCTCCTGCGCCTGGCCTTGGAGCAGCTGCTG
GAGCAACTGCCTCCTGCCCACCCTTTGCGCAGCAGAGTGACCCGAGAGTTGCGGGCTGCG
GTGCCTGGATACCCCCAGCCTTCAGGGACACCTGTGAAGCCCACCGCCCTAACAGGGACA
CTGCAGGTCCGCCTCCTGGGCTGTGAACAGTTGCTGACAGCCGTGCCTGGGCGCTCCCCA
GCGGCCGCACTGGCCAGCAGCCCCTCCGAGGGCTGGCTTCGGACCAAGGCCAAGCACCAG
CGTGGCCGAGGCGAGCTTGCCAGTGAGGTGCTGGCTGTGCTAAAGGTGGACAACCGTGTT
GTGGGCAGACGGGCTGGGGGCAGGTGGCCGAACAGTCCTGGGACCAGACCTTTGTCATC
CCACTGGAGCGAGCCCGTGAGCTGGAGATTGGGGTACACTGGCGGGACTGGCGGCAGCTA
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CTGCTGCCCCCCTGCAGCTCCCCGAGCACAATCAGCCCCCCTAAAGGATGCCCTCGGACC
CCAACAACACTGCGAGAGGCCTCTGACCCTGCCACTCCCAGTAATTTCCTGCCCAAGAAG
ACCCCCTTGGGTGAAGAGATGACACCCCCACCCAAGCCCCCACGCCTCTACCTCCCCCAG
GAGCCAACATCCGAGGAGACTCCGCGCACCAAACGTCCCCATATGGAGCCTAGGACTCGA
CGTGGGCCATCTCCACCAGCCTCCCCCACCAGGAAACCCCCTCGGCTTCAGGACTTCCGC
TGCTTAGCTGTGCTGGGCCGGGGACACTTTGGGAAGGTCCTCCTGGTCCAGTTCAAGGGG
ACAGGGAAATACTACGCCATCAAAGCACTGAAGAAGCAGGAGGTGCTCAGCCGGGACGAG
ATAGAGAGCCTGTACTGCGAGAAGCGGATCCTGGAGGCTGTGGGCTGCACAGGGCACCCT
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ATTTACAGGGACCTGAAGTTGGATAACCTTCTGCTGGATGCCCAGGGATTCCTGAAGATC
GCAGACTTTGGACTCTGCAAGGAAGGGATCGGCTTCGGGGACCGGACTAGCACCTTCTGT
GGCACCCCGGAGTTCCTGGCTCCCGAGGTGCTGACCCAGGAGGCATACACACAGGCCGTC
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GGGGACACAGAGGAAGAGGTGTTTGACTGCATCGTCAACATGGACGCCCCCTACCCCGGC
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CGCCTCGGGGCAGGTGAGCAGGATGCCGAGGAGATCAAGGTCCAGCCATTCTTCAGGACC
ACCAACTGGCAAGCCCTGCTCGCCCGCACCATCCAGCCCCCCTTCGTGCCTACCCTGTGT
GGCCCTGCGGACCTGCGCTACTTTGAGGGCGAGTTCACAGGGCTGCCGCCTGCCCTGACC
CCACCTGCACCCCACAGCCTCCTCACTGCCCGCCAACAGGCCGCCTTCCGGGACTTCGAC
TTTGTGTCAGAGCGATTCCTGGAACCCTGA

SEQ ID NO: 13_AI021023_M PKNBETA_M
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GCTGGGTGTGCTGCTCTACGAGATGCTGGTGGGTGAGTGCCCGTTCCCAGGGGACACAGA
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CCTGCGCTACTTTGAGGGCGAGTTCACAGGGCTGCCGCCTGCCCTGACCCCACCTGCACC
CCACAGCCTCCTCACTGCCCGCCAACAGGCCGCCTTCCGGGACTTCGACTTTGTGTCAGA
GCGATTCCTGGAACCCTGAGGGCATCTCCTGGCACCTCTGTCCCCTTCCCCCACAGACTG
TTAGAGCCTCTGCTCGTTCACCCGTGCGCCCTGCCTGGAGGTCCAGGCCTTGCTGGGTAC
TTCTGAGCCCTTGGGATTCAAAGTGGCAGCCATGGGGCCACTGTTGTGGGCTTTGCTCAG

FIGURE 2K

TGTCACTGGGCAAAGTGTGTCCCTTCCCCCTCCAGCTCGCCCTCTTCTACCTCCCAGCGA
GACCTGGCCCAGAAAGGGTGCCGCAGCAAGGAGTGATATGGTTTGTCTTTTTAAGACTGG
ACTTGCTTTATATTAAATTTGTAAAAGTG

SEQ ID NO: 14_H19102_H
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CTGAAGATTTTAGGCCTCGTGGCTAAAGGCTCCTTTGGAACTGTCCTCAAGGTGCTAGAT
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CGTCTCTTTGCTGCCGAGTTGGTGCTGGTACTGTGTTATCTCCATGACTTGGGCATCATG
CATCGAGATGTGAAGATGGAGAATATTCTTCTAGATGAACGAGGCCATCTGAAACTGACA
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CTTCAGTACATGGCCCCAGAGGTCCTAAGTGGAGGACCTTACAACCATGCTGCTGATTGG
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GAGCTCCTACAGAAGCAGCCAGTGAACTTTGTCACGGAGACACAAGCTACCCAGCCCAGT
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CCTATCCCTGCTTGA

SEQ ID NO: 15_AA476563_H
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TGTGACAGCGATGCCATAGAGAGAATGTACTGTGCCCCAGAGGTTGGAGCAATCACTGAA
GAAACTGAAGCCTGTGATTGGTGGAGTTTGGGTGCTGTCCTCTTTGAACTTCTCACTGGC
AAGACTCTGGTTGAATGCCATCCAGCAGGAATAAATACTCACACTACTTTGAACATGCCA
GAATGTGTCTCTGAAGAGGCTCGCTCACTCATTCAACAGCTCTTGCAGTTCAATCCTCTG

FIGURE 2L

GAACGACTTGGTGCTGGAGTTGCTGGTGTTGAAGATATCAAATCTCATCCATTTTTTACC
CCTGTGGATTGGGCAGAACTGATGAGATGA

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GTTAAGGAAGGCTATGAGAAAGCAGATCCTGCACAGTTTGAGTTGCTCAAGGTTCTTGGT
CAGGGGTCATTTGGAAAGGTTTTTCTTGTTAGAAAGAAGACCGGTCCTGATGCTGGGCAG
CTCTATGCAATGAAGGTGTTAAAAAAAGCCTCTTTAAAAGTTCGAGACAGAGTTCGGACA
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TTCACAAGATTATCCAAAGAGGTTCTGTTTACAGAGGAAGATGTGAAATTCTACCTCGCA
GAACTGGCCCTTGCTTTGGATCATCTGCACCAATTAGGAATTGTTTATAGAGACCTGAAG
CCAGAAAACATTTTGCTTGATGAAATAGGACATATCAAATTAACAGATTTTGGACTCAGC
AAGGAGTCAGTAGATCAAGAAAAGAAGGCTTACTCATTTTGTGGTACAGTAGAGTATATG
GCTCCTGAAGTAGTAAATAGGAGAGGCCATTCCCAGAGTGCTGATTGGTGGTCATATGGT
GTTCTTATGTTTGAAATGCTTACTGGTACTCTGCCATTTCAAGGTAAAGACAGAAATGAG
ACCATGAATATGATATTAAAAGCAAAACTTGGAATGCCTCAATTTCTTAGTGCTGAAGCA
CAAAGTCTTCTAAGGATGTTATTCAAAAGGAATCCAGCAAATAGATTGGGATCAGAAGGA
GTTGAAGAAATCAAAAGACATCTGTTTTTTGCAAATATTGACTGGGATAAATTATATAAA
AGAGAAGTTCAACCTCCTTTCAAACCTGCTTCTGGAAAACCAGATGATACTTTTTGTTTT
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GCTCATCAGCTCTTCAAAGGATTCAGCTTTGTTGCAACTTCTATTGCAGAAGAATATAAA
ATCACTCCTATCACAAGTGCAAATGTATTACCAATTGTTCAGATAAATGGAAATGCTGCA
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ATTACTTTGAAGGATGTCTTTGATGATGGTAGATATGTTTACCTTGTTACGGATTTAATG
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AGTGATATACTATATGTAATAAGTAAGACAGTTGACTATCTTCATTGTCAAGGAGTTGTT
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ATCAGGATATGTGATTTTGGGTTTGCAAAACAACTTCGAGGAGAAAATGGACTTCTCTTA
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GCTGCTTGTGATATCTGGAGTTTAGGAGTCCTTTTTTACACAATGTTGGCTGGCTACACT
CCATTTGCTAATGGCCCCAATGATACTCCTGAAGAGATACTGCTGCGTATAGGCAATGGA
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TCCCATATGCTTCATATGGACCCACATCAGCGGTATACTGCTGAACAAATATTAAAGCAC
TCATGGATAACTCACAGAGACCAGTTGCCAAATGATCAGCCAAAGAGAAATGATGTGTCA
CATGTTGTTAAGGGAGCAATGGTTGCAACATACTCTGCCCTGACTCACAAGACCTTTCAA
CCAGTCCTAGAGCCTGTAGCTGCTTCAAGCTTAGCCCAGCGACGGAGCATGAAAAAGCGA
ACATCAACTGGCCTGTAA

SEQ ID NO: 17_AA215680_H
ATGAGCCTGGTGGCCTGTGAGTGCCTGCCCAGCCCCGGCCTGGAGCCTGAGCCTTGCTCA
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GTGCCTGACATGACAAAACGTGACTATCTGGTGGATGCGGCCACGCAGATCCGGCTGGCC
CTGGAGCGCGATGTTAGTGAGGACTATGAGGCGGCCTTCAACCACTATCAGAATGGCGTG
GACGTGCTGCTCCGTGGCATACACGTTGACCCCAACAAGGAGCGACGTGAGGCTGTGAAG
CTGAAAATTACCAAATACCTGCGGCGGGCAGAGGAGATCTTCAACTGCCACCTGCAGCGG

FIGURE 2M

CCGCTGAGCAGTGGAGCCAGCCCCAGCGCGGGTTTCAGCAGCCTGAGGCTCCGGCCCATT
CGCACGCTGAGCTCTGCCGTGGAGCAGCTGAGGGGCTGCAGGGTGGTCGGGGTCATCGAG
AAGGTGCAGCTGGTCCAGGACCCGGCAACCGGAGGGACCTTTGTGGTGAAGAGCCTACCC
AGGTGCCACATGGTGAGCAGGGAGCGGCTGACCATCATCCCACACGGAGTCCCCTACATG
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CAAGGAGGCACTCTCTGGTCCCACCTGCTCTCCCAGGCGCACTCCCGACATTCTGGGCTC
AGCTCTGGCTCTACCCAGGAGAGGATGAAGGCTCAGCTCAACCCCCACCTCAACCTCCTG
ACCCCAGCGAGGCTTCCCTCAGGCCATGCCCCTGGCCAGGACAGAATCGCCCTGGAGCCT
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GCCCCAGGTGGCCACCTGCACCTTCAAGCTAGGAGGGCTGGCCAGAACTCAGACGCTGGG
GCCCCTCGGCTGGCTCACTTGGGTCCTGAGGGGGCCGGCCCGGTGCTAGGCGGCTCTGGC
CGAGGCATGGATCAGAGCTGCCTGTCAGCAGATGGGGCCGGCCGGGGCTGTGGCAGGGCC
ACCTGGAGTGTGAGAGAGGAGCAGGTGAAGCAGTGGGCGGCAGAGATGCTGGTAGCGCTG
GAGGCGCTGCACGAGCAGGGGGTGCTGTGCCGGGACCTCCACCCCGGGAACCTGCTCCTG
GACCAGGCAGGTCACATCCGGCTCACATATTTTGGCCAGTGGTCAGAGGTGGAGCCCCAG
TGCTGCGGGGAGGCCGTGGACAATCTCTACAGCGCCCCAGAGGTGGGTGGGATTTCCGAG
CTGACGGAAGCCTGTGACTGGTGGAGCTTTGGGTCTCTACTGTATGAACTGCTGACGGGA
ATGGCACTGTCCCAGAGCCACCCTTCAGGAATCCAGGCCCACACCCAGCTCCAGCTGCCC
GAGTGGCTCAGTCGCCCAGCGGCCTCTCTGCTGACTGAGCTGCTGCAGTTCGAGCCTACC
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ACCATCCAATGGAGCAAGCTGGTGGGGTAA

SEQ ID NO: 18_SGK_H
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GGTGGAGAGTTGTTCTACCATCTCCAGAGGGAACGCTGCTTCCTGGAACCACGGGCTCGT
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AGAGACTTAAAACCAGAGAATATTTTGCTAGATTCACAGGGACACATTGTCCTTACTGAT
TTCGGACTCTGCAAGGAGAACATTGAACACAACAGCACAACATCCACCTTCTGTGGCACG
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TGGTGCCTGGGAGCTGTCTTGTATGAGATGCTGTATGGCCTGCCGCCTTTTTATAGCCGA
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ACAAATTCCGCAAGACACCTCCTGGAGGGCCTCCTGCAGAAGGACAGGACAAAGCGGCTC
GGGGCCAAGGATGACTTCATGGAGATTAAGAGTCATGTCTTCTTCTCCTTAATTAACTGG
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GAGCTACGGCACTTTGACCCCGAGTTTACCGAAGAGCCTGTCCCCAACTCCATTGGCAAG
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TTTTCCTATGCGCCTCCCACGGACTCTTTCCTCTGA

SEQ ID NO: 19_AA107515_M
CGGGTCGACCCACGCGTCCGCCGGTTTCACTGCTCCCCTCAGTCTCTTTTGGGCTCTTTC
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FIGURE 2N

GAATGAGGGGAATGGTAGCGATTCTCATCGCTTTTATGAAACAGAGAAGGATGGGCCTGA
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ATGCAGGTCTAAGAGGAATCCCCGCAGGTCTGTCTGAGCTGTGATCAAGAATATTCTGCA
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TGAGAACATTCTGCACCAGCCGCTACAGATCCCCGGAGGCCGGACAGTGGCCGCCTGTGA
CCTCCTGCAAAGCCTTCTCCACAAGGACCAGAGGCAGCGGCTGGGCTCCAAAGCAGACTT
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FIGURE 2O

GAGGCTAACTCCACCCTTCAACCCAAATGTGACAGGACCTGCTGACTTGAAGCATTTTGA
CCCAGAGTTCACCCAGGAAGCTGTGTCCAAGTCCATTGGCTGTACCCCTGACACTGTGGC
CAGCAGCTCTGGGGCCTCAAGTGCATTCCTGGGATTTTCTTATGCGCCAGAGGATGATGA
CATCTTGGATTGCTAGAAGAGAAGGACCTGTGAAACTACTGAGGCCAGCTGGTATTAGTA
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SEQ ID NO: 21_AA887783_H
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CCCTGAAGATTCCTGCCAAGAGAATATTTGGTGATAATTTTGATCCAGATTTTATTAAAC
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FIGURE 2P

GGAGTTGGAGACCAGCCTGACCAACATGGACAAACCCCGTCTCTACTAAAAATACAAAAT
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CCTGGGCAACAAGAGTGAAACTCCATCTCC

SEQ ID NO: 22_R47805_H
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SEQ ID NO: 23_H60215_H
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ACAGCATCCCGCAGGAGCTCTTCCGCAAGATCAAGGCTGCCGAGTATACCATTCCTGAGG
ATGGACGGGTTTCTGAGAACACCGTGTGTCTCATCCGGAAGCTGCTGGTCCTTGACCCCC
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FIGURE 2Q

AGTCCCTGTCATCTCTGAGTGGGCCTTTGCAAGTGGTTCCTGACATTGATGACCAAATGA
GCAATGCGGATAGCTCCCAGGAGGCGAAGGTGACGGAGGAGTGCTCCCAGTACGAGTTTG
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FIGURE 2R

GTGAGTGGAAGGCGGCAGGTCTGGCCTGACTGCGGAGCCGGCCTTGAAGTTTTTGAATTA
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CTGGCTGGGCCCTCTGGGCAGCTGCTTCCACTCTTGTCTCTGCCTTCTCATCTAGAGAGA
CTCCCAAGCCCTGGAGGGGTGTGTTGTGTTAGGAATTAACTCCCTGCCTACCCCAAGGCC
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TAAAGGTACATAATCAAGGAAAAAAATATATATTCATTTTTCAGGGTTGGTAACATTTTA
TGAGATGTCAGTGACAACGATGGCCTTATTTTTTTCAGCCTTTTCTTCTTCCAAAATGTT
TCTTAAGGCAACTCTCCTAAATACATAAACACAACAAATTAAAATGAAAAGTGACATGAG
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ACCAACCTGGCAGACTTGAAGAACAGAGGGCAGTATGTGGCCGCTGGATTTGAACGATTC

FIGURE 2S

CACAAGCTCCCCCCTTACCAGGCTTTTTGTCTCAGTGTGTTCAGGAATGGGGACCTGGTA
AGTCCCCCATTTAGTCTGAAGCTGTCCCAGGCTGCCAGCCAGGACTGGGAAACTGTGTTG
AAGCTCCTGACTGAGAAGGTCAAGTTGCAGAGTGGGGCTGTGAGACTCTGCACCCTAGAG
GGGCTCCCACTGTCAGCAGGGAAGGAGCTGGTAACTGGCCATTACTATGTGGCTGTCGGA
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SEQ ID NO: 28_AA197883_M
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GGACCTCTGGAGAAGCCAGTTCTGGGGCCACGTGGTGCCGTCATGCCGCTGTTCAGCCCT
CAGAGCAGCCTCCACTCAGTCCGCGCAGAGCACAGCCCACTGAAGCCCAGGGTGGTGACG
GTGGTGAAGCTGGGTGGGCAGCCCCTCCGTAAGGCCACCCTGCTCCTCAACCGGCGCTCA
GTGCAGACCTTTGAGCAGCTCCTATCAGACATCTCCGAAGCCTTGGGCTTCCCACGCTGG
AAGAACGACCGTGTGCGGAAGCTGTTCACCCTCAAGGGCAGGGAGGTGAAGAGTGTGTCT
GACTTCTTCCGGGAGGGTGATGCTTTCATAGCTATGGGCAAAGAGCCGCTGACATTGAAG
AGTATCCAGTTGGCCATGGAGGAGCTGTATCCTAAGAACCGGGCTCTTGCCCTGGCCCCT
CACAGTAGAGTCCCCTCCCCAAGGCTGAGAAGCAGACTTCCCAGCAAGCTTCTGAAAGGA

FIGURE 2T

AGTCACCGCTGTGGGGAGGCAGGAAGCTATAGCGCGGAAATGGAGAGTAAGGCAGTCTCT
AGGCATCAGGGCAAGACTTCCACAGTGCTGGCCCCAGAAGACAAGGCGAGGGCCCAGAAG
TGGGTAAGAGGGAAACAGGAGTCAGAACCTGGTGGCCCGCCTTCACCCGGGGCAGCCACT
CAGGAGGAGACTCATGCAAGTGGAGAGAAACATCTGGGGGTGGAGATCGAAAAGACCTCC
GGGGAGATTGTCAGATGTGAGAAGTGTAAGAGAGAAAGAGAGCTGCAGTTGGGCCTGCAG
AGGGAGCCGTGCCCGCTGGAACCAGTGAGCTGGACCTGGGGAGAGCTCAGAAGAGGGAT
TCCGAGAAGTTGGTGAGGACCAAGAGCTGCAGGAGGCCTTCTAAGGCAAAATTTACAGAT
GGAGAGGAAGGGTGGAAGGGTGACAGCCATCGGGGCAGTCCCAGGGACCCCCCTCAGGAA
ATGAGGAGGCCCAACAGCAACTCAGACAAGAAAGAGATCAGAGGCTCAGAAAGTCAGGAC
AGTTATCCTCAGGGGGCACCCAAGGCCCAGAAGGACTTCGTGGAAGGGCCACCAGCTGTA
GAGGAGGGGCCGATAG[illegible]CATGAGGAGAGAGGACCGGCACACATGCAGGAGCAACC[illegible]TGCC
GC[illegible]GGTCCGGAGAGAGCAGCAGGCCGAACCCC[illegible]ACAGCTC[illegible]CCCAGAA[illegible]
GAGAAGCAAGCAGAGCACGAGAAGAAGCCAGGCGGCTTAGGAGAGAGGAGGGCGCCAGAG
AAGGAGTCTAAGAGGAAGCTAGAAGAGAAGAGGCCAGAACGACCCAGTGGCCGGAAGCCG
AGGCCCAAGGGCATCATCTCAGCGGATGTGGAGAAGCACTATGACATAGGTGGGGTCATT
GGGGATGGCAACTTTGCCACCGTGAAGGAATGCAGGCACCGAGAGACCAAGCAGGCTTAC
GCCATGAAGATGATTGACAAGTCCCAGCTGAAGGGTAAGGAGGACATTGTCGACAGTGAG
ATTTTAATCATCCAGAGTCTCTCTCATCCCAACATTGTGAAACTGCATGAGGTCTACGAA
ACGGAGGCGGAGATCTACCTGATCATGGAGTATGTGCAGGGAGGGGACCTTTTTGATGCC
ATCGTTGAAAATGTGAAGTTTCCAGAGCCCGAGGCTGCAGTTATGATCACAGACTTGTGT
AAGGCCTTCGTCCACATGCACGACAAGAATATCGTCCACCGGGACGTGAAACCAGAAAAC
CTCCTGGTTCAGCGAAATGAAGACAAGTCTATCACCTTGAAGCTGGCTGATTTTGGCTTG
GCCAAATATGTGGTGAGGCCTATATTTACTGTGTGTGGGACGCCAACATATGTAGCTCCT
GAAATTCTTTCTGAGAAAGGTTACGGCCTGGAGGTGGACATGTGGGCGGCAGGTGTGATC
CTATACATCCTCTTGTGTGGCTTCCCCCCTTTCCGAAGTCCTGAGAGGGACCAAGACGAG
CTCTTCAACATCATCCAAGTGGGCCAGTTTGAGTTCCTCTCTCCTTACTGGGACAACATT
TCTGATGCTGCCAAAGATCTGGTGAGAAATTTGCTGGAGGTGGACCCTAAGAAGCGGTAC
ACGG[illegible]CGAACAGGTC[illegible]GAGA[illegible]GG[illegible]GGGCATACC[illegible]GGG
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GTTGCAGAGCAGATGCCATAA

SEQ ID NO: 29_DRAK2_H
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TCTGGAAAAGTAAAAGTGGATCCTGCCACGTTCGGAGCTCCCTGGCGCCTCGCCCGGCTG
GAGCTAGAGAACTCGTCCTGTGGCGGCCCCCGGCGTGGGCGGGACAGCGGCCCCCTGGA
GGGGGCAGTCCCGGGAGAACCTGCGGCGGCCGGAGCGGTAAAAATAAGTGACTAAAGAAG
CAGACCTGGGAATCACCTAACATGTCGAGGAGGAGATTTGATTGCCGAAGTATTTCAGGC
CTACTAACTACAACTCCTCAAATTCCAATAAAAATGGAAAACTTTAATAATTTCTATATA
CTTACATCTAAAGAGCTAGGGAGAGGAAAATTTGCTGTGGTTAGACAATGTATATCAAAA
TCTACTGGCCAAGAATATGCTGCAAAATTTCTAAAAAAGAGAAGAAGAGGACAGGATTGT
CGGGCAGAAATTTTACACGAGATTGCTGTGCTTGAATTGGCAAAGTCTTGTCCCCGTGTT
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GCAGGTGGAGAAATTTTCAGCCTGTGTTTACCTGAGTTGGCTGAAATGGTTTCTGAAAAT
GATGTTATCAGACTCATTAAACAAATACTTGAAGGAGTTTATTATCTACATCAGAATAAC
ATTGTACACCTTGATTTAAAGCCACAGAATATATTACTGAGCAGCATATACCCTCTCGGG
GACATTAAAATAGTAGATTTTGGAATGTCTCGAAAAATAGGGCATGCGTGTGAACTTCGG
GAAATCATGGGAACACCAGAATATTTAGCTCCAGAAATCCTGAACTATGATCCCATTACC
ACAGCAACAGATATGTGGAATATTGGTATAATAGCATATATGTTGTTAACTCACACATCA
CCATTTGTGGGAGAAGATAATCAAGAAACATACCTCAATATTTCTCAAGTTAATGTAGAT
TATTCGGAAGAAACTTTTTCATCAGTTTCACAGCTGGCCACAGACTTTATTCAGAGCCTT

FIGURE 2U

TTAGTAAAAAATCCAGAGAAAAGACCAACAGCAGAGATATGCCTTTCTCATTCTTGGCTA
CAGCAGTGGGACTTTGAAAACTTGTTTCACCCTGAAGAAACTTCCAGTTCCTCTCAAACT
CAGGATCATTCTGTAAGGTCCTCTGAAGACAAGACTTCTAAATCCTCCTGTAATGGAACC
TGTGGTGATAGAGAAGACAAAGAGAATATCCCAGAGGATAGCAGCATGGTTTCCAAAAGA
TTTCGTTTCGATGACTCATTACCCAATCCCCATGAACTTGTTTCAGATTTGCTCTGTTAG
CACTTTTTTCTTTGACTCATTTGGACTGAATTTGAAATTTTATATCCACTCCAGTGAGAT
TATGATTTGTAGCTTCATATATGACATGTTTATATTGTAAATGCACTTTTCCATGGAATA
ATTTAGGGAAGTGTTTTAATGTTAAATTACTAGTTGCTAGCATGTTATGATTTCATATCC
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GTGAAAG

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GAGTGCGAGGTAAAAGTCTGCCTAGAGAAGCAGGTCTGGCAGTCATCAACATGTCTCGGA
GGAGATTCGATTGCCGAAGTGTCTCAGGCTTGCTAACTACAACCCCTCAAACGCCGATTA
AAACAGAGAATTTTAATAATTTCTATACTCTTACCCCAAAAGAACTTGGGAGAGGAAAAT
TTGCTGTGGTTAGACAATGTATATCAAAATCAACTGGACAAGAGTATGCTGCCAAATCCC
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TGGAGCTGGCCAGGTCTTGTCCCCACGTGATTAATCTGCATGAGGTCTACGAAAATGCAA
CGGAAATCATTTTGGTGTTAGAATATGCTGCGGGTGGAGAAATTTTCAACCTGTGTTTAC
CTGAGTTAGCCGAAATGGTATCTGAAAATGATGTTATCAGACTCATTAAACAAATCCTTG
AAGGAGTTCATTATCTACATCAGAATAACATTGTTCACCTTGATTTAAAGCCACAGAATA
TACTTTTGAGCAGTATATACCCACTCGGGGACATAAAAATTGTAGATTTTGGAATGTCTC
GAAAAATTGGGAATGCAAGTGAGCTTCGGGAAATCATGGGAACACCTGAATACTTAGCTC
CAGAAATCCTCAACTATGATCCCATTACCACAGCAACAGATATGTGGAATATTGGCATAA
TAGCGTATATGTTGTTAACTCATACATCACCATTTGTAGGAGAAGATAATCAAGAAACAT
[illegible]ATATTTCTCAAGTGAATGTAGATTATTCAGA[illegible]
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CAGAATCCTGCCTATCCCACTCATGGCTGCAGCAGTGGGACTTTGGAAGCTTGTTTCATC
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AGACCTCCAAGTCCTCCTGTAATGGAGCTGTGGAGCCCGGGAGGACAAGGAGAACATCC
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ATGAACTTGTTCCAGATTTGTTCTGTTAGCATTTTTCTCTGTGACTCATCTGGACTGACT
CGGAAATTTGAAATCTCTGGTGTGAGATTGTGTTTGTAGCTTCATATATTATGTTTATAT
TATAAATGCACTTCTGCTTAGAAGAACTTAAGGAACAGTTTAAATGCTAGGCTTCTGTTG
GCTAGCATATCATTTCTTGTCCTGAAATTGTTTTGCAGAGGAAAATATTTAAGTATATGA
CAAAAAATGTAAATTGTGTTTAAGAGAACACATGCAACTGAAAGAACTCAAGTTCAGTCA
GACTTATAAAATGGGTTATATTATGGTTAGTAAAAGTTGAAAAAAAAATGAAAACAGGAAT
TTAGTAGGTTCTAAGGTAAGCCCTATACCATAACTCTATTACAGAGAATCTGTTTGGGGA
AATGCTGTCAAGGGTAAACCACAACATATACTGCTTTATAAATACTCCAGAGAGAGTTTA
TAGTTGAAAGTATTTCCCAGTTACCAATAATAGCTTGAAACTGTAAGATTTTCTTTGTGT
GCCATGTGCTCGGTGAGAGGACACAGTCAACCAGAGCAGGGTTGATCCAGGCTGTTTCTC
TGCAAACCGAGTCAAAACTCGACATCATTTCCAGCTCATGTATTTTGTACGTGCATCATA
TATCAGATCTAATAAGATCTGGAAGATGGATATGCAAATAAGAGGCCTTTGTCTTCTAGA
ATGATTAGAGTAGAGGAGAATTGGATAGTACAGAATATGCTCTAGTTTCAGTCAGACATA
TTCATAAAGGGAAATGTTAAGTTCTGGCAGCTGACTTAGTGTTGGATGTCTCCTAAGTCT
CAGGATAGAAGCCCATCATTAGAGCATAGGCACTTCAGGAATTCTTGTGTGAAATTCTAG
TGAGTGAGGAGGTGTGACATGCAGCTATCTTTGGGCTCCTTTTGTGTGTGTTCTGCTGGA
CACAACACATGGGAGTGTTCAGTGTTGTCCGTGGTCAATATCTATGTTCAGTCCTGATGG

FIGURE 2V

GAGGGGCCTAGGGACTGCTTTGGAGATTTCCCACTGGTGTCCATTTTAAGGTCTGTAATA
ATGTCATGTTAAGATAACAGATCTCATAAATATGCTACTCTATCAGACTCCGTTGCCAAA
ACAAATTAAAAGCCTGTGTATTGAAGTGGGTGTTAGTCTAACAACCTGTAAATTCTTGAA
ATTGTTACTAAAATTCCAAATTCTTTAGATAACTTTAAACTATTTAAATTGAGCATTGCT
GTCTTTGTTTGATTAAAGGTTGAGTTCCTTTATATCTGTTATTTTTAAAGGAAAAGTTGT
TTGCCTTTTGTATATGTGTGTGCATATGTGTATGTGTACAGGTATATGTATATATGTATT
GATAGATAAAATACAGCCTTTAAACAACTTC

SEQ ID NO: 31_H01248_H, DRAK1_H
ATGATCCCTTTGGAGAAGCCAGGCAGCGGCGGCTCCTCCCCAGGCGCCACCTCAGGCTCG
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GGGCTGCTGACAGAGATAC[illegible]CACCGAGCCCTTCCAGGACGGCTA[illegible]C
CTGTGCCCGGGCCGGGAGCTGGGCAGGGGGAAATTTGCAGTGGTGAGAAAATGTATAAAG
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TGTCGGATGGAAATAATTCATGAGATTGCTGTACTTGAACTAGCACAAGACAATCCTTGG
GTCATTAATTTACATGAAGTTTATGAGACTGCATCAGAAATGATCTTAGTTCTGGAATAT
GCTGCTGGGGGTGAAATCTTTGACCAGTGTGTTGCAGACAGAGAAGAAGCCTTTAAAGAA
AAAGATGTTCAAAGACTTATGCGACAGATTTTAGAAGGTGTTCACTTTTTACACACTCGT
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GGTGACATTAAGATTGTTGATTTTGGCCTTTCAAGAATATTGAAGAACAGTGAAGAGCTC
CGAGAAATTATGGGTACCCCTGAATATGTGGCTCCTGAAATTCTTAGTTATGATCCTATA
AGCATGGCAACAGATATGTGGAGCATTGGAGTGTTAACATATGTCATGCTTACAGGAATA
TCACCTTTCTTAGGCAATGATAAACAAGAAACATTCTTAAACATCTCACAGATGAATTTA
AGTTATTCTGAGGAAGAATTTGATGTTTTGTCTGAGTCGGCTGTTGATTTCATCAGGACA
CTTTTAGTTAAGAAACCTGAAGATCGAGCCACTGCTGAAGAATGTCTAAAGCACCCCTGG
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[illegible]CATTGTAACCGAAGAGTTAAT[illegible]A
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SEQ ID NO: 32_AA021445_H
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CCCAGCCCCGGCCTCCCGCGGACCCATGCCCGCCCGTATCGGCTACTACGAGATCGACCG
CACCATCGGCAAGGGCAACTTCGCGGTGGTCAAGCGGGCCACGCACCTCGTCACCAAGGC
CAAGGTTGCTATCAAGATCATAGATAAGACCCAGCTGGATGAAGAAAACTTGAAGAAGAT
TTTCCGGGAAGTTCAAATTATGAAGATGCTTTGCCACCCCCATATCATCAGGCTCTACCA
GGTTATGGAGACAGAACGGATGATTTATCTGGTGACAGAATATGCTAGTGGAGGGGAAAT
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ACAGATCGTCACAGCTGTCTATTTTTGTCACTGTCGGAACATTGTTCATCGTGATTTAAA
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GATCTGCAAGCACAAGTGGATGAAGCTAGGGGACGCCGATCCCAACTTTGACAGGTTAAT
AGCTGAATGCCAACAACTAAAGGAAGAAAGACAGGTGGACCCCCTGAATGAGGATGTCCT
CTTGGCCATGGAGGACATGGGACTGGACAAAGAACAGACACTGCAGTCATTAAGATCAGA

FIGURE 2W

TGCCTATGATCACTATAGTGCAATCTACAGCCTGCTGTGTGATCGACATAAGAGACATAA
AACCCTGCGTCTCGGAGCACTTCCTAGCATGCCCCGAGCCCTGGCCTTTCAAGCACCAGT
CAATATCCAGGCGGAGCAGGCAGGTACTGCTATGAACATCAGCGTTCCCCAGGTGCAGCT
GATCAACCCAGAGAACCAAATTGTGGAGCCGGATGGGACACTGAATTTGGACAGTGATGA
GGGTGAAGAGCCTTCCCCTGAAGCATTGGTGCGCTATTTGTCAATGAGGAGGCACACAGT
GGGTGTGGCTGACCCACGCACGGAAGTTATGGAAGATCTGCAGAAGCTCCTACCTGGCTT
TCCTGGAGTCAACCCCCAGGCTCCATTCCTGCAGGTGGCCCCTAATGTGAACTTCATGCA
CAACCTGTTGCCTATGCAAAACTTGCAACCAACCGGGCAACTTGAGTACAAGGAGCAGTC
TCTCCTACAGCCGCCCACGCTACAGCTGTTGAATGGAATGGGCCCCCTTGGCCGGAGGGC
ATCAGATGGAGGAGCCAACATCCAACTGCATGCCCAGCAGCTGCTGAAGCGCCCACGGGG
ACCCTCTCCGCTTGTCACCATGACACCAGCAGTGCCAGCAGTTACCCCTGTGGACGAGGA
GAGCTCAGACGGTGAGCCAGACCAGGA[illegible]TGT[illegible]GG[illegible]TAGGTCCA[illegible]
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GCTAGGACAGCAGCCTTTCCGTTCCCGGGTCTGGCCTCCTCACCTGGTACCTGATCAGCA
TCGCTCTACCTACAAGGACTCCAACACTCTGCACCTCCCTACGGAGCGTTTCTCCCCTGT
GCGCCGGTTCTCAGATGGGGCTGCGAGCATCCAGGCCTTCAAAGCTCACCTGGAAAAAAT
GGGCAACAACAGCAGCATCAAACAGCTGCAGCAGGAGTGTGAGCAGCTGCAGAAGATGTA
CGGGGGGCAGATTGATGAAAGAACCCTGGAGAAGACCCAGCAGCAGCATATGTTATACCA
GCAGGAGCAGCACCATCAAATTCTCCAGCAACAAATTCAAGACTCTATCTGTCCTCCTCA
GCCATCTCCACCTCTTCAGGCTGCATGTGAAAATCAGCCAGCCCTCCTTACCCATCAGCT
CCAGAGGTTAAGGATTCAGCCTTCAAGCCCACCCCCCAACCACCCCAACAACCATCTCTT
CAGGCAGCCCAGTAATAGTCCTCCCCCCATGAGCAGTGCCATGATCCAGCCTCACGGGGC
TGCATCTTCTTCCCAGTTTCAAGGCTTACCTTCCCGCAGTGCAATCTTTCAGCAGCAACC
TGAGAACTGTTCCTCTCCTCCCAACGTGGCACTAACCTGCTTGGGTATGCAGCAGCCTGC
TCAGTCACAGCAGGTCACCATCCAAGTCCAAGAGCCTGTTGACATGCTCAGCAACATGCC
AGGCACAGCTGCAGGCTCCAGTGGGCGCGGCATCTCCATCAGCCCCAGTGCTGGTCAGAT
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[illegible]GTC[illegible]TGAC[illegible]GTGCAGAGGCTCACAGCTTG[illegible]
TGCTAACTACGACCAGGCGCATTTACACCCCCATCTGTTTTCGGA[illegible]CAGTCCCGGC[illegible]
CCCCAGCAGCTACAGCCCTTCAACAGGAGTGGGGTTCTCTCCAACCCAAGCCCTGAAAGT
CCCTCCACTTGACCAATTCCCCACCTTCCCTCCCAGTGCACATCAGCAGCCGCCACACTA
TACCACGTCGGCACTACAGCAGGCCCTGCTGTCTCCCACGCCGCCAGACTATACAAGACA
CCAGCAGGTACCCCACATCCTTCAAGGACTGCTTTCTCCCCGGCATTCGCTCACCGGCCA
CTCGGACATCCGGCTGCCCCCAACAGAGTTTGCACAGCTCATTAAAAGGCAGCAGCAACA
ACGGCAGCAGCAGCAGCAACAGCAGCAACAGCAAGAATACCAGGAACTGTTCAGGCACAT
GAACCAAGGGGATGCGGGGAGTCTGGCTCCCAGCCTTGGGGGACAGAGCATGACAGAGCG
CCAGGCTTTATCTTATCAAAATGCTGACTCTTATCACCATCACACCAGCCCCCAGCATCT
GCTACAAATCAGGGCACAAGAATGTGTCTCACAGGCTTCCTCACCCACCCCGCCCCACGG
GTATGCTCACCAGCCGGCACTGATGCATTCAGAGAGCATGGAGGAGGACTGCTCGTGTGA
GGGGGCCAAGGATGGCTTCCAAGACAGTAAGAGTTCAAGTACATTGACCAAAGGTTGCCA
TGACAGCCCTCTGCTCTTGAGTACCGGTGGACCTGGGGACCCTGAATCTTTGCTAGGAAC
TGTGAGTCATGCCCAAGAATTGGGGATACATCCCTATGGTCATCAGCCAACTGCTGCATT
CAGTAAAAATAAGGTGCCCAGCAGAGAGCCTGTCATAGGGAACTGCATGGATAGAAGTTC
TCCAGGACAAGCAGTGGAGCTGCCGGATCACAATGGGCTCGGGTACCCAGCACGCCCCTC
CGTCCATGAGCACCACAGGCCCCGGGCCCTCCAGAGACACCACACGATCCAGAACAGCGA
CGATGCTTATGTACAGCTGGATAACTTGCCAGGAATGAGTCTCGTGGCTGGGAAAGCACT
TAGCTCTGCCCGGATGTCGGATGCAGTTCTCAGTCAGTCTTCGCTCATGGGCAGCCAGCA
GTTTCAGGATGGGGAAAATGAGGAATGTGGGGCAAGCCTGGGAGGTCATGAGCACCCAGA
CCTGAGTGATGGCAGCCAGCATTTAAACTCCTCTTGCTATCCATCTACGTGTATTACAGA
CATTCTGCTCAGCTACAAGCACCCCGAAGTCTCCTTCAGCATGGAGCAGGCAGGCGTGTA

FIGURE 2X

ACAAGAAACAGAGAGTTTTGTGTACAGCTTGGGAATGAAAAGGTTGATTGTAAACCCACA
GTATCTAGCAGCGTTGTGCCAAATTGCCCTTGTGTTTCTCTCCACCCAAAATATCACAGC
TGCTTTCCTCACATTTGGTTCATCCGTGTGCTGTTCTTTTGGGTTCTGAGAGGGTTTTGC
CATGTTTGCTTGTATGACCAAGTCACCAAGGAAATAAACAGGAAGGAAATCCATGTTCTC
C

SEQ ID NO: 33_2R22-5-11_H
CTGGGCCGCTGCCGGTCAGGTCGGCCGCCCCTGACAGCTCCGGGAGCCTCAAGCGCGACA
GGGCGCCCTCACCTCGGGACATCCACACACCGACCGCTCCTGCTCCAGAGGCAACAACCC
AGCGCGCCTAGCCTGGCGCCGTGCAGCGAAGCCCAAGAGCTGGCCTCGCCACGAAGGTTG
[illegible]GCC[illegible]ATTTTCGAGACAGCTCACGGCTTAGAGGAAGG[illegible]
GGCTAAAGTGACATTGCAGGGATTAAATCCTTCTTTGGCTGCCTGTGTGACCAGAAGGCT
TATTTGCAAGTTTCTTCTTTCCTGGGGTCCAGATTATTAGGTCTCCAGCGCCCTGCAGCT
TGACAGAAAGAGAAGCATGAAATGAAGGTCAGAGATGAGATCCCGCAGCAGGGACGTGGG
GGCCTCCCAGGGGCATTTACGCACCAGAGTGCAAGATTCTCTGGCCATCAAGGGAAATAG
CAAACAGAAGCCTTTGTCCTGGGGCACAGCCACCTACCACAAAGCATCAGACTCCACGTC
TGGCCAGAAAGTTCCTGGAGTCCCATCAGGCCAGTGGGTATGTAACATGTGCCTAATTGT
ACAGCTAGAGCCTGCAAGTTCAACGTGAGGGAAGGTGGGAAATGTCTTGAGTGAGGCGAG
CAGCTCCTGGCTGGGCTGGGCAGACTCAGCTACCACGTTCACTGCCTTCCTCTCACTAAA
GCCGAGAGGGAGGCTGCTCAGCTCTCAGGAAAACTCTTTTGAACCCTGGGCACCTGCTGT
CCTCAGTTGGCATCTCCCACCCTCTGAGCCTCTTCTGCTCCTGCACAACCTGCCTCTTCG
CTGAGATGGAGACGTGAGCCCCCGTGGACGATGACTGCAGTGTATATGAATGGAGGTGGC
CTGGTGAACCCCCACTATGCCCGGTGGGATCGGCGCGACAGTGTAGAAAGTGGCTGTCAG
ACCGAGAGTAGCAAGGAGGGTGAGGAGGGACAGCCCCGCCAGCTGACGCCCTTCGAGAAA
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GAC[illegible]ACCCAGAGGC[illegible]TATCCCG[illegible]GAAATCTCCAGCATGGAAA[illegible]
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CAAATTATTCATAGAGATCTGAAAGCAGAAAATGTATTCTATACCAGTAATACTTGTGTG
AAGGTGGGCGATTTTGGATTCAGCACAGTAAGCAAAAAAGGTGAAATGCTGAACACTTTC
TGTGGGTCTCCTCCCTACGCTGCGCCTGAACTCTTCCGGGACGAGCACTACATCGGCATT
TACGTGGATATCTGGGCCTTGGGGGTGCTTTTGTACTTCATGGTGACTGGCACCATGCCA
TTTCGGGCAGAAACCGTGGCCAAACTAAAAAAGAGCATCCTCGAGGGCACATACAGTGTA
CCGCCGCACGTGTCAGAGCCCTGCCACCGACTCATCCGAGGAGTCCTTCAGCAGATCCCC
ACGGAGAGGTACGGAATCGACTGCATCATGAATGATGAATGGATGCAAGGGGTGCCATAC
CCTACACCTTTGGAACCTTTCCAACTGGATCCCAAACATTTGTCGGAAACCAGCACTCTC
AAGGAAGAAGAAAATGAGGTCAAAAGCACTTTAGAACATTTGGGCATTACAGAAGAGCAT
ATTCGAAATAACCAAGGGAGAGATGCTCGCAGCTCAATCACAGGGGTCTATAGAATTATT
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CCTAAAGAAAGAGACCTCAAAAAAGGGTCCCGTGTCTACAGAGGGATAAGACACACATCC
AAATTTTGCTCGATTTTATAAATTGCACTAGACTGCTTGTAACTAACCAAGATGATTGTT
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SEQ ID NO: 34_R31237_1_H, AAC33487
ATGTCCACTAGGACCCCATTGCCAACGGTGAATGAACGAGACACTGAAAACCACACGTCA
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FIGURE 2Y

AACTCTATAGCCTCCTGTGCAGATGAACAACCTCACATCGGAAACTACAGACTGTTGAAA
ACAATCGGCAAGGGGAATTTTGCAAAAGTAAAATTGGCAAGACATATCCTTACAGGCAGA
GAGGTTGCAATAAAAATAATTGACAAAACTCAGTTGAATCCAACAAGTCTACAAAAGCTC
TTCAGAGAAGTAAGAATAATGAAGATTTTAAATCATCCCAATATAGTGAAGTTATTCGAA
GTCATTGAAACTGAAAAAACACTCTACCTAATCATGGAATATGCAAGTGGAGGTGAAGTA
TTTGACTATTTGGTTGCACATGGCAGGATGAAGGAAAAAGAAGCAAGATCTAAATTTAGA
CAGATTGTGTCTGCAGTTCAATACTGCCATCAGAAACGGATCGTACATCGAGACCTCAAG
GCTGAAAATCTATTGTTAGATGCCGATATGAACATTAAAATAGCAGATTTCGGTTTTAGC
AATGAATTTACTGTTGGCGGTAAACTCGACACGTTTTGTGGCAGTCCTCCATACGCAGCA
CCTGAGCTCTTCCAGGGCAAGAAATATGACGGCCAGAAGTGGATGTGTGGAGTCTGGGG
GTCATTTTATACACACTAGTCAGTGGCTCACTTCCCTTTGATGGCAAAACCTAAACGAA
CTGAGAC[illegible]GAGAGTATTAAGAGGGAAATACAGAATT[illegible]CTGT
GAAAACCTTCTCAAACGTTTCCTGGTGCTAAATCCAATTAAACGCGGCACTCTAGAGCAA
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GAACCAGAGCTAGACATCTCAGACCAAAAAAGAATAGATATTATGGTGGGAATGGGATAT
TCACAAGAAGAAATTCAAGAATCTCTTAGTAAGATGAAATACGATGAAATCACAGCTACA
TATTTGTTATTGGGGAGAAAATCTTCAGAGCTGGATGCTAGTGATTCCAGTTCTAGCAGC
AATCTTTCACTTGCTAAGGTTAGGCCGAGCAGTGATCTCAACAACAGTACTGGCCAGTCT
CCTCACCACAAAGTGCAGAGAAGTGTTTCTTCAAGCCAAAAGCAAAGACGCTACAGTGAC
CATGCTGGACCAGCTATTCCTTCTGTTGTGGCGTATCCGAAAAGGAGTCAGACAAGCACT
GCAGATGGTGACCTCAAAGAAGATGGAATTTCCTCCCGGAAATCAAGTGGCAGTGCTGTT
GGAGGAAAGGGAATTGCTCCAGCCAGTCCCATGCTTGGGAATGCAAGTAATCCTAATAAG
GCGGATATTCCTGAACGCAAGAAAAGCTCCACTGTCCCTAGTAGTAACACAGCATCTGGT
GGAATGACACGACGAAATACTTATGTTTGCAGTGAGAGAACTACAGCTGATAGACACTCA
GTGATTCAGAATGGCAAAGAAAACAGCACTATTCCTGATCAGAGAACTCCAGTTGCTTCA
ACACACAGTATCAGTAGTGCAGCCACCCCAGATCGAATCCGCTTCCCAAGAGGCACTGCC
AGTCGTAGCACTTTCCACGGCCAGCCCCGGGAACGGCGAACCGCAACATATAATGGCCCT
CCTG[illegible]AGCCACACCATTG[illegible]CCAGA[illegible]
TCCACTAATCTCTTTACTATATTAACTTCAAAACTCACAAGGAGTCGCAA[illegible]TATCTGCT
GAGCAAAAAGATGAAAACAAAGAAGCAAAGCCTCGATCCCTACGCTTCACCTGGAGCATG
AAAACCACTAGTTCAATGGATCCCGGGGACATGATGCGGGAAATCCGCAAAGTGTTGGAC
GCCAATAACTGCGACTATGAGCAGAGGGAGCGCTTCTTGCTCTTCTGCGTCCACGGAGAT
GGGCACGCGGAGAACCTCGTGCAGTGGGAAATGGAAGTGTGCAAGCTGCCAAGACTGTCT
CTGAACGGGGTCCGGTTTAAGCGGATATCGGGGACATCCATAGCCTTCAAAAATATTGCT
TCCAAAATTGCCAATGAGCTAAAGCTGTAA

SEQ ID NO: 35_W90839_M
AAAGGGCCGTCCTGGTCCAGCCGTTCCCTGGGTGCCCGTTGCCGGAACTCTATCGCTTCC
TGCCCTGAGGAACAACCCCATGTGGGCAACTATAGGCTGCTAAGGACCATCGGGAAGGGC
AACTTCGCCAAAGTCAAGCTGGCTCGGCATATCCTCACGGGCCGGGAGGTCGCTATTAAG
ATCATTGATAAGACCCAGCTGAACCCCAGTAGCTTGCAGAAGCTGTTCAGAGAAGTCCGA
ATTATGAAGGGACTCAACCACCCCAACATCGTGAAGCTTTTTGAGGTGATAGAGACGGAG
AAGACGCTATACCTGGTGATGGAATACGCTAGCGCAGGAGAAGTGTTTGACTACCTCGTG
TCGCACGGCCGCATGAAGGAGAAGGAGGCTCGAGCCAAGTTCCGGCAGATCGTGTCAGCC
GTGCACTACTGTCATCAGAAGAACATTGTACACAGGGATCTAAAGGCTGAAAACCTGTTG
CTGGATGCCGAGGCCAACATCAAAATCGCCGACTTCGGCTTCAGCAATGAGTTCACGCTG
GGCTCCAAGCTGGACACCTTCTGTGGGAGCCCCCCATACGCCGCCCCAGAGCTGTTCCAG
GGCAAGAAGTATGATGGGCCAGAGGTGGACATCTGGAGCCTGGGTGTCATCCTGTACACG
CTGGTCAGCGGCTCCCTGCCCTTCGATGGGCACAACCTCAAGGAGCTGCGGGAGCGAGTC
CTCAGAGGAAAGTACCGGGTCCCCTTCTACATGTCTACAGACTGCGAGAGCATTCTGCGG

FIGURE 2Z

AGATTTCTGGTGCTGAACCCCGCAAAACGCTGTACTCTGGAGCAAATCATGAAAGACAAA
TGGATCAACATCGGCTATGAGGGTGAGGAGCTGAAGCCAGACACGGAGCTCAAAGAAGAG
CGGATGCCGGGTCGGAAAGCGAGCTGCAGTGCAGTGGGCAGTGGAAGTCGAGGCTTGCCC
CCCTCCAGCCCCATGGTCAGCAGTGCCCACAACCCCAATAAGGCAGAGATCCCTGAGCGG
CGGAAGGACAGCACTAGCACCCCTAACAACCTCCCCCCCAGCATGATGACCCGAAGAAAC
ACCTATGTGTGCACAGAGCGACCAGGATCTGAACGCCCGTCCTTGTTGCCAAATGGCAAA
GAAAATAGCTCCGGTACCTCGCGGGTGCCCCCTGCCTCGCCTTCCAGTCATAGCCTGGCT
CCCCCGTCAGGCGAGCGGAGCCGCCTGGCTCGGGGCTCCACCATCCGCAGCACCTTCCAT
GGGGGCCAGGTCCGAGACCGGCGGGCAGGGAGCGGGAGTGGCGGGGGTGTGCAGAATGGA
CCCCCAGCCTCACCCACGCTTGCCCACGAGGCCGCACCCCTGCCCTCCGGGCGGCCTCGC
CCCACCACCAACCTCTTCACCAAGCTGACCTCCAAACTGACCCGAAGCGTCACAGACG[illegible]
CCTGAGAGAATCGGGGACCTGAGGTCA[illegible]AAGTTGCCATCTACC[illegible]A
ACCGCCCCCAGGCTGCTCCGATTCCCCTGGAGTGTGAAGCTGACCAGCTCGCGACCTTCC
TGAGGCCCTGATGGCTGCCCTGCGACAGGCCACA

SEQ ID NO: 36_406786.5_H
GTAGCCGGCTTGGCGTGACCGTCGCCTGATCCAGTTGTTAGAGGTGGAAGCTTGGCAGTT
GGCCTCCCTTCTTCCCATGGAGGTCGGGGCTTAACAGTCTTTGAAGAGGACCAGAGATG
CCTTTCCCAGAGCCTCCCCTTGCCAGTGTCAGCAGAGGGCCCAGCTGCACAGACCACTGC
TGAGCCCAGCAGGTCGTTTTCCTCAGCCCACAGACACCTGAGCAGAAGGAATGGGCTTTC
CAGACTCTGCCAGAGCAGGACGGCGCTCTCTGAAGACAGATGGAGCTCCTATTGTCTATC
ATCACTGGCTGCCCAGAATATTTGTACAAGTAAACTGCACTGCCCTGCTGCCCCTGAGCA
CACGGACCCGTCCGAACCGCGGGGCAGTGTGTCCTGCTGCTCCCTGCTGCGGGGACTGTC
CTCAGGGTGGTCCTCACCTCTGCTTCCGGCCCCTGTGTGCAACCCTAACAAGGCCATCTT
CACGGTGGATGCCAAGACCACAGAGATCCTCGTTGCTAACGACAAAGCTTGCGGGCTCCT
GGGGTACAGCAGCCAGGACCTGATTGGCCAGAAGCTCACGCAGTTCTTTCTGAGGTCAGA
TTCTGATGTGGTGGAGGCCCTCAGCGAGGAGCACATGGAGGCCGACGGCCACGCTGCGGT
GGTGTTTGG[illegible]CGACATC[illegible]CAC[illegible]GTGGGAGAAG[illegible]AGTG[illegible]
GTGGATGAAGAGGATGCGGCAGGAGCGCCGCCTATGCTGCGTGGTGGTCCTGGAGCCCGT
GGAGAGGGTCTCGACCTGGGTCGCTTTCCAGAGCGATGGCACCATCACGTCATGTGACAG
TCTCTTTGCTCATCTTCACGGGTACGTGTCTGGGGAGGACGTGGCTGGGCAGCATATCAC
AGACCTGATCCCTTCTGTGCAGCTCCCTCCTTCTGGCCAGCACATCCCAAAGAATCTCAA
GATTCAGAGGTCTGTTGGAAGAGCCAGGGACGGTACCACCTTCCCTCTGAGCTTAAAGCT
GAAATCCCAACCCAGCAGCGAGGAGGCGACCACCGGTGAGGCGGCCCCTGTGAGCGGCTA
CCGGGCATCTGTCTGGGTGTTCTGCACCATCAGTGGCCTCATCACCCTCCTGCCGGATGG
GACCATCCACGGCATCAACCACAGCTTCGCGCTGACACTGTTTGGTTACGGAAAGACGGA
GCTCCTGGGCAAGAATATCACTTTCCTGATTCCTGGTTTCTACAGCTACATGGACCTTGC
GTACAACAGCTCATTACAGCTCCCAGACCTGGCCAGCTGCCTGGACGTCGGCAATGAGAG
TGGGTGTGGGGAGAGAACCTTGGACCCGTGGCAGGGCCAGGACCCAGCTGAGGGGGGCCA
GGATCCAAGGATTAATGTCGTGCTTGCTGGTGGCCACGTTGTGCCCCGAGATGAGATCCG
GAAGCTGATGGAAAGCCAAGACATCTTCACCGGGACTCAGACTGAGCTGATTGCTGGAGG
CCAGCTCCTTTCCTGCCTCTCACCTCAGCCTGCTCCAGGGGTGGACAATGTCCCAGAAGG
AAGCCTGCCAGTGCACGGTGAACAGGCGCTGCCCAAGGACCAGCAAATCACTGCCTTGGG
GAGAGAGGAACCTGTGGCAATAGAGAGCCCCGGACAGGATCTTCTGGAGAAAGCAGGTC
TGAACCAGTGGATGTGAAGCCATTTGCTTCCTGCGAAGATTCTGAAGCTCCAGTCCCAGC
TGAGGATGGGGGCAGTGATGCTGGCATGTGTGGCCTGTGTCAGAAGGCCCAGCTAGAGCG
GATGGGAGTCAGTGGTCCCAGCGGTTCAGACCTTTGGGCTGGGGCTGCCGTGGCCAAGCC
CCAGGCCAAGGGTCAGCTGGCGGGGGGCAGCCTCCTGATGCACTGCCCTTGCTATGGGAG
TGAATGGGGCTTGTGGTGGCGAAGCCAGGACTTGGCCCCCAGCCCCTCTGGGATGGCAGG
CCTCTCGTTTGGGACACCTACTCTAGATGAGCCGTGGCTGGGAGTGGAAAACGACCGAGA

FIGURE 2AA

AGAGCTGCAGACCTGCTTGATTAAGGAGCAGCTGTCCCAGTTGAGCCTTGCAGGAGCCCT
GGATGTCCCCCACGCCGAACTCGTTCCGACAGAGTGCCAGGCTGTCACCGCTCCTGTGTC
GTCCTGCGATCTGGGAGGCAGAGACCTGTGCGGTGGCTGCACGGGCAGCTCCTCAGCCTG
CTATGCCTTGGCCACGGACCTCCCTGGGGGCCTGGAAGCAGTGGAGGCCCAGGAGGTTGA
TGTGAATTCGTTTTCCTGGAACCTCAAGGAACTCTTTTTCAGTGACCAGACAGACCAAAC
GTCATCAAATTGTTCCTGTGCTACGTCTGAACTCAGAGAGACACCCTCTTCCTTGGCAGT
GGGCTCCGATCCAGATGTAGGCAGTCTCCAGGAACAGGGGTCGTGTGTCCTGGATGACAG
GGAGCTGTTACTACTGACCGGCACCTGTGTTGACCTTGGCCAAGGCCGACGGTTCCGGGA
GAGCTGTGTGGGACATGATCCAACAGAACCGCTTGAGGTTTGTTTGGTGTCCTCTGAGCA
TTATGCAGCAAGCGACAGAGAAAGCCCAGGACACGTTCCTTCCACGTTGGATGCTGGCCC
TGAGGACACGTGCCCATCAGCAGAGGAGCCAAGGCTGAACGTCCAGGTCACCTCCACGCC
[illegible]CGTGATGCGGGGGCTGCTGGCCTGCAGCGGGAGATCCAGGA[illegible]
CGGGAGCTGCTACCATCGAGATGGCTTACGGCTGAGTATACAGTTTGAGGTGAGGCGGGT
GGAGCTCCAGGGCCCCACACCTCTGTTCTGCTGCTGGCTGGTGAAAGACCTCCTCCACAG
CCAACGCGACTCAGCCGCCAGGACCCGCCTGTTCCTTGCCAGCCTGCCCGGCTCCACCCA
CTCTACCGCTGCTGAGCTCACCGGACCCAGCCTGGTGGAAGTGCTCAGAGCCAGACCCTG
GTTTGAGGAGCCCCCCAAGGCTGTGGAACTGGAGGGGTTGGCGGCCTGTGAGGGCGAGTA
CTCCCAAAAGTACAGTACCATGAGCCCGCTGGGCAGTGGGGCCTTCGGCTTCGTGTGGAC
TGCTGTGGACAAGGGAAAAAACAAGGAGGTGGTGGTGAAGTTTATTAAGAAGGAGAAGGT
CTTGGAGGATTGTTGGATTGAGGATCCCAAACTTGGGAAAGTTACTTTAGAGATCGCAAT
TCTATCCAGGGTGGAGCACGCCAATATCATCAAGGTATTGGATATATTTGAAAACCAAGG
GTTCTTCCAGCTTGTGATGGAGAAGCACGGCTCCGGCCTAGACCTCTTCGCTTTCATCGA
CCGCCACCCCAGGCTGGATGAGCCCCTGGCGAGCTACATCTTCCGACAAGTGAGAGCAGG
CCAGAGCCGTCTAGTGTCAGCAGTGGGATACCTGCGCTTGAAGGACATCATCCACCGTGA
CATCAAGGATGAGAACATCGTGATCGCTGAGGACTTCACAATCAAGCTGATAGACTTTGG
CTCGGCCGCCTACTTGGAAAGGGGAAAATTATTTTATACTTTTTGTGGGACCATCGAGTA
CTGTGCACCGGAAGTTCTCATGGGGAATCCCTACAGAGGGCCGGAGCTGGAGATGTGGTC
TCTGGGAGTCACTCTGT[illegible]TGAGG[illegible]CCCTTCTGTCAGCTGCAGGA
GACCGTGGAGGCTGCCATACACCCGCCATACCTGGTGTCCAAAGAACTCATGAGCCTTGT
GTCTGGGCTGCTGCAGCCAGTCCCTGAGAGACGCACCACCTTGGAGAAGCTGGTGACAGA
CCCGTGGGTAACACAGCCTGTGAATCTTGCTGACTATACATGGAAGAGGTGTTTCGAGT
AAACAAGCCAGAAAGTGGAGTTCTGTCCGCTGCGAGCCTGGAGATGGGGAACAGGAGCCT
GAGTGATGTGGCCCAGGCTCAGGAGCTTTGTGGGGGCCCCGTTCCAGGCGAGGCTCCTAA
TGGCCAAGGCTGTTTGCATCCCGGGGATCCCCGTCTGCTGACCAGCTAAACACCAATTTC
TTCCTGCTTTTCTCCACTTGGTTTGGAAAATCACACAGTTTTCAGGCTCCATCTGTTTG

SEQ ID NO: 37_AA544838_M 406786_M
CCACGCGTCCGCATCCCTGCTTGGATGAGCCCCTGGCGAGTTTCATCTTTCGACAACTAG
TGTCTGCTGTAGGATACCTGCACTCCCAAGGCATCATCCATAGAGACATCAAGGATGAGA
ACATTGTGATTGCTGAGGACTTCACAATTAAGCTGATAGATTTTGGCTCAGCTGCCTACT
TAGAGAGGGGCAAACTATTTTATACCTTTTGTGGAACAATCGAATACTGTGCACCTGAGG
TTCTCATTGGAAATCCCTACAGAGGGCCAGAGCTGGAGATGTGGTCTCTGGGGGTCACCC
TGTACACGCTCATCTTCGAGGAGAATCCCTTCTGTGAGGTGGAGGAGACCATGGAGGCAG
TTATTCATCCCCCATTCCTGGTTTCCCAAGAACTTATGAGTCTTCTGTCTGGACTGCTGC
AGCCTTGCCCTGAGCAGCGGACCACTTTGGAGAAGCTGATCAGGGACCCCTGGGTGACAC
AGCCTGTGAACCTTGCTAGCTATACTTGGGAAGAGGTGTGTAGGACCAACCAGCCAGAAA
GTGGCCTGCTGTCAGCTGCAAGTCTGGAGATTGGGAGTAGGAGTCCAAGTGAAATGGCTC
AGAGAGAGGGTCTCTGTGGGCCTCCTGCTCCCAGGGAGACTCGTGGTGACCAGCACTGCT
TGCATCTTAAGGACCCCTCTTTGCCAGTCAGCTGAGCAAGCTCTCCTGCTCTTTGGTTTG
GGCAGTTGTATGGATTTCAGGGCTTTCTACCTGGAGAAAGGAAGTTGTGAAGGATTGGGA

FIGURE 2BB

TGACTTCTGCTTCTAGATTCCTATGCAAATGCTACAAGAGCCTGCGATGCTAGTTTTCTT
AGGTTTATGATATAGACTTGTAATTCATGTTTTTTATAACCTTGAAAATCATTCTAATG
TTCAGTTATACTGTACTATTAAAGGGCTTTAAGTTGTAAGCCTCAGAAAGACACAAGGAG
TGTTTAAGTTCTCTATTTTTGTTGTTTGTTTTTGCTTGTAAGTTTTTGAGACAGGATCTC
ACCATGTAACTTTGGCTGGCCTGGAACTCAACTATGTAGACCAGGTAGACCTTAAACTGA
CAGATCTGCCTGCGCTTGCCTCCCAAGCATTAGGACTGATGGTGTGTGTCACCATGCCCA
GTTCTTCCTGGTTTTGTGTGTAGGTTTCTTTCCCACTGACTTGGTACATGTGACATGTGA
CAGATGTATGGAGTCTATAGAAGTGGCCAGACAAAAATGGCCAGAATATTTATTTATTTT
CTTAAAAATTTTCCAAATTAAAGCTACTTAGTTAACAGTTAAACTGGCCAGGACTATATG
AGATAAACTTGGTTTTCTATTTCTTTTTGT

SEQ ID NO: 38_AA785735_H
GGCACGAGGCGCGCCTGGCTGGGCCCTGCGGAGGANGGGAAGGAGCGAAGGAGCGAAGGA
GCAAGCGGAGCGCAGTTCGCCCAAGCCAAGCCGCGCTGCCAACCCTCCCGCCCGCCCGCG
CTCCTGTCCGCCGTGTCTAGCAGCGGGGCCCAGCATGGTCATGGCGGATGGCCCGAGGCA
CTTGCAGCGCGGGCCGGTCCGGGTGGGGTTCTACGACATCGAGGGCACGCTGGGCAAGGG
CAACTTCGCTGTGGTGAAGCTGGGGCGGCACCGGATCACCAAGACGGAGGTGGCAATAAA
AATAATCGATAAGTCTCAGCTGGATGCAGTGAACCTTGAGAAAATCTACCGAGAAGTACA
AATAATGAAAATGTTAGACCACCCTCACATAATCAAACTTTATCAGGTAATGGAGACCAA
AAGTATGTTGTACCTTGTGACAGAATATGCCAAAAATGGAGAAATTTTTGACTATCTTGC
TAATCATGGCCGGTTAAATGAGTCTGAAGCCAGGCGAAAATTCTGGCAAATCCTGTCTGC
TGTTGATTATTGTCATGGTCGGAAGATTGTGCACCGTGACCTCAAAGCTGAAAATCTCCT
GCTGGATAACAACATGAATATCAAAATAGCAGATTTCGGTTTTGGAAATTTCTTTAAAAG
TGGTGAACTGCTGGCAACATGGTGTGGCAGCCCCCCTTATGCAGCCCCAGAAGTCTTTGA
AGGGCAGCAGTATGAAGGACCACAGCTGGACATCTGGAGTATGGGAGTTGTTCTTTATGT
CCTTGTCTGTGGAGCTCTGCCCTTTGATGGACCGACTCTTCCAATTTTGAGGCAGAGGGT
TCTGGAAGGAAGATTCCGGATTCCGTATTTCATGTCAGAAGATTGCGAGCACCTTATCCG
AAGGATGTTGGTCCTAGACCCATCCAAACGGCTAACCATAGCCCAAATCAAGGAGCATAA
ATGGATGCTCATAGAAGTTCCTGTCCAGAGACCTGTTCTCTATCCACAAGAGCAAGAAAA
TGAGCCATCCATCGGGGAGTTTAATGAGCAGGTTCTGCGACTGATGCACAGCCTTGGAAT
AGATCAGCAGAAARCCATTGAGTCTTTGCAGAACAAGAGCTATAACCACTTTGCTGCCAT
TTATTTCTTGTTGGTGGAGCGCCTGAAATCACATCGGAGCAGTTTCCCAGTGGAGCAGAG
ACTTGATGGCCGCCAGCGTCGGCCTAGCACCATTGCTGAGCAAACAGTTGCCAAGGCACA
GACTGTGGGGCTCCCAGTGACCATGCATTCACCGAACATGAGGCTGCTGCGATCTGCCCT
CCTCCCCCAGGCATCCAACGTGGAGGCCTTTTCATTTCCAGCATCTGGCTGTCAGGCGGA
AGCTGCATTCATGGAAGAAGAGTGTGTGGACACTCCAAAGGTCAATGGCTGTCTGCTTGA
CCCTGTGCCTCCTGTCCTGGTGCGGAAGGGATGCCAGTCACTGCCCAGCAACATGATGGA
GACCTCCATTGACGAAGGGCTGGAGACAGAAGGAGAGGCCGAGGAAGACCCCGCTCATGC
CTTTGAGGCATTTCAGTCCACACGCAGCGGGCAGAGACGGCACACTCTGTCAGAAGTGAC
CAATCAACTGGTCGTGATGCCTGGGGCAGGGAAAATTTTCTCCATGAATGACAGCCCCTC
CCTTGACAGTGTGGACTCTGAGTATGATATGGGGTCTGTTCAGAGGGACCTGAACTTTCT
GGAAGACAACCCTTCCCTTAAGGACATCATGTTAGCCAATCAGCCTTCACCCCGCATGAC
ATCTCCCTTCATAAGCCTGAGACCTACCAACCCAGCCATGCAGGCTCTGAGCTCCCAGAA
ACGAGAGGTCCACAACAGGTCTCCAGTGAGCTTCAGAGAGGGCCGCAGAGCATCAGATAC
CTCCCTCACCCAGGGAATTGTAGCATTTAGACAACATCTTCAGAATCTGGCTAGAACCAA
AGGAATTCTAGAGTTGAACAAAGTGCAGTTGTTGTATGAACAAATAGGACCGGAGGCAGA
CCCTAACCTGGCGCCGGCGGCTCCTCAGCTCCAGGACCTTGCTAGCAGCTGCCCTCAGGA
AGAAGTTTCTCAGCAGCAGGAAAGCGTCTCCACTCTCCCTGCCAGCGTGCATCCCCAGCT
GTCCCCACGGCAGAGCCTGGAGACCCAGTACCTGCAGCACAGACTCCAGAAGCCCAGCCT
TCTGTCAAAGGCCCAGAACACCTGTCAGCTTTATTGCAAAGAACCACCGCGGAGCCTTGA

FIGURE 2CC

GCAGCAGCTGCAGGAACATAGGCTCCAGCAGAAGCGACTCTTTCTTCAGAAGCAGTCTCA
ACTGCAGGCCTATTTAATCAGATGCAGATAGCAGAGAGCTCCTACCCACAGCCAAGTCA
GCAGCTGCCCCTTCCCCGCCAGGAGACTCCACCGCCTTCTCAGCAGGCCCCACCGTTCAG
CCTGACCCAGCCCCTGAGCCCCGTCCTGGAGCCTTCCTCCGAGCAGATGCAATACAGCCC
TTTCCTCAGCCAGTACCAAGAGATGCAGCTTCAGCCCCTGCCCTCCACTTCCGGTCCCCG
GGCTGCTCCTCCTCTGCCCACGCAGCTACAGCAGCAGCAGCCGCCACCGCCACCACCCCC
TCCACCACCACGACAGCCAGGAGCTGCCCCAGCCCCCTTACAGTTCTCCTATCAGACTTG
TGAGCTGCCAAGCGCTGCTTCCCCTGCGCCAGACTATCCCACTCCCTGTCAGTATCCTGT
GGATGGAGCCCAGCAGAGCGACCTAACGGGGCCAGACTGTCCCAGAAGCCCAGGACTGCA
AGAGGCCCCCTCCAGCTACGACCCACTAGCCCTCTCTGAGCTACCTGGACTCTTTGATTG
TGAAATGCTAGACGCTGTGGATCCACAACACAACGGGTATGTCCTGGTGAATTAGTCTCA
GCACAGGAATTGAGGTGGGTCAGGTGAAGGAAGAGTGTATGTTCCTATTTTT[illegible]CCAGC
CTTTTAAATTTAAAGCTTATTTTCTTGCCCTCTCCCTAACGGGGAGAAATCGAGCCACCC
AACTGGAATCAGAGGGTCTGGCTGGGGTGGATGTTGCTTCCTCCTGGTTCTGCCCCACCA
CAAAGTTTTCTGTGGCAAGTGCTGGAACATAGTTGTAGGCTGAGGCAGGAGAATGGCGTG
AACCCGGGAGGCGGAGCTTGCAGTGAGCCAAGATCGTGCCACTGCACTCCAGCCTGGGCG
ACTGAGCAAGACTCCACCTCAAAAAAAAAAAAAAAAGGACAAGAGCAGTATCATCTGCCTC
TGTTTCTAAACTGGACAAAGAGATTTTCTTAAAGTTTCTATCATCTCCCTTCTGACAGGT
TCTACAGTGTGGTCTGAAGCACCTGTAATGTCAGAGCCCTTGTCTGGCCCTTGGTGGCAG
GTGAACGAAAGCAGTGGAGCCTCTCACCTTCCAGTAGCCTCTCACATTCTTATTTTACCA
TTTTTGTCCTAATTAAGGTAGCCTAGCTGATTCTAGAAGACAGCCATCCTACGTGCACCC
CCACCTTGTGTCCACATCTTCTCCAGGCAGGTTTCAACCTATCAGCAGACTCAGGCACAC
ACTGGGGCACAGATAGAGAACCAGGCGGCAGCAGTGCTCGCAGACCCACCCAGGGAGAGC
TGTGATGGGTTCTGCCCAGATACTCTGCTCGCCCACCCACAAGGGAGCAATAGCTTATAT
TTGTACATTAGTTTTACCAAGCACTTTCTCTTCTAACCCTCACAACAATTCTATGAAATT
AGCTGGGGAGATACTGTCCTTATTTTTCACAGCTGAAGAAACCAAAGCTTTGGGAAGTTT
GTGACTTCTCTGAGATCACAGCTGGTGATAGAAGGAGCTGGGACACGCGCTTGGGTTGAC
TGGCTTCTGGTTTTGGTTCTGTGGCTTCTAGTGCTGGAAGAAGCCCTCTCTTTCCCTTCT
CTTTCCTCAGTAGCATCTGACTCTTTTCATAAGCAAACAGCTGTATAAACAAAGCCCCCA
TTTTGGTCAAGCACAGGGTGAATGTGATATTGTTCCCACAACCTTATTCTCCACTCAACA
GCCGCCTGGCTTTGGGGAAGAGGCCGCCTTCAGGTGACAGTGCAGCTGTCCAGGTGGCCG
TGCACTGAACCAGGCTGAGGGAGACAAAAACCCCGCAGACCCGCCTGCCTTTCAGCGTCC
AGTTAACTGCAGAAGTTTAGGCTCACCTCAAAGATGTCTAGTTTTTCCAAGTTACAATAC
AGCAGTTTCCTACAGAACACCCCCTTCCTCAATTGCCAAGGGGCCGCATCGCACGGCATC
AGGCCACCACTGCAGGCCAGCAGATTCCACCCCAGGAACGGTCATGAACTCAGCCTTTGT
CTCAACGAGGGGCGTAACATTTCCTTACAGTCAAGCCCCATCAACTAGAAGTGCTTATTA
CTTTTAGGATTAAAAAAGTAATAACAGACTTTGACTTAATACTCTGTCTTTTCAGAGGCA
AAGTGGGTGGGTAGAGGGGAGCTTTAAAAATAGAAGTACAAAACAACATCCTGGAAACAT
ATGACCCCAGATGGAATAATGTCACATTCCCCAGTGCAGATAATGGGCTGCTGCTGGCTC
TGTGGTGTCTGTCTGCAGAAGATTTGCTCAGTCAAGGAAATTCAAGTGGTGAGACCTTTC
CACCATGGGTGGTAAGAGAAACCTGCCTTCACCAAAATCTCTGAAGGGGAAAGAAGTGGA
GAGAAAGGTTTGCTTCACTTCGGGGACTGCAGTTTGAGAAATAAAAGGGATACAGAGATA
TCTGCACTTTGTAGAAAGGGCAAGATTATTTGCTTATATCTGAAGGGAGGTGGGTGGTTT
TGCTGGATGTTTGGTCTGAAAGAGTTACTTTTGATAAAGTTAATCTAATTGTAGTTATAT
TTTCTGTGTGCTTTTTTTTAATTACTAAGAAAAAAATTGGTGAGTTCAGTAGCTTTGGTA
TTATGAGTGCAAATCATAATAGCTCCAATGTGAAAAAAAAAAATCAAAAGTATAACTTGTC
ACTTAATGTTAGAAAATTGCCTAAAATGCAGTGTAATAAATAATCTCTGTACCAAATAGT
AATTTAAATGGGGTAATTTTCTGCAAGGAAAATGTACTGTTTTTATGTTTCCAACCCTCT
TGA

FIGURE 2DD

SEQ ID NO: 39_AA207220_H
GCTGTGGCTCCCCGTCCTGGTGCGGACCTGTGCCCCGCGCTTCAGCCCTCCCCGCAAGC
CTATTGATTCCCCTGCCGCCCTTGCTCCACCTCCTGCTCGCCATGGAGTCGCTGGTTTTC
GCGCGGCGCTCCGGCCCCACTCCCTCGGCCGCAGAGCTAGCCCGGCCGCTGGCGGAAGGG
CTGATCAAGTCGCCCAAGCCCCTAATGAAGAAGCAGGCGGTGAAGCGGCACCACCACAAG
CACAACCTGCGGCACCGCTACGAGTTCCTGGAGACCCTGGGCAAAGGCACCTACGGGAAG
GTGAAGAAGGCGCGGGAGAGCTCGGGGCGCCTGGTGGCCATCAAGTCAATCCGGAAGGAC
AAAATCAAAGATGAGCAAGATCTGATGCACATACGGAGGGAGATTGAGATCATGTCATCA
CTCAACCACCCTCACATCATTGCCATCCATGAAGTGTTTGAGAACAGCAGCAAGATCGTG
ATCGTCATGGAGTATGCCAGCCGGGGCGACCTTTATGACTACATCAGCGAGCGGCAGCAG
CTCAGTGAGCGCGAAGCTAGGCATTTCTTCCGGCAGATCGTCTCTGCCGTGCACTATTGC
CATCAGAACAGAGTTGTCCACCGAGATCTCAAGCTGGAGAACATCCTCTTGGATGCCAAT
GGGAATATCAAGATTGCTGACTTCGGCCTCTCCAACCTCTACCATCAAGGCAAGTTCCTG
CAGACATTCTGTGGGAGCCCCCTCTATGCCTCGCCAGAGATTGTCAATGGGAAGCCCTAC
ACAGGCCCAGAGGTGGACAGCTGGTCCCTGGGTGTTCTCCTCTACATCCTGGTGCATGGC
ACCATGCCCTTTGATGGGCATGACCATAAGATCCTAGTGAAACAGATCAGCAACGGGGCC
TACCGGGAGCCACCTAAACCCTCTGATTGCCTGNNTGGCCTGATCCGGTGGCTGTTGATG
GTGAACCCCACCCGCCGGGCCACCCTGGAGGATGTGGCCAGTCACTGGTGGGTCAACTGG
GGCTACGCCACCCGAGTGGGAGAGCAGGAGGCTCCGCATGAGGGTGGGCACCCTGGCAGT
GACTCTGCCCGCGCCTCCATGGCTGACTGGCTCCGGCGTTCCTCCCGCCCCCTCCTGGAG
AATGGGGCCAAGGTGTGCAGCTTCTTCAAGCAGCATGCACCTGGTGGGGGAAGCACCACC
CCTGGCCTGGAGCGCCAGCATTCGCTCAAGAAGTCCCGCAAGGAGAATGACATGGCCCAG
TCTCTCCACAGTGACACGGCTGATGACACTGCCCATCGCCCTGGCAAGAGCAACCTCAAG
CTGCCAAAGGGCATTCTCAAGAAGAAGGTGTCAGCCTCTGCAGAAGGGGTACAGGAGGAC
CCTCCGGAGCTCAGCCCAATCCCTGCGAGCCCAGGGCAGGCTGCCCCCCTGCTCCCCAAG
AAGGGCATTCTCAAGAAGCCCCGACAGCGCGAGTCTGGCTACTACTCCTCTCCCGAGCCC
AGTGAATCTGGGGAGCTCTTGGACGCAGGCGACGTGTTTGTGAGTGGGATCCCAAGGAG
CAGAAGCCTCCGCAAGCTTCAGGCTGCTCCTCCATCGCAAAGCCATCCTCAAACTCAAT
GGCAAGTTCTCCCAGACAGCCTTGGAGCTCGCGGCCCCCACCACCTTCGGCTCCCTGGAT
GAACTCGCCCCACCTCGCCCCCTGGCCCGGGCCAGCCGACCCTCAGGGGCTGTGAGCGAG
GACAGCATCCTGTCCTCTGAGTCCTTTGACCAGCTGGACTTGCCTGAACGGCTCCCAGAG
CCCCCACTGCGGGGCTGTGTGTCTGTGGACAACCTCACGGGGCTTGAGGAGCCCCCCTCA
GAGGGCCCTGGAAGCTGCCTGAGGCGCTGGCGGCAGGATCCTTTGGGGGACAGCTGCTTT
TCCCTGACAGACTGCCAGGAGGTGACAGCGACCTACCGACAGGCACTGAGGGTCTGCTCA
AAGCTCACCTGAGTGGAGTAGGCATTGCCCCAGCCCGGTCAGGCTCTCAGATGCAGCTGG
TTGCACCCCGAGGGGAGATGCCTTCTCCCCCACCTCCCAGGACCTGCATCCCAGCTCAGA
AGGCTGAGAGGGTTTGCAGTGGAGCCCTGAGCAGGGCTGGATATGGGAAGTAGGCAAATG
AAATGCGCCAAGGGTTCAGTGTCTGTCTTCAGCCCTGCTGAACGAAGAGGATACTAAAGA
GAGGGGAACGGGAATGCCCGCGACAGAGTCCACATTGCCTGTTTCTTGTGTACATGGAGG
GGCCACAGAGA

SEQ ID NO: 40_AA426580_H, MAK_V_H
ATGCCGGCGGCGGCGGGGGACGGGCTCCTGGGGGAGCCGGCGGCGCCTGGGGGCGGCGGC
GGCGCGGAGGACGCGGCCAGGCCCGCGGCGGCCTGCGAGGGAAGTTTCCTGCCTGCCTGG
GTGAGCGGCGTGCCCCGCGAGCGGCTCCGCGACTTCCAGCACCACAAGCGCGTGGGCAAC
TACCTCATCGGCAGCAGGAAGCTGGGCGAGGGCTCCTTTGCCAAGGTGCGCGAGGGGCTG
CACGTGCTGACCGGGGAGAAGGTGGCCATAAAAGTCATTGATAAGAAGAGAGCCAAAAAG
GACACCTATGTCACCAAAAACCTGCGGCGAGAGGGTCAGATCCAGCAGATGATCCGCCAC
CCCAATATCACTCAGCTCCTTGATATTTTAGAAACGGAAAACAGCTACTACCTGGTCATG
GAGCTGTGCCCTGGGGGCAACCTGATGCACAAGATCTATGAGAAGAAGCGGCTGGAGGAG

FIGURE 2EE

TCCGAAGCCCGCAGATACATCCGACAGCTCATCTCTGCCGTAGAGCACCTGCACCGGGCC
GGGGTGGTCCACAGAGACTTGAAGATAGAGAATTTGCTACTAGATGAAGACAATAATATC
AAGCTGATTGACTTTGGTTTGAGCAACTGCGCAGGGATCCTGGGTTACTCGGATCCGTTC
AGCACACAGTGTGGCAGCCCTGCCTACGCTGCACCTGAACTGCTCGCCAGGAAGAAATAC
GGCCCCAAAATCGATGTCTGGTCCATAGGTGTGAACATGTATGCCATGTTGACCGGGACG
CTGCCTTTCACGGTGGAGCCTTTCAGCCTGAGGGCTTTGTACCAGAAGATGGTAGACAAA
GAAATGAACCCCCTCCCCACTCAGCTCTCCACAGGTGCCATCAGTTTCCTGCGCTCTCTC
CTGGAACCGGATCCTGTGAAGAGGCCAAATATTCAGCAGGCACTGGCGAATCGCTGGCTT
AATGAGAATTACACGGGCAAAGTGCCCTGTAATGTCACCTATCCCAACAGGATTTCTCTG
GAAGATCTGAGCCCGAGCGTCGTGCTGCACATGACCGAGAAGCTGGGTTACAAGAACAGC
GACGTGATCAACACTGTGCTCTCCAACCGCGCCTGCCACATCCTGGCCATCTACTTCCTC
TTAAACAAGAAAC[illegible]GCAGCGCTATTTGTCAGGGAAATCTGACATCCAGGACAGCCTCTGC
TACAAGACCCGGCTCTACCAGATAGAAAAGTACAGGGCCCCCAAGCAGTCCTATGAGGCC
TCTCTGGACACCTGGACACGAGATCTTGAATTCCATGCCGTGCAGGATAAAAAGCCCAAA
GAACAAGAAAAAAGAGGGGATTTTCTTCATCGACCATTCTCCAAGAAGTTGGACAAGAAC
CTGCCCTCGCACAAACAGCCCTCAGGCTCGCTTATGACACAGATTCAGAACACCAAAGCC
CTCCTGAAGGACCGGAAGGCCTCCAAGTCCAGCTTCCCCGACAAAGATTCCTTTGGCTGC
CGCAATATTTTCCGCAAAACCTCAGATTCCAATTGTGTGGCTTCTTCTTCCATGGAGTTC
ATCCCCGTGCCACCGCCCAGGACCCCGAGGATTGTGAAGAAACCGGAGCCCCATCAGCCA
GGGCCCGGAAGCACTGGCATCCCCCACAAGGAAGACCCCCTGATGCTGGACATGGTGCGC
TCCTTCGAGTCTGTGGATCGCGACGACCACGTAGAAGTGCTGTCTCCCTCTCATCACTAC
AGGATTCTGAACTCCCCGGTCAGCTTGGCTCGCAGAAATTCCAGCGAGAGGACGCTGTCC
CCGGGTCTGCCATCCGGAAGCATGTCGCCTCTCCATACTCCTTTGCATCCAACTCTGGTC
TCTTTTGCTCACGAAGATAAGAACAGCCCCCCAAAAGAGGAGGGCCTGTGTTGCCCACCT
CCGGTTCCCAGCAATGGCCCCATGCAGCCTCTGGGGAGCCCCAATTGTGTGAAAAGCCGA
GGCCGGTTCCCTATGATGGGCATCGGACAGATGTTAAGGAAGCGCCATCAGAGTCTGCAG
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GCCCAGCACGGTGCCAGGCTGGAGGCCCTCTTCAGGATGGTGGCTGCGGTGGACAGGGCC
ATCGCTTTGGTGGGGGCCACGTTCCAGAAATCAAAGGTGGCGGATTTCCTCATGCAGGGG
CGTGTGCCCTGGAGGAGAGGCAGCCCAGGTGACAGCCCTGAGGAGTGGGTAAAAGAGGAG
GAGGTCTGTTTCATGCCTCCAGTTCCCCCAGCTCCGGGGGCAGCAGGACAGAGCCTGCAG
AAGGATAAGGGGGAGCTGTCTGCCGAGCAGGGGATCTGGGCCACATTGATGACGCTGGTG
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GTGCTGAGCACCAGTGGGGTGCAGTCTGATGCCAGGGAGCCTGGGGAAGAGAGCCAGAAG
GCGGACGTGCTGGAGGGGACAGCGGAGAGGCTGCCCCCCATCAGAGCGTCAGGGCTGGGA
GCTGACCCCGCCCAGGCAGTGGTCTCACCGGGCCAGGGAGATGGTGTTCCTGGCCCAGCC
CAGGCATTCCCTGGCCACCTGCCCCTGCCCACAAAGGTGGAAGCCAAGGCTCCTGAGACA
CCCAGCGAGAACCTCAGGACTGGCCTGGAATTGGCTCCAGCACCCGGCAGGGTCAATGTG
GTCTCCCCGAGCCTGGAGGTTGCACCAGGTGCAGGACAAGGAGCATCGTCCAGCAGGCCT
GACCCTGAGCCCTTAGAGGAAGGCACGAGGCTGACTCCAGGGCCTGGCCCTCAGTGCCCA
GGGCCTCCAGGGCTGCCAGCCCAGGCCAGGGCAACCCACAGTGGTGGAGAAACACCTCCA
AGGGCAGCCCTGCTGAAGGGCGCTGTGGCCCCGGGCTTCTCTCGGAGGGACCTGGTGTTT
CCTAGCATCTTCTGCGCCTGCCTAGGGATCTCCATCCACATACAAGAGATGGATACTCCT

FIGURE 2FF

GGGGAGATGCTGATGACAGGCAGGGGCAGCCTTGGACCCACCCTCACCACAGAGGCTCCA
GCAGCTGCCCAGCCAGGCAAGCAGGGCCCACCTGGGACCGGGCGCTGCCTCCAAGCCCCT
GGGACTGAGCCCGGAGAACAGACCCCTGAAGGAGCCAGAGAGCTCTCCCCGCTGCAGGAG
AGCAGCAGCCCCGGGGGAGTGAAGGCAGAGGAGGAGCAAAGGGCTGGGGCCGAGCCTGGC
ACGAGACCAAGCTTGGCCAGGAGTGACGACAATGACCACGAGGTTGGGGCCCTGGGCCTG
CAGCAGGGCAAAAGCCCAGGGGCGGGAAACCCTGAGCCTGAGCAGGACTGTGCAGCCAGG
GCTCCGGTGAGAGCTGAAGCAGTAAGGAGGATGCCCCCAGGCGCCGAGGCTGGCAGCGTG
GTTCTGGATGACAGTCCGGCCCCACCAGCTCCTTTTGAACACCGGGTAGTGAGCGTCAAG
GAGACCTCCATCTCTGCGGGTTACGAGGTGTGCCAGCACGAAGTCTTGGGAGGGGGTCGG
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ATCAAAGTGAAGAGCGCCAAGGACCGGGAGGACGTGAAGAACGAGATCAACATCATGAAC
CAGCTC[illegible]GCCACGTGAACCTGA[illegible]TCTATG[illegible]CGCCTTCCAGAGCAAGCACAGCT[illegible]C
ACCCTTGTCATGGAGTACGTGGACGGGGGTGAGCTCTTCGACCGGATCACAGATGAGAAG
TACCACCTGACTGAGCTGGATGTGGTCCTGTTCACCAGGCAGATCTGTGAGGGTGTGCAT
TACCTGCACCAGCACTACATCCTGCACCTGGACCTCAAGCCGGAGAACATATTGTGCGTC
AATCAGACAGGACATCAAATTAAGATCATTGACTTTGGGCTGGCCAGAAGGTACAAGCCT
CGAGAGAAGCTGAAGGTGAACTTCGGCACTCCTGAGTTCCTGGCCCCAGAAGTCGTCAAT
TATGAGTTTGTCTCATTCCCCACAGACATGTGGAGTGTGGGAGTCATCACCTACATGCTA
CTCAGTGGCTTGTCCCCATTTCTAGGGGAAACAGATGCAGAGACCATGAATTTCATTGTA
AACTGTAGCTGGGATTTTGATGCTGACACCTTTGAAGGGCTCTCGGAGGAGGCCAAGGAC
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SEQ ID NO: 42_SGK088_H
GGGGAGATGGCGCTGTTTGAGTGCCTGGTGGCGGGGCCCACTGACGTGGAGGTGGATTGG
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CGCAAATGCAAGCTGCTACTTACATCTGTACATGAGGACGACAGTGGCGTCTACACCTGC
AAGCTCAGCACGGCCAAAGATGAGCTGACCTGCAGTGCCCGGCTGACCGTGCGGCCCTCG
TTGGCACCCCTGTTCACACGGCTGCTGGAAGATGTGGAGGTGTTGGAGGGCCGAGCTGCC
CGTTTCGACTGCAAGATCAGTGGCACCCCGCCCCCTGTTGTTACCTGGACTCATTTTGGC
TGCCCCATGGAGGAGAGTGAGAACTTGCGGCTGCGGCAGGACGGGGGTCTGCACTCACTG
CACATTGCCCATGTGGGCAGCGAGGACGAGGGGCTCTATGCGGTCAGTGCTGTTAACACC
CATGGCCAGGCCCACTGCTCAGCCCAGCTGTATGTAGAAGAGCCCCGGACAGCCGCCTCA
GGCCCCAGCTCGAAGCTGGAGAAGATGCCATCCATTCCCGAGGAGCCAGAGCAGGGTGAG
CTGGAGCGGCTGTCCATTCCCGACTTCCTGCGGCCACTGCAGGACCTGGAGGTGGGACTG
GCCAAGGAGGCCATGCTAGAGTGCCAGGTGACCGGCCTGCCCTACCCCACCATCAGCTGG
TTCCACAATGGCCACCGCATCCAGAGCAGCGACGACCGGCGCATGACACAGTACAGGGAT
GTCCATCGCTTGGTGTTCCCTGCCGTGGGCCTCAGCACGCCGGTGTCTACAAGAGCGTC
ATTGCCAACAAGCTGGGCAAAGCTGCCTGCTATGCCCACCTGTATGTCACAGATGTGGTC
CCAGGCCCTCCAGATGGCGCCCCGCAGGTGGTGGCTGTGACGGGGAGGATGGTCACACTC
ACATGGAACCCCCCCAGGAGTCTGGACATGGCCATCGACCCGGACTCCCTGACGTACACA
GTGCAGCACCAGGTGCTGGGCTCGGACCAGTGGACGGCACTGGTCACAGGCCTGCGGGAG
CCAGGGTGGGCAGCCACAGGGCTGCGTAAGGGGGTCCAGCACATCTTCCGGGTCCTCAGC
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CACGGCCCAACCCTGGAGGAGGCCCCTGCCATGCTGGACAAACCAGACATCGTGTATGTG
GTGGAGGGACAGCCTGCCAGCGTCACCGTCACATTCAACCATGTGGAGGCCCAGGTCGTC
TGGAGGAGCTGCCGAGGGGCCCTCCTAGAGGCACGGGCCGGTGTGTACGAGCTGAGCCAG
CCAGATGATGACCAGTACTGTCTTCGGATCTGCCGGGTGAGCCGCCGGGACATGGGGGCC

FIGURE 2GG

CTCACCTGCACCGCCCGAAACCGTCACGGCACACAGACCTGCTCGGTCACATTGGAGCTG
GCAGAGGCCCCTCGGTTTGAGTCCATCATGGAGGACGTGGAGGTGGGGCTGGGAAACT
GCTCGCTTTGCGGTGGTGGTCGAGGGAAAACCACTGCCGGACATCATGTGGTACAAGGAC
GAGGTGCTGCTGACCGAGAGCAGCCATGTGAGCTTCGTGTACGAGGAGAATGAGTGCTCC
CTGGTGGTGCTCAGCACGGGGGCCCAGGATGGAGGCGTCTACACCTGCACCGCCCAGAAC
CTGGCGGGTGAGGTCTCCTGCAAAGCAGAGTTGGCTGTGCATTCAGCTCAGACAGCTATG
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AGCTCCGGCCTGGAGTTTGCGGCCAAGTTCATCCCCAGCCAGGCCAAGCCAAAGGCATCA
GCGCGTCGGGAGGCCCGGCTGCTGGCCAGGCTCCAGCACGACTGTGTCCTCTACTTCCAT
GAGGCCTTCGAGAGGCGCCGGGGACTGGTCATTGTCACCGAGCTCTGCACAGAGGAGCTG
CTGGAGCGAATCGCCAGGAAACCCACCGTGT[illegible]ATGCGG
CAGGTGCTAGAGGGAATACACTACCTGCACCAGAGCCACGTGCTGCACCTCGATGTCAAG
CCTGAGAACCTGCTGGTGTGGGATGGTGCTGCGGGCGAGCAGCAGGTGCGGATCTGTGAC
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GAGTTTGTAGCACCCGAGATTGTCAATCAGAGCCCCGTGTCTGGAGTCACTGACATCTGG
CCTGTGGGTGTTGTTGCCTTCCTCTGTCTGACAGGAATCTCCCCGTTTGTTGGGGAAAAT
GACCGGACAACATTGATGAACATCCGAAACTACAACGTGGCCTTCGAGGAGACCACATTC
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GAGGTGAGCACGGATCACCTGAAGCTATTCCTCTCCCGGCGGAGGTGGCAGCGCTCCCAG
ATCAGCTACAAATGCCACCTGGTGCTGCGCCCCATCCCCGAGCTGCTGCGGGCCCCCCCA
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TCGGATTCTGAAGAGGAAGAGCTGGAAGAGCTGCCCTCAGTGCCCCGCCCACTGCAGCCC
GAGTTCTCTGGCTCCCGGGTGTCCCTCACAGACATTCCCACTGAGGATGAGGCCCTGGGG
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CAGGACCAGGAGGCTCCCAGCCCAGAGGCCCTCCCCTCCCCAGGCCAGGAGCCCGCAGCT
GGCGCTAGC[illegible]CTCCGCAGGGGCAGCTCGGCTGA[illegible]
CGGGCCGGGCCGCGGGAGCTGGGCCGGGGCCTGCACAAGGCGGCGTCTGTGGAGCTGCCG
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CACCGCCGAGCGGGGGCGCCCCTCGAGATCCCCGTGGCCAGGCTTGGGGCCCGTAGGCTA
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CTGGAGCTGGTGCGACGGCCTGAGCGCTCACGCTCGGTGCAGGACCTCAGGGCTGTCGGA
GAGCCTGGCCTCGTCCGCCGCCTCTCGCTGTCACTGTCCCAGCGGCTGCGGCGGACCCCT
CCCGCGCAGCGCCACCCGGCCTGGGAGGCCCGCGGCGGGGACGGAGAGAGCTCGGAGGGC
GGGAGCTCGGCGCGGGGCTCCCCGGTGCTGGCGATGCGCAGGCGGCTGAGCTTCACCCTG

FIGURE 2HH

GAGCGGCTGTCCAGCCGATTGCAGCGCAGTGGCAGCAGCGAGGACTCGGGGGGCGCGTCG
GGCCGCAGCACGCCGCTGTTCGGACGGCTTCGCAGGGCCACGTCCGAGGGCGAGAGTCTG
CGGCGCCTTGGCCTTCCGCACAACCAGTTGGCCGCCCAGGCCGGCGCCACCACGCCTTCC
GCCGAGTCCCTGGGCTCCGAGGCCAGCGCCACGTCGGGCTCCTCAGCCCCAGGGGAAAGC
CGAAGCCGGCTCCGCTGGGGCTTCTCTCGGCCGCGGAAGGACAAGGGGTTATCGCCACCA
AACCTCTCTGCCAGCGTCCAGGAGGAGTTGGGTCACCAGTACGTGCGCAGTGAGTCAGAC
TTCCCCCCAGTCTTCCACATCAAACTCAAGGACCAGGTGCTGCTGGAGGGGGAGGCAGCC
ACCCTGCTCTGCCTGCCAGCGGCCTGCCCTGCACCGCACATCTCCTGGATGAAAGACAAG
AAGTCCTTGAGGTCAGAGCCCTCAGTGATCATCGTGTCCTGCAAAGATGGGCGGCAGCTG
CTCAGCATCCCCCGGGCGGGCAAGCGGCACGCCGGTCTCTATGAGTGCTCGGCCACCAAC
GTACTGGCAGCATCACCAGCTCCTGTACCGTGGCTGTGGCCCCAGTCCCAGGAAAGCTA
GCTCCTCCAGAGGTAACCCAGACCTACCAGGACACGGCGCTGGTGCTGTGGAACCCGGGA
GACAGCCGGGCACCTTGCACGTATACGCTGGAGCGGCGAGTGGATGGGGAGTCTGTGTGG
CACCCTGTGAGCTCAGGCATCCCCGACTGTTACTACAACGTGACCCACCTGCCAGTTGGC
GTGACTGTGAGGTTCCGTGTGGCCTGTGCCAACCGTGCTGGGCAGGGGCCCTTCAGCAAC
TCTTCTGAGAAGGTCTTTGTCAGGGGTACTCAAGATTCTTCAGCTGTGCCATCTGCTGCC
CACCAAGAGGCCCCTGTCACCTCAAGGCCAGCCAGGGCCCGGCCTCCTGACTCTCCTACC
TCACTGGCCCCACCCCTAGCTCCTGCTGCCCCCACACCCCCGTCAGTCACTGTCAGCCCC
TCATCTCCCCCCACACCTCCTAGCCAGGCCTTGTCCTCGCTCAAGGCTGTGGGTCCACCA
CCCCAAACCCCTCCACGAAGACACAGGGGCCTGCAGGCTGCCCGGCCAGCGGAGCCCACC
CTACCCAGTACCCACGTCACCCCAAGTGAGCCCAAGCCTTTCGTCCTTGACACTGGGACC
CCGATCCCAGCCTCCACTCCTCAAGGGGTTAAACCAGTGTCTTCCTCTACTCCTGTGTAT
GTGGTGACTTCCTTTGTGTCTGCACCACCAGCCCCTGAGCCCCCAGCCCCTGAGCCCCCT
CCTGAGCCTACCAAGGTGACTGTGCAGAGCCTCAGCCCGGCCAAGGAGGTGGTCAGCTCC
CCTGGGAGCAGTCCCCGAAGCTCTCCCAGGCCTGAGGGTACCACTCTTCGACAGGGTCCC
CCTCAGAAACCCTACACCTTCCTGGAGGAGAAAGCCAGGGGCCGCTTTGGTGTTGTGCGA
GCGTGCCGGGAGAATGCCACGGGGCGAACGTTCGTGGCCAAGATCGTGCCCTATGCTGCC
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ACGGACATCTGGGGAGCGGGTGTGCTCACTTACATTATGCTCAGTGGACGCTCCCCGTTC
TATGAGCCAGACCCCCAGGAAACGGAGGCTCGGATTGTGGGGGGCCGCTTTGATGCCTTC
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GCATCTCAGGGAGAACCAAGGAAGGTGGGCATGGCTGGAGAGGAGGAAAAGGAAGGAGCC
CCAGGTGTCAGGGCAGTAGGCTGGGAGTCAGTGTGGCAAAGCGGGGGCAGGACACAGATA
CAGTGGCAGGGGCCCAGGGCTGGACATGAGAGAAGGCAGCGAGGCGGCAGAGGGAGAAG
AGAGGACTCAGGTGGAGGTGGGGTGGGTCAGCTGTCAGCATCCCTCAGAGGAGAAATGTG

FIGURE 2II

GAGAGCTGGAGGCCAGCAGTCACTCACACTCGCTCTGTCCTCCTGTCCAGTGGATACAGC
CCTGGGCGCTCTGCTGGCCCAAGGATGTCCCCACTGCCCCTCCATGGCCTTTGGCCTTCT
TCCCATTCATATTTATTTATTTATTGACTTTTATGAAGTTTCCCCTTCCATCCGATCCCT
ACTGCCCATGTTGTCCTGACCATCCCTCCCAGCCATCCAGCTGTCTGTCTGTCTGCCACA
AGGAAATAAAAATGGCAAGCAGCAAAAAAA

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TTCCAGTTGTATCCTAACACATCCCAGAGTGCCACCCTCTTCTTGAGAAAGGTCCTCTCA
CTACATCCCTGGAGCCGGCCCTCTCTGCAGGACTGCTTGGCCCACCCATGGCTGCAAGAT
GCCTACCTGATGAAGCTGCGCCGCCAGACACTCACCTTCACCACCAACCGGCTCAAGGAA
TTCCTGGGCGAGCAGCGGCGACGTCGGGCTGAGGCTGCTACCCGTCACAAGGTGCTGCTC
CGCTCCTACCCTGGCAGCCCCTAGGTGGCACAGACCGCAGCCCGGCCACGGGCTTCAACT
TGGGTTCTCACTCGCGCTGCCAAGGGACATTCCAGAGCCCATGCTGAGCTGGACAGGCAG
GGGCTTCAGATACCAGCAGCAGCAGCAGCAGCAGCAGCAGCAACATCTGGCTGGGCTATT
ACCTCATGGACCTAAGAGGACAAGGCCCTGGGGCTTCAGCCGAATGTCACCCCGGCCATA
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GGGAGTTGGGAAGTGAAGAATGAGACGGAGGATAGAGAGGGAGGAGTTTGAGGAAGGTTC
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CAGGAGCCAGAGCAGAGACATAAGGGAGGGCAGAAGGGTAGAAGGCAACAGGAGTGGGCT
CAGGGGTGGCAGGGCAGGCCAGCAGCTGCATCTTCAGAAAGAGAGAGGAGAAAGGCAAAG
AGACGAAAGGCCGCTCCAGCTGGTCTCCTGTCCCAGCCGATGCAGTTCTGGGCGTTCTCC
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SEQ ID NO: 44_R19772_H
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CAGACAGAGAAAGACTATGTCAAGGATCTGGGCATTGTGGTGGAGGGCTTCATGAAGAGA
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TTTGAGGAGGTAAAACAGGAGATAAATCAGAGGCTGACACTGAGTGACTTCCTCATCAAG
CCCATTCAGAGAATAACAAAATACCAGTTGCTCCTCAAGGACTTCCTGAGATACAGTGAG
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FIGURE 2JJ

AAACGCTGCAATGACATGATGAATCTAGGACGTCTGCAGGGCTTTGAGGGCACTCTGACT
GCTCAGGGGAAGCTACTGCAGCAGGACACATTCTATGTGATCGAGCTGGATGCAGGCATG
CAGTCCCGGACCAAAGAGAGGCGCGTGTTCCTCTTCGAGCAGATTGTCATCTTCAGTGAA
CTGCTCAGGAAGGGATCCCTCACCCCTGGCTACATGTTCAAAAGGAGCATCAAGATGAAT
TACTTGGTCCTGGAGGAGAATGTGGACAATGATCCCTGCAAGTTTGCACTCATGAACAGA
GAGACTTCTGAGAGGGTTGTTCTGCAAGCCGCCAACGCTGACATCCAGCAGGCCTGGGTG
CAGGACATCAATCAAGTCTTAGAAACACAGCGAGACTTTTTGAATGCACTGCAATCGCCC
ATTGAGTATCAACGGAAAGAAAGGAGCACAGCTGTGATGAGGTCTCAACCTGCCAGGCTT
CCCCAAGCCAGCCCCAGGCCCTACTCCTCTGTTCCTGCGGGCTCAGAGAAGCCCCCAAAG
GGCTCCAGCTATAACCCACCTCTGCCTCCCCTGAAGATATCTACCTCCAATGGCAGTCCA
GGGTTTGAATACCACCAGCCTGGGGACAAGTTCGAAGCCAGCAAGAACGACCTGGGAGGC
TGCAATGGACCTCGTCCATGGCCGTGATCAAAGATTACTATGCACTGAAGCAGGAATGAA
ATCTGTGTGAGCCAAGGTGAGGTGGTCCAGGTCCTCGCCGTCAACCAGCAGAACATGTGT
CTGGTGTACCAGCCTGCCAGCGACCATTCCCCCGCCGCCGAGGGCTGGGTCCCAGGCAGC
ATCCTGGCGCCCCTCACCAAAGCCACAGCAGCAGAAAGTAGTGACGGGAGCATCAAGAAG
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ACATACACGGTCTCCTCTTGTGATTCTGGAGAAATCACCCTGAAGATCTGTAATCTGATG
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GTAGCTTTCTATATCCGAGACATCATGGAGGCTCTGCAGTACCTTCACAACTGCAGGGTT
GCACATTTGGACATAAAGCCTGAAAACCTGCTCATTGACCTACGGATTCCAGTGCCTCGA
GTGAAGCTCATTGACTTGGAGGATGCTGTCCAGATCTCGGGTCACTTCCACATTCACCAC
CTGCTGGGGAACCCTGAGTTTGCTGCCCCAGAAGTCATTCAAGGCATCCCCGTCTCCCTG
GGGACAGACATCTGGAGCATCGGGGTTCTGACATATGTCATGCTGAGTGGGGTCTCCCCC
TTCTTGGATGAGAGCAAAGAGGAGACATGTATCAACGTATGCAGGGTGGATTTCAGCTTC
CCCCATGAATACTTCTGTGGTGTGAGCAATGCTGCCAGAGATTTCATCAATGTGATCTTA
CAGGAAGATTTTCGGAGGCGGCCCACAGCAGCCACATGCTTGCAGCATCCATGGCTGCAG
CCCCATAATGGCAGCTACTCTAAGATCCCCCTGGACACCTCCCGCCTAGCATGCTTCATA
GAACGTCGCAAGCACCAGAATGATGTGCGGCCTATCCCCAATGTCAAGAGCTACATTGTC
AACCGGGTGAACCAAGGGACGTAG

SEQ ID NO: 45_5R72_8_2_H
CGCCGCTGTTTGTCCTCGCGCGGCCCCGTCCACTGCCCTGCGGTTGCTCTGCGGGCTGAA
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GTCGGAGACCCGCCAGTCCGCCGGCCCCGGCTTTGTTCGTGCGGAACTGTAGTGGTGAGA

FIGURE 2KK

AAAACTCCATGTCTGGGCACGCCTGGCTGATCTTCACCTCTTTCTTCTAGGACCTTCCTC
TGGGCTGTCACGTGTGAATATGTGTCTAGTGCATCCTTAACCTGAGGACTTCACCAGTTC
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CAGTGGAAACATTTTTAAAGTTGCTTTTGTTGCAGAGTTAAACAAATGGCTGATAGTGGC
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ATAGCATATCTTCACAATAATGATATTGTACATAGAGATCTGAAACTGGAAAATATAATG
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GCCCTGTCCAGAACCAAAAAGAAACTCTAAGGTTCCCTCCAGTGTTGGACAGTACAAAAA
CAAAGCTGCTCTTGTTAGCACTTTGATGAGGGGGTAGGAGGGGAAGAAGACAGCCCTATG
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TGAAGCTGCTTATCTCCAAAGCAGCATAAGCTGCACATGGCATTAAAGGACAGCCACCAG
TAGGCTTGGCAGTGGGCTGCAGTGGAAATCAACTCAAGATGTACACGAAGGTTTTTTAGG
GGGGCAGATACCTTCAATTTAAGGCTGTGGGCACACTTGCTCATTTTTACTTCAAATTCT
TATGTTTAGGCACAGCTATTTATAGGGGAAAACAAGAGGCCAAATATAGTAATGGAGGTG
CCAAATAATTATGTGCACTTTGCACTAGAAGACTTTGTTAGAAAATTACTAATAAACTTG
CCATACGTATTACAGCAGAAGTGCTTCAGTCATTCACATGTGTTCGTGAGATTTTAGGTT
GCTATAGATTGTTTAAGACAGCTTATTTTAAATGTAGAAAAATAGGAGATTTTGTAACTG
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TTACTC

SEQ ID NO: 46_SGK309_H
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CAGCCCAAGCAGGTCCTCAAGATGGAGGTGGCCGTGCTCAAGAAGTTGCAAGGTTCGGGC
CTCGGGCAGGGGGATGGAAGGAAGAGATGATGAAGCCAGGGGCTAAGAGAGGGAAGGAC

FIGURE 2LL

CATGTGTGCAGGTTCATTGGCTGTGGCAGGAACGAGAAGTTTAACTATGTAGTGATGCAG
CTCCAGGGCCGGAACCTGGCCGACCTGCGCCGTAGCCAGCCGCGAGGCACCTTCACGCTG
AGCACCACATTGCGGCTGGGCAAGCAGATCTTGGAGTCCATCGAGGCCATCCACTCTGTG
GGCTTCCTGCACCGTGACATCAAGCCTTCAAACTTTGCCATGGGCAGGCTGCCCTCCACC
TACAGGAAGTGCTATATGCTGGACTTCGGGCTGGCCCGGCAGTACACCAACACCACGGGG
GATGTGCGGCCCCCTCGGAATGTGGCCGGGTTTCGAGGAACGGTTCGCTATGCCTCAGTC
AATGCCCACAAGAACCGGGAGATGGGCCGCCACGACGACCTGTGGTCCCTCTTCTACATG
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GGGATGATCAAGGAGAAGTATGAGCACCGGATGCTGCTGAAGCACATGCCGTCAGAGTTC
CACCTCTTCCTGGACCACATTGCCAGCCTCGACTACTTCACCAAGCCCGACTACCAGTTG
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TTTCTCTCACCCCCGATTCCCAGCCTTGTGCCCCTGCCCTGTTCCTCCTAAGCACCCTGT
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SEQ ID NO: 47_AA234451_H
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ATGGATGCCAACAAAAACAAGATAAAGCTTGGAATTTGTAAGGCTGCTACTGAAGAGGAG
AACAGCCATGGCCAGGCAAATGGTCTTCTCAATGCTCCAAGCCTTGGGTCACCAATTCGT

FIGURE 2MM

GTCCGCTCAGAGATTACTCAGCCAGACAGAGATATTCCACTGGTGCGAAAGTTACGTTCC
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TTCCTTGAGACCTGGTATAAAATAGTGTATTTTTCTTTTTAAAGCTTCTAAGGTACCATT
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SEQ ID NO: 48_AA435956_H
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TTACTCATCAGTCACCTGGGAGAGCTCAAACTGGCTGATTTTGGTCTTGCCCGGGCCAAG
TCCATTCCCAGCCAGACATACTCTTCAGAAGTCGTGACCCTCTGGTACCGGCCCCCTGAT
GCTTTGCTGGGAGCCACTGAATATTCCTCTGAGCTGGACATATGGGGTGCAGGCTGCATC
TTTATTGAAATGTTCCAGGGTCAACCTTTGTTTCCTGGGGTTTCCAACATCCTTGAACAG
CTGGAGAAAATCTGGGAGGTGCTGGGAGTCCCTACAGAGGATACTTGGCCGGGAGTCTCC
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GTCTGGAACAGGCTGGGCAGGGTTCCTGAAGCTGAAGACCTGGCCTCCCAGATGCTAAAA
GGCTTTCCCAGAGACCGCGTCTCCGCCCAGGAAGCACTTGTTCATGATTATTTCAGCGCC
CTGCCATCTCAGCTGTACCAGCTTCCTGATGAGGAGTCTTTGTTTACAGTTTCAGGAGTG
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ATTTCTGCAGTTTCGGTTTTCATTTGCTTCAGCTTACTAAGAAGCTTCAAATCTAACTCC
ATACTGAACAAGGGGCTTTATGTCCTCACCTATGACCTGGAATAGTTTAAATATGGTGTT
CAAGGCAATAGTACATAATAGTGGAAGAAAATTCAGTGGAAGGTTATTGCTATTGTCATT
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SEQ ID NO: 49_AA626859_H
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GTACACATTTTGTACAAGTGAGATAGGAATTCTCAGTGTTTCAAATGCAAATGAGCCATA

FIGURE 2NN

TGAAAATTAAGATGCCTTCTAGAATTGGTTTGCTCTGATCATTGCTGATTCCTTTCCCCA
TGCTTTTACAT

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TGTAAAACCTGAAAACATCCTAATAACCAAGCAAGGGATGATAAAGATTTGTGACTTTGG
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CGTCGGCTGTGTTTTTGCAGAGCTCCTGACGGGTCAGCCACTCTGGCCGGGAAAATCCGA
CGTGGACCAGCTTTACCTGATCATCAGGACGTTGGGGAAGCTGATTCCAAGACACCAGTC
TATCTTTAGGAGTAACCAGTTTTTCCGCGGCATCAGCATACCTGAACCAGAGGACATGGA
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CCTGAAGATGAATCCTGATGAGAGGCTGACCTGTGCCCAGCTGCTGGACAGTGCCTACTT
TGAGTCTTTTCAAGAGGATCAAATGAAAAGAAAAGCCCGCAGTGAGGGGAGAAGCCGAAG
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FIGURE 2OO

SEQ ID NO: 51_AA397553_H
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GACACCTTCTCCGATGACATGGCCTTCAAACTAGACCGAAGGGAGAACGACGAACGTCGT
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TCTCAGCCCCCTGTACAGGTTTCTGTGAAGACTCAAGTATCTGTAACAGCTGCTATTCCA
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GACAATGAGAAAGAGGGCTTCCCAATCACAGCCATTCGTGAAATCAAAATCCTTCGTCAG
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TACCGACCTCCAGAACTACTGCTAGGAGAGGAACGTTACACACCAGCCATAGATGTTTGG
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CCTGATGTTATCAAACTGCCCTACTTCAACACCATGAAACCGAAGAAGCAATATCGAAGG

FIGURE 2PP

CGTCTACGAGAAGAATTCTCTTTCATTCCTTCTGCAGCACTTGATTTATTGGACCACATG
CTGACACTAGATCCTAGTAAGCGGTGCACAGCTGAACAGACCCTACAGAGCGACTTCCTT
AAAGATGTCGAACTCAGCAAAATGGCTCCTCCAGACCTCCCCCACTGGCAGGATTGCCAT
GAGTTGTGGAGTAAGAAACGGCGACGTCAGCGACAAAGTGGTGTTGTAGTCGAAGAGCCA
CCTCCATCCAAAACTTCTCGAAAAGAAACTACCTCAGGGACAAGTACTGAGCCTGTGAAG
AACAGCAGCCCAGCACCACCTCAGCCTGCTCCTGGCAAGGTGGAGTCTGGGGCTGGGGAT
GCAATAGGCCTTGCTGACATCACACAACAGCTGAATCAAAGTGAATTGGCAGTGTTATTA
AACCTGCTGCAGAGCCAAACCGACCTGAGCATCCCTCAAATGGCACAGCTGCTTAACATC
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AGCACACCAGCTGACATGCAGAATATATTGGCAGTTCTCTTGAGTCAGCTGATGAAAACC
CAAGAGCCAGCAGGCAGTCTGGAGGAAAACAACAGTGACAAGAACAGTGGGCCACAGGGG
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CCACCAGAGAAGAGGCCCCCTGAGCCCCCCGGACCTCCACCGCCGCCACCTCCACCCCCT
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CAGGACCTCCGTTTTGCCAGGGTCCCCTTAGCGTTACACCCGGTGGTCGGGCAACCATTC
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GGGGAGCTGGGGCCAGGAACCACTGGGGCCAGCAGCTCAGGAGCAGGCCTTCACTGGGGG
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AGAGGGGGAAGAGGGAGAGGAGTTCCTTACTAA

SEQ ID NO: 52_AA789239_H

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AAGTTATGCCTAATAGCAGGCAAGAGGATCCAGGTCCTATTCAAAGCCAAATGGAGAAGG
GTATATTTAATGAGCGAACAGGTCACAGTGACCAAATGGCAAATGAGAACAAAAGGAAGC

FIGURE 2QQ

TGAATTTTTCCAGATCTGACAGGAAAGAATTCCATTTTCCAGAATTGCCTGTCACAATAC
AGTCAAAAGATACAAAAGGAATGGAAGTTAAACAGATAAAAATGCTGAAGAGGGAGTCAA
AGAAAACAGAGTCATCTAAGATACCAACTTTACTTAACGTGGATCAAAATCAAGAAAAAC
AAGAGTTTATTCCCTTATCTCTGCTGTCTGCCTGCTGTCCTATTTTCACAAATATTTGCT
CTCAGCTAACTATCAGGGTGGAGATGGCCATTGCGAGGGGAAGAATTTGAAGAGAAACAG
GTTTTTTTTCTGGTAGTGTCTTTTCTTTTACATAGTCCAAAAAATACAAGATGACAACTC
TTCCCGTTTTATTTATCTACAATAGAAGTGTGATGTGAGTTGTTGTTAAGACAGCCATCC
ATGTGCATGAGCATCATCCAGCTTTTTTTGTTAGCAAAACATTTACTGTTTTCTTTTCCC
TTTTAAGACTCTGTTGATGTGATAATTTGATTTGGAATTATAAAGTCATCTCTTCTCTGC
CTTGAA

SEQ ID NO: 53_AA124976_M
CTGGCAGATATAGTTCATGCTTGTTTACAAATTGATCCTGCTGAGAGGACATCATCTACT
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CTGAGAGCTAAATTATTACAGGAAGCAAAGGTTAATTCATTTATAAAGCCAAAAGAGAAT
TTTAAAGAAAATGAACCTGTGAGAGATGAGAAGAAATCAGTTTTTACCAACACCCTGCTC
TATGGAAATCCATCACTTTATGGCAAGGAAGTGGACAGAGACAAAAGGGCCAAGGAGCTC
AAAGTCAGAGTCATTAAGGCCAAAGGGGGCAAAGGAGATGTCCCAGACCAGAAGAAGCCA
GAGTATGAAGGCGACCACCGCCAGCAGGGCACAGCTGATGACACACAGCCCTCATCACTG
GACAAGAAGCCTTCTGTCTTGGAACTGACAAACCCTCTCAATCCCAGTGAGAATTCTGAC
GGTGTCAAAGAAGACCCACACGCTGGGGGTTGTATGATAATGCCACCTATCAACCTGACA
AGCAGTAATTTGTTGGCCGCAAATCTCAGTTCAAACCTTTCCCACCCCAATTCACGGTTA
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AGCAGACAAGAGGACACAGGTCCCACACAAGTCCAAACAGAGAAAGGTGCATTTAATGAG
CGAACAGGTCAGAATGACCAAATATCGAGTGGGAACAAAAGAAAGCTGAATTTTCCCAAA
TGCGACAGGAAAGAATTCCATTTCCCTGAACTGCCATTCACAGTGCAGGCGAAGGAGATG
AAAGGGATGGAAGTTAAACAGATAAAAGTGCTGAAGAGAGAATCAAAGAAAACAGATTCA
TCT[illegible]AA[illegible]TACCAACTTTACTTAGTATGGACCCAAATC[illegible]GTGGAGAT
GGCGATTGTGAGGGGAAGAATTTGAAGAGGAACAGATTTTTTTTTCCCGATAGTGCTTT
GTCTTTTAAGTAATCTTAAAAATACAAGCTTGACAATTCCTTCCTTTTTATTTTATATAC
ACTAGAATGTACATAGGTTGCTGCTAAGATAGCCACCCATCCCATCTGCATCAACATCAT
CTATTTTTTTGGTTTTGCTAGCAAAATTTTCACAATTTTTCTCTATCTTCCAAAAACTGT
TATTTTGATGCTGTGATTTGAAATTATAAAGTCACCTCCTCTGTCTGCTTCCTTCCTTGC
CATGATTACTGAGTGGGTAGTCACATGATGTGCCCTGCTCGCACTGCTCTCAGACTGCTG
AGACTCAAACCTCATAAGCCAGGGGTCTCCTGGGAAGCACTGGCCTCTTCAAGTGGATGC
TCGATGAACCTTCTTATCTGTTGTCTTAGTAACCACTCGTTGCCATCACATGATGAAAGA
CATTCTATTGTCCCCAGTGAAGCATTTATAGTACTTACATAACATGTTACAGTGATATGA
TGTTCCTAGGTTAAACTCCTTGAGATGAAACTATTTCCTGCATTCTCTGACTCCCCTAGT
CTAATAGTTCCTTCCATTTAGCCAGAAGAATTTCCTGAAGAAGCGATGCACAACCTGGGA
AAGGTTTACTTTCTATCCTGGGCTGTTTTCTGTTGCTAAATAATATAGACTGGGTAGTTA
GTTAACAT

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AGCGCCTCAGGCCAGCTCAAGATAGCTGACTTTGGCCTGGCCCGGGTCTTCTCTCCGGAT
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GAGCTGTTGAATGGGTCCCCCCTGTTCCCGGGCGAAAACGACATTGAACAACTGTGCTGT
GTGCTTCGCATCCTGGGTACCCCGAGTCCTCGAGTCTGGCCGGAGATCACAGAGCTGCCT
GACTACAACAAGATCTCCTTCGAGGAGCAGGCACCAGTGCCCCTGGAGGAGGTGCTGCCT
GATGCCTCTCCCCAGGCCTTGGACCTGCTGGGCCAGTTCCTCCTCTACCCTCCACGACAG

FIGURE 2RR

CGTATTGCAGCCTCCCAGGCCCTTCTGCATCAGTACTTCTTCACAGCGCCTCTGCCTGCC
CATCCATCCGAGCTGCCAATTCCTCAGCGCCCAGGGGGACCTGCACCCAAGGCTCACCCA
GGGCCCCCCCATGTCCACGACTTCCATGTGGATCGACCTATTGAGGAGTCACTGTTGAAC
CCAGAACTGATTCGGCCCTTCATCCCAGAGGGGTGAGATGCTGGTCCAGGCCTTCCTGCT
CGCCCTAGGAGCACCTCTTTCTGATTTGCCTCCATGGCCTCCCCACGGCTATATATACCA
CACCTGGTCCTGCTCCTGAGTGTGCTTGAGGGCTGGGCTCTGGGAGGCAGAACCGTGAGA
TGTTCATCCCAGCAGAGAAAGAGACTCACGTCCTACAGACAAAGCCTCCAGAAACTGCTA
GCTGTGTCCTTCTCCAGGGCCACCCCTCAGTGGTGCCACCCGGCCTTAGAGATGATTGTC
AGGCTCTGTCCCCTCTTCAAGGACATTGGTACTACAGCACCACCTGGTGGAAGCACAGAG
TATAAGCTGTCTTCATACTGGGGACACAGCTGGGAAGTCAGACATGTTTTAGTTTTGGTT
CCACTGGGTCAGGATTTGAGGTTCATATAAAAGCCCTGGGTGTTTCTGTCTAATTGCACC
TTGTCTGTTGCTGTTAGGGAAAGGACAATGGTGGCCCTTGATTCACAGGGGTCAGGTACT
CAGAAGGGGCCTCCTGTCAAGGCCATTTGGGTCCTCAGGCTTCCCATGCTATTCACGGGA
CTTGAGTGCTCATTTGGGAGCGAGGGTCCAGAAGCTGAGGCCCAGGGATGGACAGTCCAG
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SEQ ID NO: 55_AA631990_H
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GGGAAGACGGCAGTTTGGCGACATTTCTCGGCCGAAGGGCCATTTGCTTTTGCGGAGATG
CGGCATTCCAAAAGAACTCACTGTCCTGATTGGGATAGCAGAGAAAGCTGGGGACATGAA
AGCTATCGTGGAAGTCACAAGCGGAAGAGGAGATCTCATAGTAGCACACAAGAGAACAGG
CATTGTAAACCACATCACCAGTTTAAAGAATCTGATTGTCATTATTTAGAAGCAAGGTCC
TTGAATGAGCGAGATTATCGGGACCGGAGATACGTTGACGAATACAGGAATGACTACTGT
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GAAAACAGCTTTCTGCCATTTCAAATTGACCACATCAGGCAGATGGCGTATCAGATCTGC
CAGTCAATAAATTTTTTACATCATAATAAATTAACCCATACAGATCTGAAGCCTGAAAAT
ATTTTGTTTGTGAAGTCTGACTATGTAGTCAAATATAATTCTAAAATGAAACGTGATGAA
CGCACACTGAAAAACACAGATATCAAAGTTGTTGACTTTGGAAGTGCAACGTATGATGAT
GAACATCACAGTACTTTGGTGTCTACCCGGCACTACAGAGCTCCCGAGGTCATTTTGGCT
TTAGGTTGGTCTCAGCCTTGTGATGTTTGGAGCATAGGTTGCATTCTTATTGAATATTAC
CTTGGTTTCACAGTCTTTCAGACTCATGATAGTAAAGAGCACCTGGCAATGATGGAACGA
ATATTAGGACCCATACCACAACACATGATTCAGAAAACAAGAAAACGCAAGTATTTTCAC
CATAACCAGCTAGATTGGGATGAACACAGTTCTGCTGGTAGATATGTTAGGAGACGCTGC
AAACCGTTGAAGGAATTTATGCTTTGTCATGATGAAGAACATGAGAAACTGTTTGACCTG
GTTCGAAGAATGTTAGAATATGATCCAACTCAAAGAATTACCTTGGATGAAGCATTGCAG
CATCCTTTCTTTGACTTATTAAAAAAGAAATGAAATGGGAATCAGTGGTCTTACTATATA
CTTCTCTAGAAGAGATTACTTAAGACTGTGTCAGTCAACTAAACATTCTAATATTTTTGT
AAACATTAAATTATTTTGTACAGTTAAGTGTAAATATTGTATGTTTTGTATCAATAGCAT
AATTAACTTGTTAAGCAAGTATGGTCTTGATAATGCATTAGAAAAATTAAAATTAATTTT
TCTTTTTGAAATTACCATTTTTAAATACCTTTGAAATATCCTTTGTGTCCAGTGATAAAT
GTGATTGATCTTGCCTTTTGTACATGGAGGTCACCTCTGAAGTGATTTTTTTGAGTAAA
AGGAAATCTTGACTACTTTATATTCTTAAAGGAATATTCTTTATATACTTCAAATTTAGA

FIGURE 2SS

ACTTAACTTTAAAAGTTTTTCTTCTGTAATTGTTGAACGGGTGATTATTATTAACTCTAG
ATAAGCAGGTACTAGAAACCAAAACTCAGAAAATGTTTACTGTTAGAATTCTATTAAATT
TTAAGTGTTGTATTCTTTTTCATTGGGTGATGTCAGGGTGATAACCAGACATTCATGGAA
AGGCATGCAGTTTGTCCATTGTGACAGTTTGTTTAATAAAACCACATACACACTTTATTT
AAGATTAAAATCTAACTGGAAAGTCAGCTTGGAAAATGGACATTTCCAAGTATGTTTGGT
GAGTCACAGATATAAAAATAGAAATTCTGATGAGAGGTTTCAGTTTTTAATACCAAGTCC
TTAGGAGTCTTAACATTGGCCAGCATCTGTTTATCAAATGACATAAATACGTAAACCTAT
AAGAATTAAGTTTATTAATTAGGCAATTTATGTCTGTGATAATTCTTACGGGAGAAAGAG
GATTTGATTGGAAAGCAGTTTGGGAAGAAAGTGCTGCTGAAATTTCCAGAATTTAATTGA
TTGGTTACATAAACTTTTTGACTTCAAT

SEQ ID NO: 56_AA557536_H
AGTAAGGCCCCGCGGGCGTCCTGGCCGCCATGTGCACCGTAGTGGACCCTCGCATTGTCC
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TCCAGGTGAGTGGCCTGGGCCCTCCAGTCCAATCCCCTTGCCCAGGTACAGATCTCTCCA
GACAGGAGAGAAACTGGCCTTCTTGGGCCCCAGAGCACAGCCCCTCCTGGCCTTCCAGCC
GCCTCCGACTCTCTCCCCAGGAGTTTGGGGACCATCCCAACATCATCAGCCTCCTTGACG
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TGAACGCAGTCATCCGGAAGGGCGGCCTGCTGCAGGACGTCCACGTGCGCTCCATCTTCT
ACCAGCTCCTGCGGGCCACCCGGTTCCTCCACTCGGGGCACGTTGTGCACCGGGACCAGA
AGCCGTCCAATGTGCTCCTGGATGCCAACTGCACAGTGAAGCTGTGTGACTTTGGCCTGG
CCCGCTCCCTGGGCGACCTCCCTGAGGGGCCTGAGGACCAGGCCGTGACAGAGTACGTGG
CCACACGCTGGTACCGAGCACCGGAGGTGCTGCTCTCTTCGCACCGCTACACCGCTTCCT
GCCCCAGATACACCCTTGGGGTGGACATGTGGAGTCTGGGCTGTATCCTGGGGGAGATGC
TGCGGGGGAGACCCCTGTTCCCCGGCACGTCCACCCTCCACCAGCTGGAGCTGATCCTGG
AGACCATCCCACCGCCATCTGAGGAGXXXAGGCCACGACAGACGCTGGATGCCCTCCTAC
CGCCAGACACCTCCCCAGAGGCCTTGGACCTCCTTAGGCGACTCCTGGTGTTCGCCCCGG
ACAAGCGG[illegible]CAGGCACTGCAGCACCCCTACGTG[illegible]AGAGGTTCC[illegible]
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GCGGCACCTCGAGAGAGAAGGGCCCGGAGGGTGTCTCCCCAAGCCAGGCACACCTGCACA
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CCCAGAGCAGCCCAGGCCATGACCCTGCCGAGCACGAGTCCCCCCGTGCAGCCAAGAACG
TTCCCAGGCAGAACTCCGCTCCCCTGCTCCAAACTGCTCTCCTAGGGAATGGGGAAAGGC
CCCCTGGGGCGAAGGAAGCGCCCCCCTTGACACTCTCGCTGGTGAAGCCAAGCGGAGGG
GAGCTGCGCCCTCCCTGACCTCCCAGGCTGCGGCTCAGGTGGCCAACCAGGCCCTGATCC
GGGGTGACTGGAACCGGGGCGGTGGGGTGAGGGTGGCCAGCGTACAACAGGTCCCTCCCC
GGCTTCCTCCGGAGGCCCGGCCCGGCCGGAGGATGTTCAGCACCTCTGCCTTGCAGGGTG
CCCAGGGGGGTGCCAGGGCTTTGCTTGGAGGCTACTCCCAAGCCTACGGGACTGTCTGCC
ACTCGGCACTGGGCCACCTGCCCCTGCTGGAGGGGCACCATGTGTGAGCCGCCCTACTCC
CTTCACCTGGCCCTCTGTTCCTGCCCCAGCNCCTTCCCCAGACCCCTCTCCAGTCTCCTG
CACCCCTTAGCCCTCCCTGCTTTGCCTGGCCCGTTGAAGTTCCAGGGAGCTTGCCCGGGT
CTCCTCGGGGGAGCAGATGAGGGCCCTGCCC

SEQ ID NO: 57_N28606_H, MOK_H
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AGTATTGAGCAAGTCAACAACCTACGAGAGATCCAAGCACTGAGGCGCCTGAATCCGCAC
CCAAACATTCTTATGTTGCATGAAGTGGTTTTTGACAGAAAATCTGGTTCTCTTGCACTA
ATATGTGAACTTATGGACATGAATATTTATGAGCTAATACGAGGGAGAAGATACCCATTA

FIGURE 2TT

TCAGAAAAAAAAATTATGCACTATATGTACCAGTTATGTAAGTCCCTGGATCATATTCAC
AGAAATGGAATATTTCACAGAGATGTAAAACCAGAAAATATACTAATAAAGCAGGATGTC
CTGAAATTAGGGGACTTTGGCTCCTGCCGGAGTGTCTATTCCAAGCAGCCGTACACGGAA
TACATCTCCACCCGCTGGTACCGGGCCCCGGAGTGTCTCCTCACTGATGGGTTCTACACG
TACAAGATGGACCTGTGGAGCGCCGGCTGTGTGTTCTACGAGATCGCCAGTCTGCAGCCC
CTCTTTCCTGGAGTAAATGAACTGGACCAAATCTCAAAAATCCACGATGTCATCGGCACA
CCCGCTCAGAAGATCCTCACCAAGTTCAAACAGTCGAGAGCTATGAATTTTGATTTTCCT
TTTAAAAAGGGATCAGGAATACCTCTACTAACAACCAATTTGTCCCCACAATGCCTCTCC
CTCCTGCACGCAATGGTGGCCTATGATCCCGATGAGAGAATCGCCGCCCACCAGGCCCTG
CAGCACCCCTACTTCCAAGAACAGAGGAAAACAGAGAAGCGGGCTCTGGGCAGCCACAGA
AAAGCTGGCTTTCCGGAGCACCCTGTGGCACCGGAACCACTCAGTAAGCGCTGCCAGCTT
TCCAAGGAGGGCAGAAAGCAGAAACAGTCCCTAAAGCAAGAGGAGGACCGTCCCAAGAGA
CGAGGACCGGCCTATGTCATGGAACTGCCCAAACTAAAGCTTTCGGGAGTGGTCAGACTG
TCGTCTTACTCCAGCCCCACGCTGCAGTCCGTGCTTGGATCTGGAACAAATGGAAGAGTG
CCGGTGCTGAGACCCTTGAAGTGCATCCCTGCGAGCAAGAAGACAGATCCGCAGAAGGAC
CTTAAGCCTGCCCCGCAGCAGTGTCGCCTGCCCACCATAGTGCGGAAAGGCGGAAGATAA

SEQ ID NO: 58_AB023153_H, ICK_H
ATGAATAGATACACAACAATCAGGCAGCTCGGGGATGGAACCTACGGTTCCGTCCTGCTG
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TCCTGGGAGGAATGCATGAACCAACGGGAGGTTAAGTCTTTAAAGAAGCTCAACCATGCC
AATGTAGTCAAATTAAAAGAAGTTATCAGGGAAAATGATCATCTTTATTTTATCTTCGAG
TACATGAAGGAAAATCTTTACCAGCTCATTAAAGAGAGAAATAAGTTGTTTCCTGAGTCT
GCTATAAGGAATATCATGTATCAGATATTACAAGGACTCGCATTTATTCACAAACTCGGC
TTCTTTCATCGAGACTTAAAGCCTGAGAACCTCCTCTGCATGGACCAGAACTTGTGAAA
ATTGCAGACTTTGGTTTGGCCCGAGAAATACGATCAAAACCTCCATATACAGATTATGTA
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ATTGACGTCTGGCGGTGGGCTGCATCATGGCAGAAGTTTACACCCTCAGGCCACTCTTC
CCTGGAGCCAGTGAAAATGACACAATATTCAAAATTTGCCAAGTGCTGGGACACCAAAA
AAGACTGACTGGCCTGAAGGCTATCAACTTTCAAGTGCAATGAACTTCCGTTGGCCACAG
TGTGTACCCAATAACTTAAAGACCTTGATTCCCAATGCTAGCAGTGAAGCAGTCCAGCTC
CTGAGAGACATGCTTCAGTGGGATCCCAAGAAACGACCAACAGCTAGTCAGGCACTTCGA
TATCCTTACTTCCAAGTTGGACACCCACTAGGCAGCACCACACAAAACCTTCAGGATTCA
GAAAAACCACAGAAAGGCATCCTGGAAAGGGCAGGCCCACCTCCTTATATTAAGCCAGTC
CCACCTGCCCAGCCACCAGCCAAGCCACACACACACGAATTTCTTCACGACAGCATCAAGCC
AGCCAGCCCCCTCTGCATCTCACGTACCCCTACAAAGCAGAGGTCTCCAGGACAGATCAC
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TTGGATGACTTGGATTTCAGTCCATCCCTCAGCAGGATTGACCTGAAAAACAAGAAAAGA
CAGAGTGATGACACTCTCTGCAGGTTTGAGAGTGTTTTGGACCTGAAGCCCTCTGAGCCT
GTGGGCACAGGAAACAGTGCCCCCACCCAGACGTCATATCAGCGGCGAGACACGCCCACC
CTGAGATCTGCAGCCAAGCAGCACTATTTGAAGCACTCTCGATACTTGCCTGGGATCAGT
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AGTTCTGGCTTGTCTGGAAAATCTTCAGGGACAATGTCAGTAATCAGCAAAGTAAATTCA
GTTGGTTCCAGCTCTACAAGTTCTAGTGGACTGACTGGAAACTATGTCCCTTCCTTTCTG
AAAAAAGAAATCGGTTCTGCTATGCAGAGGGTACACCTAGCACCTATTCCAGACCCTTCC
CCTGGTTATTCCTCCCTGAAGGCCATGAGACCTCATCCTGGGCGACCATTCTTGGACACC
CAGCCTAGAAGCACTCCTGGGTTGATACCACGGCCTCCAGCCGCCCAGCCAGTGCATGGC
CGGACAGACTGGGCTTCCAAGTACCCATCCCGGCGGTGA

FIGURE 2UU

SEQ ID NO: 59_AA839940_M
AGCAGCAACAATGGTGGCATGAGTGCAGAGGAGGAGATAGGGCCTGGGGCTGAGCCTATG
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CAGCAAGGCATAGACCCAGGAGCAGTGAGCCCTGAGCCTGGGAAGGACCACGCAGCCCAG
GGCCCAGGAAGAACTGAAGCTGGAAGGGTATCTTCTGCTGCAGAGGCTGCCATTGTGGTT
CTAGATGACAGCGCAGCACCCCCAGCCCCTTTTGAACACCGGGTAGTGAGCATCAAAGAT
ACCCTGATCTCAGCAGGCTACACGGTATCCCAACATGAAGTCTTAGGAGGGGGTCGGTTT
GGCCAGGTGCACAGGTGTACAGAGAGGTCTACAGGCCTTGCACTGGCAGCCAAGATCATC
AAAGTGAAGAACGTAAAGGACCGGGAGGATGTGAAGAATGAGGTCAACATCATGAACCAG
CTCAGCCACGTAAACTTGATCCAACTTTATGATGCGTTTGAGAGCAAGAACAGCTTCACT
CTGATCAGGGAGTATGTGGATGGAGGCGAACTCTTTGACCGGATCAGGGATCAGAAGTAC
CACCTCACTGAGTTGGATGTGGTCTTGTTCACGAGGCAGATCTGTGAGGGTGTGCATTAC
CTGCATCAGCACTATATCCTGCACCTGGACCTCAAGCCTGAGAACATATTGTGTGTCAGC
CAGACAGGGCATCAAATTAAGATCATTGACTTTGGGCTGGCTAGAAGATACAAGCCTCGG
GAGAAGCTAAAGGTGAACTTTGGTACTCCGGAGTTCCTGGCCCCAGAAGTTGTTAACTAT
GAGTTTGTGTCATTTCCAACAGACATGTGGAGTGTGGGAGTTATCACCTACATGCTACTC
AGTGGTTTGTCCCCATTTCTAGGGGAGACAGATGCAGAGACCATGAATTTTATTGTGAAC
TGCAGCTGGGATTTCGATGCTGATACCTTCAAAGGGCTGTCGGAGGAAGCCAAGGACTTT
GTTTCCCGGTTACTGGTCAAAGAGAAGAGCTGTAGGATGAGCGCCACACAGTGCCTGAAA
CACGAGTGGTTAAATCACCTGCCTGCCAAAGCCTCGGGCTCCAACGTTCGCCTCAGATCC
CAACAACTGCTGCAGAAATATATGGCTCAGAGTAAATGGAAGAAACATTTCCACGTGGTG
GCTGCAGTCAACAGGCTACGGAAATTTCCAACGTGTCCCTAATCTTCAACTCTGGTGTTC
CACTGGGCCTGGGAATTCTTGAGGCAACACGAAGTGGTAATATGAAGAGATTACTCAAGA
TTTTATGTAGATTGGCGCTTTGCTATTATTGATTTTTCTTATTTTGCAAAGAATGATGGA
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GGAAACAGGCTACGTTGTTGCTCTTCTTGTAGGTGAAAGTGTTTTTATTAAAAGCCCTAG
GAATGTTTTTCTGCCTCGTAAGGTCAGCAGGTCTCATATGCTGCTTGCTACCCCGCACCC
TTCCTTTTGGTAATAAGAGCAGGCAGGCTCAGGATGGGCAGGGAAATCCTACTTGGCTTT
TGGTCAAATTTGAATTCTAAACTTGTCATGATTAAAGAAGCCAGTAGGGAGGGAGGTATG
GAAGAGGGAGGAATTAGGTCCAACAGTGGGGGATGAATTTGACCGAAACATTGTATAAAA
TTCTTAAAGAATTAATAAAATATATTTTTAAAGGAG

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GGATTTCCGAAGCGAGCCGAAGCATCGCGACAGTTTTCAGAGACAGCTGATCGGTTGGAG
CTGTTGCGCCGAGCAGTCATGGCGGCGGCCAGAGCTACTACGCCGGCCGATGGCGAGGAG
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CGCGCGGCGGTGATCAAGCACCGCTTCCCCAAGGGCTACCGGCACCCGGCGCTGGAGGCG
CGGCTTGGCAGACGGCGGACGGTGCAGGAGGCCCGGGCGCTCCTCCGCTGTCGCCGCGCT
GGAATATCTGCCCCAGTTGTCTTTTTTGTGGACTATGCTTCCAACTGCTTATATATGGAA
GAAATTGAAGGCTCAGTGACTGTTCGAGATTATATTCAGTCCACTATGGAGACTGAAAAA
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GATGAAGACCTCATTCATGGTGATCTCACCACCTCCAACATGCTCCTGAAACCCCCCCTG
GAACAGCTGAACATTGTGCTCATAGACTTTGGGCTGAGTTTCATTTCAGCACTTCCAGAG
GATAAGGGAGTAGACCTCTATGTCCTGGAGAAGGCCTTCCTCAGTACCCATCCCAACACT
GAAACTGTGTTTGAAGCCTTTCTGAAGAGCTACTCCACCTCCTCCAAAAAGGCCAGGCCA
GTGCTAAAAAAATTAGATGAAGTGCGCCTGAGAGGAAGAAAGAGGTCCATGGTTGGGTAG
AAGAATGTGTATGACAACCACACACAGTGAAGCTCTTTTTTCAAAGTAAATTTGAAGAAA

FIGURE 2VV

TGCTACAAGTATGAGATGAGATCTAAGTAAAGGTGTTAAGATATTTTTAAGTGGTATGTG
ATCGTGTCATTATCATCTGCACTTCACTCAAGAGCTTACTATGTGTCTAAGTCATGTTCT
AGGCAGAATTGGGTATTTAAAGTAAATTGAGGACAGGCTTCTCCCAGATTGTGACATGTA
TATCTCAGATACATGGGTGTGGCATTGAACCACATAATGAGAACATTATTCTCTTTTTAG
TCCTTGTGAGACAAGGATGAAGTCTCAGTTGCTGATACTCGCTGAGCTTACTGGCCCTCT
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AATGGGATACAACCAGCATTTTAAAAAATGAAATAGAATACAGCATGG

SEQ ID NO: 61_SGK034_H
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CCGAACATCGTGAAGTTGCACAAGTACTGGCTGGATACCTCTGAGGCCTGCGCGAGGGTC
ATCTTCATCACAGAGTACGTGTCATCAGGCAGCCTCAAGCAATTCCTCAAAAAGACCAAG
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GCGCTCAGCTTCCTGCACGCCTGCAGCCCCCCAATCATCCACGGGAACCTGACCAGCGAC
ACCATCTTCATTCAGCACAACGGCCTCATCAAGATCGGCTCCGTGTGGCACCGAATCTTC
TCCAATGCACTTCCAGATGATCTCCGAAGCCCCATCCGCGCTGAGCGAGAGGAACTTCGG
AACCTGCACTTCTTCCCCCCAGAGTATGGAGAGGTGGCCGATGGGACCGCTGTGGACATC
TTCTCCTTTGGGATGTGTGCGCTGGAGATGGCTGTACTGGAAATCCAGACCAATGGGGAC
ACCCGGGTCACAGAGGAGGCCATTGCTCGCGCCAGGCACTCGCTGAGTGACCCCAACATG
CGGGAGTTCATCCTTTGCTGCCTGGCCCGGGACCCTGCCCGCCGGCCCTCTGCCCACAGC
CTCCTCTTCCACCGCGTGCTCTTCGAGGTGCACTCGCTGAAGCTCCTGGCAGCCCACTGC
TTCATCCAGCACCAGTACCTCATGCCTGAGAATGTGGTGGAGGAGAAGACCAAGGCCATG
GACCTGCACGCGGTCTTGGCGGAGCTTCCCCGGCCCCGCAGGCCCCCGCTGCAGTGGCGG
TACTCGGAAGTCTCCTTCATGGAGCTGGACAAATTCCTGGAGGATGTCAGGAATGGAATC
TACCCACTGATGAACTTTGCAGCCACTCGACCCCTGGGGCTGCCCCGTGTGCTGGCCCCA
CCCCCGGAGGAGGTCCAAAAGGCCAAGACCCCGACGCCAGACCCTTTGACTCTGAGACC
AGAAAGGTCATCCAGATGCAGTGCAACCTGGAGAGAAGCGAGGACAAGGCGGCTGGCAT
CTCACTCTGCTTCTGGTGCTGGAAGACCGGCTGCACCGGCAGCTGACCTACGACCTGCTC
CCAACGGACAGCGCCCAGGACCTCGCCTCGGAGCTCGTGCACTATGGCTTCCTCCACGAG
GACGACCGGATGAAGCTGGCCGCCTTCCTGGAGAGCACCTTCCTCAAGTACCGTGGGACC
CAGGCCTGACCCGGAGCCCCAGCCCCAGGGGACCATGCCGGGGTGCTGCCCGGGCAGGCC
ATGTTGGGGAGACTCCAGCACCGTGGGGCTGCCCTCCTCCATGCGCCTGGGAGCACAAAG
GCCCCGGTAGTGAAGGAACCCCCCGTCTCCTGAGAGTGGGGCTGACCCTGCCTTGGGCGC
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GTTGCCCCCAGAACCCCTTCCCATATCCTCCATTCTCCGCCCTGAGTTCCTACCCAGGCT
GCCTGGCTGGGGCCACTGCCTCCTCAGCATGCAGGAGGCTGCCCTGTAGGGAACCCCAGC
TCTGGGGCTTGGGGGTGAGGGTCAGCCCTGGACAGACCTCTGCCCAGGGAACTGCTCCAT
GGGGTCTGGGAGAGCAGCCATCCCCTGCTGGCACCATAGACCCACACAAGGAGCCTGCAC
AGCAAGCCAGCGGTGACACACCTGCAGGTGTCAGGCATGGCACTGGGCACAACAGGGACC
TGGCAGGAGAAACAGACCACAGAGAGGTCTGGAGTTGAGGCTGTTGTCAGCAAAGCCCCT
GGTCCCACACAGCTCTGCCCTAGAGCCACCTCTTTGACCCTTTACCCACCCTGAGACCAG
AACTTGCAGCCCCTCTGCAGATCTCCTCTGGCCACTGCAGCCCCTCCAATGGGCTTTTTC
TCTCATGCATTCCCTGGCCTGGAGGCGTCAGGGACCCCACATCCTCCCTGCTCCTCAGAC
TCACAGCCCCTCCATGTTACCTCCCGCACCTCCTCCCTGGGGCAGCTGCTCCCTGGGCCT
CTGAGGATGTCAGCTCCTGGCTCCCTGCCTCTCTCCCACTCCACTCCTGGCTCAGTCTTA
GAGATTTCTATGCCCTCATGGATTCTACCCCTGCCTTCCTGGCCTCTTGATTCTTGGCTT
GCCTCTCCTCCAATTCCAAACTTAGTGAAATGGCCTTAAGCATTTTAAACTGTATGTATA
CATTAGCGCATTCATGCCTTTCTAAACGCATTTCAAATGTCAACCAGGAAGGCACACCAC

FIGURE 2WW

TGTATTAGTTTTATACTGCCGCTGTAAAATTTACCACAAACTTAGTGACTTAACACAAAT
TTATTGCAATTCTGTAGGCTGGAAGTCTGACTATGGGTCTCACTGGACTAGAATCAAGGC
TGGCAGGCTGCCTTCCTTCCTGGAGGTTCTAGGGGAGACTCTGTCTCCTGCTCCTTCAGG
CTGCTGGCAGAATCCACATCCTTTCGGTGGCAGGGCCAAGGTCCCCACTTTCTTGCTGAC
TGTAAACTAAGGCCACTTCCAGCTTGTAGAGGCTGCCTACATTCCTTGGCTCTTGGCCCC
CTCCTCCATCTTCAGAGCTAGCAGGTTCAGTCTGTGTCACGAACCATTTCTCTGGTTCCC
TGCAGACAGGAAAGGTTGTCCCTAAGGACTCATGAGATTAGGTTGGGCCCAGCCAGATAA
TACATGATAATCTCCCTCCTCAAGGTTTTTAATATTAAACACATCTGCAGGACACATTTT
GCCATGTAAACTAACATTCACTGGTTCCAGGGATTAAGGAATGAACCTCTTTTGTTGGGG
AAGGGTGGCATTCTGCTGACCACAGCACTCCAACCAAAAGCCAAAAACCAAAGCAAGACT
TACTAACGCATATCAAATAAATTAAAGGTACAAAATCGTGAATCTCAGTTATCTTAAATA
T[illegible]ACTA[illegible]AATTATTCAAATTCTCACGC[illegible]TTCCAACTC[illegible]
CTAAAGTAATTTCCATATCCTAGATGGAAACCCTCATGCTAAACTGTCTGATTATGCATG
GTTCTAAATGGTTTCAGTGGCAAATACATAACATTGTACTACTGATTAAACTGAACTTAA
AAGC

SEQ ID NO: 62_AA103218_M SGK034_M
CCACGCGTCCGCACCAGAGTATGGCGAAGTCAATGATGGGACTGGCTTTGTGGACATCTT
CTCCTTCGGGATGTGTGCACTGGAGATGGCTGTACTCGAGATCCAAGCCAACGGGGATAC
CAGAGTCACAGAAGAGGCCATCGCTCGAGCCAGGCACTCACTGAGTGACCCCAACATGCG
GGAATTCATCCTCTCCTGCCTGGCCCGGGACCCTGCCCGCCGACCCTCAGCCCACAACCT
CCTCTTCCACCGAGTGCTCTTTGAGGTGCACTCGCTGAAGCTGCTGGCAGCTCACTGCTT
CATCCAGCACCAGTACCTCATGCCTGAGAATGTGGTAGAGGAAAAGACCAAGGCCATGGA
CCTCCATGCAGTTTTGGCTGAGATGCCGCAGCCCCATGGACCCCCAATGCAGTGGCGGTA
CTCAGAGGTCTCCTTCTTGGAGCTGGACAAATTCCTAGAGGATGTCAGGAACGGGATCTA
TCCACTGATGAACTTTGCGGCTGCTCGGCCCTTGGGGCTTCCCCGTGTGTTGGCCCCACC
CCCAGAGGAAGCCCAAAAGGCCAAAACTCCAACGCCAGAACCCTTTGACTCGGAGACCAG
GAAGGTGGTCCAGATGC[illegible]GTGCAACCTGGAAGAAG[illegible]GA[illegible]ACAACGCTCGGTG[illegible]ACCT
TACTCTGCTCTTGGTGCTTGAGGACCGGCTACATCGGCAGCTGACCTATGATCTGCTCCC
AACGGACAGTGCCCAGGACCTCGCTGCTGAACTAGTGCATTATGGCTTCCTGCACGAGGA
TGACAGGACAAAGCTAGCAGCCTTTCTGGAGACCACTTTTCTCAAGTACCGAGGGACGCA
AGCGTGACCTTCCCAGTCCTGACGGCCCAGCAGAGATACAGGGGCTCAGGGTTGTCCACT
TGGCAAAGAGCCCCCACACTGCTCAAAGCTGCCTTCTGCCTGTGTTCCCTGGAACTGAAC
ACAGGCCCTGCTAGTGAAGACACCCCCACCCCCCAGCTTTCTGCAGCAGTGTGGGACCCT
GGGGTGGTGATGGAGCCCTGAGCCTGGACGAGAGTGGATACAGGTCAGTTAGGGGAACCG
CTCCATCTGGTACTAGACAACAGCCATGCCTTCAGGTGGCATAGAAACCTAGGGAAGGAG
CCTGAACTCAGGTGTCACAGTGCTGGGCATCAGGCAGACCAGACCTGACCTGATTGGAGA
ACTGTAGACTAGATAGCTTGGAGTTGAACCCATGGCCAGGGAATTCCTTGGTCCTGCTCA
GACCAGTCCTGATCCCTTGCAGACCTGCCTTGAGCCCTCTTTCTGATCTTCCACACTCTT
GAGACCAGGACCTGTGTCCTCCCCAAAGCCCTTGGGAAGGATCTTTCTATTCATCATCCC
TCTGGCCTAGGGGCTCAGGGGTCAGGCATCCTCCACATTCCCTCCCTGGGGAAGTTGTGT
GTTTGAGTTGAGGATGTGGGTTCCTGGCTCCCTCTTTCTCCCCAGCCCAACTTGTCTCTT
TCTTACTGGTTTCAAAGTCCTGATGAACGCTTCCCCTCAGAGCCACCCTGGTTTCCTTGG
TTCTTGAACTGCCTCTCTCCCAACTTCAAACCAGGTCTTAAACGTTTTTTAAATGCATAT
ATAAATGTAATGCAGTCACGGTCCTTTTTAAACACTTTGTGTATGAAACCAGGAAAGCTC
ACTATTGTATTAGGAATAGTTCCACATTGCTGCTGTTAACAGATATCATAAACCCAGTGG
TTTGAGACGACACACACACACACACACACACACACACACACAGAGAGAGAGAGAGTTCTGTA
CATCAAGTGTGATCCAGGCTCTCACTAGATTAATACCCAGGCTAAGTTCCTTTCTGGAAG
CTGGGACTTACCTCCTGCTCCTTCAAGCTATTGGCAGAACTCACTTCCCTGCAATGGTAA
GGCAGAAATCCCTATTTTCTCAACAGCTGCCAACTAAGAACCCCTCTCAGCTTCTAGAGG

FIGURE 2XX

CCACCAACTTTTCTTAGTTCTTCTTTCTCCCCCCTCAAGACCAGCAGCGTCAAGTTGAAT
CTTTGTCCTGGGCTAGCTGACTGGCTTGCCACTGCTGGGAAGAGTTGGGGCCTTTTGTGA
GTAGGTTGGACCCACCAGGATAACCGAGGATGATCCCCTTCTCAGGGTCTATAGATGAAC
CACACCTGCGCAGTTCCTTCTGCTGTCATCCTGGGCTTTGGTGCTTGGAGAACAGCCGTG
GGCGGTGGGTGTTGTTACTGTGGTACCTACCATGCCATCTTAACCGAAACCAAGACCTAA
AATAAAACAGATTTGTCATGGGACATCTAATAAATTAAATGAACTCTG

SEQ ID NO: 63_NEK7_H, N34132_H
CACGAATCCGAGCCCGCTCGCCTCTCTCCAGCGAACCGACCATGTCTGGCGGCGCCGCAG
AGAAGCAGAGCAGCACTCCCGGTTCCCTGTTCCTCTCGCCGCCGGCTCCTGCCCCCAAGA
ACGGCTCCAGCTCCGATTCCTCCGTGGGGGAGAAACTGGAGCCCGCGGCCGCCGACGCTG
TG[illegible]CCGG[illegible]AGGA[illegible]GAGG[illegible]TACAGGCGC[illegible]GCCG[illegible]CCACACTATG[illegible]ACA[illegible]ACA[illegible]CCGT[illegible]
GGGCGGCCGCGACCACTACCACCACTGAGCACCGCTTCTTCCGCCGGAGCGTCATCTGCG
ACTCCAATGCCACTGCACTGGAGCTTCCCGGCCTTCCTCTTTCCCTGCCCCAGCCCAGCA
TCCCCGCGGCTGTCCCGCAGAGTGCTCCACCGGAGCCCCACCGGGAAGAGACCGTGACCG
CCACCGCCACTTCCCAGGTAGCCCAGCAGCCTCCAGCCGCTGCCGCCCCTGGGGAACAGG
CCGTCGCGGGCCCTGCCCCCTCGACTGTCCCCAGCAGTACCAGCAAAGACCGCCCAGTGT
CCCAGCCTAGCCTTGTGGGGAGCAAAGAGGAGCCGCCGCCGGCGAGAAGTGGCAGCGGCG
GCGGCAGCGCCAAGGAGCCACAGGAGGAACGGAGCCAGCAGCAGGATGATATCGAAGAGC
TGGAGACCAAGGCCGTGGGAATGTCTAACGATGGCCGCTTTCTCAAGTTTGACATCGAAA
TCGGCAGAGGCTCCTTTAAGACGGTCTACAAAGGTCTGGACACTGAAACCACCGTGGAAG
TCGCCTGGTGTGAACTGCAGGATCGAAAATTAACAAAGTCTGAGAGGCAGAGATTTAAAG
AAGAAGCTGAAATGTTAAAAGGTCTTCAGCATCCCAATATTGTTAGATTTTATGATTCCT
GGGAATCCACAGTAAAAGGAAAGAAGTGCATTGTTTTGGTGACTGAACTTATGACGTCTG
GAACACTTAAAACGTATCTGAAAAGGTTTAAAGTGATGAAGATCAAAGTTCTAAGAAGCT
GGTGCCGTCAGATCCTTAAAGGTCTTCAGTTTCTTCATACTCGAACTCCACTTATCATTC
ACCGCGATCTTAAATGTGACAACATCTTTATCACCGGCCCTACTGGCTCAGTCAAGATTG
[illegible]CTCGGTCTG[illegible]CAA[illegible]CTGAACCGG[illegible]TTTTG[illegible]AG[illegible]AGGTACCC
CAGAGTTCATGGCCCCTGAGATGTATGAGGAGAAATATGATCA[illegible]CCGTTGACGTTTATG
CTTTTGGGATGTGCATGCTTGAGATGGCTACATCTGAATATCCTTACTCGGAGTGCCAAA
ATGCTGCGCAGATCTACCGTCGCGTGACCAGTGGGGTGAAGCCAGCCAGTTTTGACAAAG
TAGCAATTCCTGAAGTGAAGGAAATTATTGAAGGATGCATACGACAAAACAAAGATGAAA
GATATTCCATCAAAGACCTTTTGAACCATGCCTTCTTCCAAGAGGAAACAGGAGTACGGG
TAGAATTAGCAGAAGAAGATGATGGAGAAAAAATAGCCATAAAATTATGGCTACGTATTG
AAGATATTAAGAAATTAAAGGGAAAATACAAAGATAATGAAGCTATTGAGTTTTGTTTTG
ATTTAGAGAGAGATGTCCCAGAAGATGTTGCACAAGAAATGGTAGAGTCTGGGTATGTCT
GTGAAGGTGATCACAAGACCATGGCTAAAGCTATCAAAGACAGAGTATCATTAATTAAGA
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GCAGTCTCAAACAGCAGGTAGAACAATCCAGTGCTTCCCAGACAGGAATCAAGCAGCTCC
CTTCTGCTAGCACCGGCATACCTACTGCTTCTACCACTTCAGCTTCAGTTTCTACACAAG
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TATCTGTGTTATCTGATGGGACGGTTGACAGTGGTCAGGGATCCTCTGTCTTCACAGAAT
CTCGAGTGAGCAGCCAACAGACAGTTTCATATGGGTTCCCAANNCATGAACAGGCACATT
CTACAGGCACAGTCCCAGGGCATATACCTTCTACTGTCCAAGCACAGTCTCAGCCCCATG
GGGTATATCCACCCTCAAGTGTGCAGCAGGGAATACAGCAGACAGCCCCTCCTCAACAGA
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AGGGAGTCTCTCAGGTTGCTCCTGCAGAGCCAGTTGCAGTAGCACAGCCCCAAGCTACCC
AGCCGACCACTTTGGCTTCCTCTGTAGACAGTGCACATTCAGATGTTGCTTCAGGTATGA
GTGATGGCAATGAGAACGTCCCATCTTCCAGTGGAAGGCATGAAGGAAGAACTACAAAAC

FIGURE 2YY

GGCATTACCGAAAATCTGTAAGGAGTCGCTCTCGACATGAAAAAACTTCACGCCCAAAAT
TAAGAATTTTGAATGTTTCAAATAAAGGAGACCGAGTAGTAGAATGTCAATTAGAGACTC
ATAATAGGAAAATGGTTACATTCAAATTTGACCTAGATGGTGACAACCCCGAGGAGATAG
CAACAATTATGGTGAACAATGACTTTATTCTAGCAATAGAGAGAGAGAGTCGTTTGTGGATC
AAGTGCGAGAAATTATTGAAAAAGCTGATGAAATGCTCAGTGAGGATGTCAGTGTGGAAC
CAGAGGGTGATCAGGGATTGGAGAGTCTACAAGGAAAGGATGACTATGGCTTTTCAGGTT
CTCAGAAATTGGAAGGAGAGTTCAAACAACCAATTCCTGCGTCTTCCATGCCACAGCAAA
TAGGCATTCCTACCAGTTCTTTAACTCAAGTTGTTCATTCTGCGGGAAGGCGGTTTATAG
TGAGTCCTGTGCCAGAAAGCCGATTACGAGAATCAAAAGTTTTCCCCAGTGAAATAACAG
ATACAGTTGCTGCCTCTACAGCTCAGAGCCCTGGAATGAACTTGTCTCACTCTGCATCAT
CCCTTAGTCTACAACAGGCCTTTTCTGAACTTAGACGTGCCCAAATGACAGAAGGACCCA
ATACAGCACCTCCAAACTTTAGTC[illegible]TAGTACCTC[illegible]TTCT
TAAGTAGCATTGCTGGAGTCCCAACCACAGCAGCAGCCACAGCACCAGTCCCTGCAACAA
GCAGCCCTCCTAATGACATTTCCACATCAGTAATTCAGTCTGAGGTTACAGTGCCCACTG
AAGAGGGGATTGCTGGAGTTGCCACCAGCACAGGTGTGGTAACTTCAGGTGGTCTCCCCA
TACCACCTGTGTCTGAATCACCAGTACTTTCCAGCGTAGTTTCAAGTATCACAATACCTG
CAGTTGTCTCAATATCTACTACATCCCCGTCACTTCAAGTCCCCACATCCACATCTGAGA
TCGTTGTTTCTAGTACAGCACTGTATCCTTCAGTAACAGTTTCAGCAACTTCAGCCTCTG
CAGGGGGCAGTACTGCTACCCCAGGTCCTAAGCCTCCAGCTGTAGTATCTCAGCAGGCAG
CAGGCAGCACTACTGTGGGAGCCACATTAACATCAGTTTCTACCACCACTTCATTCCCAA
GCACAGCTTCACAGCTGTCCATTCAGCTTAGCAGCAGTACTTCTACTCCTACTTTAGCTG
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ATATTTCTCAGCCTGGTGGGCTGCATCCTTTGGTCATTCCATCAGTGATAGCTTCTACTC
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TCCCACCCTTGGTACAGCCTGTTGCCAATGTGCCTGCTGTACAGCAGACACTAATTCATA
GTCAGCCTCAACCAGCTTTGCTTCCCAACCAGCCCCATACTCATTGTCCTGAAGTAGATT
[illegible]TACACAACCGGAAAGCCTCCTGCAATTGATGACAT[illegible]AAGC[illegible]GC
GGTCTCTGTTCAGTGAACACAGCTCATCTGGAGCTCAGCATGCCTCTGTCTCACTGGAGA
CCTCACTAGTCATAGAGAGCACTGTCACACCAGGCATCCCAACTACTGCTGTTGCACCAA
GCAAACTCCTGACTTCTACCACAAGTACTTGCTTACCACCAACCAATTTACCACTAGGAA
CAGTTGCTTTGCCAGTTACACCAGTGGTCACACCTGGGCAAGTTTCTACCCCAGTCAGCA
CTACTACATCAGGAGTGAAACCTGGAACTGCTCCCTCCAAGCCACCTCTAACTAAGGCTC
CGGTGCTGCCAGTGGGTACTGAACTTCCAGCAGGTACTCTACCCAGCGAGCAGCTGCCAC
CTTTTCCAGGACCTTCTCTAACCCAGTCCCAGCAACCTCTAGAGGATCTTGATGCTCAAT
TGAGAAGAACACTTAGTCCAGAGATGATCACAGTGACTTCTGCGGTTGGTCCTGTGTCCA
TGGCGGCTCCAACAGCAATCACAGAAGCAGGAACACAGCCTCAGAAGGGTGTTTCTCAAG
TCAAAGAAGGCCCTGTCCTAGCAACTAGTTCAGGAGCTGGTGTTTTTAAGATGGGACGAT
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CAAAGTCTGTTCATTTTGAATCCAGCACCTCAGAGTCCTCAGTGCTATCAAGTAGTAGTC
CAGAGAGTACCTTGGTGAAACCAGAGCCGAATGGCATAACCATCCCTGGTATCTCTTCAG
ATGTGCCAGAGAGTGCCCACAAAACTACTGCCTCAGAGGCAAAGTCAGACACTGGGCAGC
CTACCAAGGTTGGACGTTTTCAGGTGACAACTACAGCAAACAAAGTGGGTCGTTTCTCTG
TATCAAAAACTGAGGACAAGATCACTGACACAAAGAAAGAAGGACCAGTGGCATCTCCTC
CTTTTATGGATTTGGAACAAGCTGTTCTTCCTGCTGTGATACCAAAGAAAGAGAAGCCTG
AACTGTCAGAGCCTTCACATCTAAATGGGCCGTCTTCTGACCCGGAGGCCGCTTTTTTAA
GTAGGGATGTGGATGATGGTTCCGGTAGTCCACACTCGCCCCATCAGCTGAGCTCAAAGA
GCCTTCCTAGCCAGAATCTAAGTCAAAGCCTTAGTAATTCATTTAACTCCTCTTACATGA
GTAGCGACAATGAGTCAGATATCGAAGATGAAGACTTAAAGTTAGAGCTGCGACGACTAC
GAGATAAACATCTCAAAGAGATTCAGGACCTGCAGAGTCGCCAGAAGCATGAAATTGAAT

FIGURE 2ZZ

CTTTGTATACCAAACTGGGCAAGGTGCCCCCTGCTGTTATTATTCCCCCAGCTGCTCCCC
TTTCAGGGAGAAGACGACGACCCACTAAAAGCAAAGGCAGCAAATCTAGTCGAAGCAGTT
CCTTGGGGAATAAAAGCCCCCAGCTTTCAGGTAACCTGTCTGGTCAGAGTGCAGCTTCAG
TCTTGCACCCCCCAGCAGACCCTCCACCCTCCTGGCAACATCCCAGAGTCCGGGCAGAATC
AGCTGTTACAGCCCCTTAAGCCATCTCCCTCCAGTGACAACCTCTATTCAGCCTTCACCA
GTGATGGTGCCATTTCAGTACCAAGCCTTTCTGCTCCAGGTCAAGGTAATAAAGCAACCA
TCATCGTCCAAAAACAATAAAATGGAGATGTTGCCATACCTGGGACAAAAGCCTGTTAAG
GCGGGTTGGGAGACTAGCTGACCAGAACACAGCCTGTGTGTTGTACACTGAAGAATCTGG
GTGAAAAGGGAAGTGGAGTGATAATGAGAATCGGTGGGCTCACTGCTCCCATTAGGTGAA
ATTACTTTTTTTCAAGGAATTACAGTGAAAAGTTACATCTGTGTGGCCTATATGACTTGC
TCATTTGGGATTTGGAACTTAGGCTTTAATATTAGGCTGAGATTTCCTGGATGAAATTCT
AAGGTGTTTTAGCAGTTTCTGAAGCTAATACATTTTCTTAGCCATTGTAGAATTTTGTTA
CTTTTAAGTATGGGAGTGGCATACTAAAATGAATAACCTTACAATTCAGTTTTTTATCCA
TAATCTACTTTCCAAATATAGCTCTGTTTATTAGTGATTGCTGAAAAAATTCCCACAGAG
GAAAGAGCTTTTAGTCATATTAGAACAAGAATTGAAAAGACTTGGGCATCTGGGTGAGAA
GAATGAAAAAAATATAGGTACTGGCTTATGTGCCTTTGCCACAGTTTCACAGAAATTAGA
GATCAGTCTCTTCACAGGAAGAATGCACTTGATTGGTAAGGAGGGCAAACTAGCTAGCAT
TATTCGAACTAAGAAAAGCTTCCGCATTTTGCAGATGGGTAGAATTAAGACCTAATATTT
CATCTCTTACATATCTGACCTTCCCCCCAGAAGCTTGTTCTTCTGTGTGCCATCTTAGTG
CATTTCACCACTCCAGCCTCAAGTTTCTAACATCTTGTAGTTGTGTTCTGTCTCTTCTCC
TCTCTCTGTTCTACCCTGTTTTCCCCTCTCACAGGCTGTGCGAAGTTTAACTGTGCATC
TGAACAGGTGACATTCAAACCTGGTGGCAGGAGGACCCGATTTCTGAGTACGCCCTGCTT
GGCTCTTTGTGTGTAACACCTTTACTCCTTCCTTGTCCTTGTGTTTCTGCTGCTTGGATC
TGATGTTTCACGCAGTCCATTTTCATTTGTCTCTTTTTGTATATCATCTACTCAGTGGCT
TGGCTGAATTACTGTTACCCTCAGAAGTTTGGGCCCCCACATTAATTATGATAAAAAATG
TCAAAATAACAAGTTATCTACAAATTTCAATGTAACTTTCTGGTAGAAGTGCTTCTTCAT
GGATCTGTGACAGAGAGTGGATATGGTATCTAGGCAATAGATTGCTGGGTCATTTAGAAT
AATGAAGACTGAACTCCACAGTCGTAGTCAGTGCTCTCTGTCTGCCCTAGCATTAGAAAT
GAGAGAAATCAGCCAGACACGGTGGCGTACACCTGTAATCCCAGCACTTTGGGAGGCCGA
GGCGGGAAGATTGCTTGAGGCCAGGAGCTCGAGACCAACCCTGGGCAACATGGTGATACC
CCATCTCT

SEQ ID NO: 64_BCON3_H
GCGGAGCGCAGCTGTGAGGGAGTCGCTGTGATCCGGGGCCCCGGAACCCGAGCTGGAGCT
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GGGGGAGTCCCAGACAGTACTTAGCAGTGGCTCAGACCCAAAGGTAGAATCCTCATCTTC
AGCTCCTGGCCTGACATCAGTGTCACCTCCTGTGACCTCCACAACCTCAGCTGCTTCCCC
AGAGGAAGAAGAAGAAAGTGAAGATGAGTCTGAGATTTTGGAAGAGTCGCCCTGTGGGCG
CTGGCAGAAGAGGCGAGAAGAGGTGAATCAACGGAATGTACCAGGTATTGACAGTGCATA
CCTGGCCATGGATACAGAGGAAGGTGTAGAGGTTGTGTGGAATGAGGTACAGTTCTCTGA
ACGCAAGAACTACAAGCTGCAGGAGGAAAAGGTTCGTGCTGTGTTTGATAATCTGATTCA
ATTGGAGCATCTTAACATTGTTAAGTTTCACAAATATTGGGCTGACATTAAAGAGAACAA
GGCCAGGGTCATTTTTATCACAGAATACATGTCATCTGGGAGTCTGAAGCAATTTCTGAA
GAAGACCAAAAAGAACCACAAGACGATGAATGAAAAGGCATGGAAGCGTTGGTGCACACA
AATCCTCTCTGCCCTAAGCTACCTGCACTCCTGTGACCCCCCCATCATCCATGGGAACCT
GACCTGTGACACCATCTTCATCCAGCACAACGGACTCATCAAGATTGGCTCTGTGGCTCC
TGACACTATCAACAATCATGTGAAGACTTGTCGAGAAGAGCAGAAGAATCTACACTTCTT
TGCACCAGAGTATGGAGAAGTCACTAATGTGACAACAGCAGTGGACATCTACTCCTTTGG
CATGTGTGCACTGGAGATGGCAGTGCTGGAGATTCAGGGCAATGGAGAGTCCTCATATGT
GCCACAGGAAGCCATCAGCAGTGCCATCCAGCTTCTAGAAGACCCATTACAGAGGGAGTT

FIGURE 2AAA

CATTCAAAAGTGCCTGCAGTCTGAGCCTGCTCGCAGACCAACAGCCAGAGAACTTCTGTT
CCACCCAGCATTGTTTGAAGTGCCCTCGCTCAAACTCCTTGCGGCCCACTGCATTGTGGG
ACACCAACACATGATCCCAGAGAACGCTCTAGAGGAGATCACCAAAAACATGGATACTAG
TGCCGTACTGGCTGAAATCCCTGCAGGACCAGGAAGAGAACCAGTTCAGACTTTGTACTC
TCAGTCACCAGCTCTGGAATTAGATAAATTCCTTGAAGATGTCAGGAATGGGATCTATCC
TCTGACAGCCTTTGGGCTGCCTCGGCCCCAGCAGCCACAGCAGGAGGAGGTGACATCACC
TGTCGTGCCCCCCTCTGTCAAGACTCCGACACCTGAACCAGCTGAGGTGGAGACTCGCAA
GGTGGTGCTGATGCAGTGCAACATTGAGTCGGTGGAGGAGGGAGTCAAACACCACCTGAC
ACTTCTGCTGAAGTTGGAGGACAAACTGAACCGGCACCTGAGCTGTGACCTGATGCCAAA
TGAGAATATCCCCGAGTTGGCGGCTGAGCTGGTGCAGCTGGGCTTCATTAGTGAGGCTGA
CCAGAGCCGGTTGACTTCTCTGCTAGAAGAGACCTTGAACAAGTTCAATTTTCCCAGGAA
CAGTACCCTCAACTCAGCCGCTGTCACCGTCTCCTCTTAGAGCTCACTCGGGCCAGGCCT
TGATCTGCGCTGTGGCTGTCCCTGGACGTGCTGCAGCCCTCCTGTCCCTTCCCCCCAGTC
AGTATTACCCTGTGAAGCCCCTTCCCTCCTTTATTATTCAGGAGGGCTGGGGGGCTCCC
TGGTTCTGAGCATCATCCTTTCCCCTCCCCTCTCTTCCTCCCCTCTGCACTTTGTTTACT
TGTTTTGCACAGACGTGGGCCTGGGCCTTCTCAGCAGCCGCCTTCTAGTTGGGGGCTAGT
CGCTGATCTGCCGGCTCCCGCCCAGCCTGTGTGGAAAGGAGGCCCACGGGCACTAGGGGA
GCCGAATTCTACAATCCCGCTGGGGCGGCCGGGGCGGGAGAGAAAGGTGGTGCTGCAGTG
GTGGCCCTGGGGGGCCATTCGATTCGCCTCAGTTGCTGCTGTAATAAAAGTCTACTTTTT
GCT

SEQ ID NO: 65_AA711829_M
CTTAAGCAGTTTCTGAAGAAGACCAAAAAGAACCACAAGACTATGAATGAAAAGGCTTGG
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ATCATCCATGGGAACCTGACCTGTGACACCATCTTCATCCAGCACAACGGACTCATCAAG
ATTGGCTCTGTGGCTCCTGACACTATCAACAATCACGTGAAGACTTGCCGGGAAGAACAG
AAGAACCTACACTTTTTTGCACCAGAGTATGGAGAAGTCACAAACGTGACAACAGCAGTG
GAGTTCTACTCCTTTGGCATGTGTGCACTGGAGATGGCAGTGCTCG[illegible]
GGCGAGTCCTCATATGTGCCACAGGAAGCCATCAGCAGTGCCATCCAGCTACTAGAAGAC
TCATTACAGAGGGAGTTTATTCAAAAGTGCCTGCAGTCTGAGCCTGCTCGGAGACCAACA
GCCAGAGAACTTCTGTTCCACCCAGCACTGTTTGAAGTGCCCTCACTCAAGCTTCTTGCT
GCTCACTGTATCGTGGGGCACCAACACATGATCCCAGAGAACGCTCTAGAGGAGATCACC
AAGAACATGGATACCAGTGCTGTACTAGCTGAAATTCCCGCAGGGCCAGGACGAGAACCA
GTTCAGACTTTGTACTCTCAGTCACCAGCCCTAGAATTAGACAAATTCCTTGAAGATGTC
AGGAATGGGATCTACCCTCTGACAGCCTTTGGGCTACCTCGGCCTCAGCAGCCACAGCAG
GAGGAGGTGACATCACCTGTTGTGCCCCCCTCTGTCAAGACTCCAACTCCTGAGCCAGCT
GAAGTGGAGACACGAAAGGTGGTGCTGATGCAGTGCAACATCGAATCTGTGGAGGAGGGA
GTCAAACACCATCTAACACTTCTGCTGAAGCTGGAGGACAAATTGAACCGGCACCTGAGC
TGTGACCTGATGCCAAATGAGAGCATCCCGGACTTGGCAGCTGAGCTGGTGCAGCTGGGC
TTCATTAGTGAGGCTGATCAGAGCCGCCTGACTTCTCTGCTGGAGGAGACGCTCAACAAG
TTCAACTTCACCAGGAACAGTACACTCAACACAGCCACTGTCACCGTCTCCTCGTAGAGC
TCACTTGAGCCAGGCCCCTAGCCAGGCTGTGGCTGTCCCTGGGCATGCTGCAGTCCTCCT
GTCCCTTCTCCCCAGTCAGTATTACCCTTCGCGCCCATATTATTTAGGAGGGCTTTAGGG
GCTCCCTGGTTGAGTATCACCCTGCCCCTTCCCCTCTCTTCCTCCCCTCTGCACTTTGTT
TACTTGTTTTGCACAGACGTGGGCCTGGGCCTTCTCAGCAGCCACCTTCTAGCTGGGGGC
TAGTAGCTGACCTGCTGCCTCCTGCCCTACTTGTGTGGACAGGAGGCCCACGGGCACTGG
GGAAGCTGAGTTCTACAATCCCGCTGGGGCGCATGGGCAGGAGAGAAAGGTGGTGCTGCA
GGGGTGGCCCCCCGGGGGGGGCATTCGAATCACCTCAGTTGCTGCTGTAATAAAGTCTAC
TTTTTGCT

FIGURE 2BBB

SEQ ID NO: 66_AA099102_H
ATGTCATCATGTGTCTCTAGCCAGCCCAGCAGCAACCGGCCGCCCCCCAGGATGAGCTG
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TCATCCTTGAGCATCCACCTGGGCATGGAGTCCTTCATTGTGGTCACCGAGTGTGAGCCG
GGCTGTGCTGTGGACCTCGGCTTGGCGCGGGACCGGCCCCTGGAGGCCGATGGCCAAGAG
GTCCCCCTTGACACCTCCGGGTCCCAGGCCCGGCCCCACCTCTCCGGTCGCAAGCTGTCT
CTGCAAGAGCGGTCCCAGGGTGGGCTGGCAGCCGGTGGCAGCCTGGACATGAACGGACGC
TGCATCTGCCCGTCCCTGCCCTACTCACCCGTCAGCTCCCCGCAGTCCTCGCCTCGGCTG
CCCCGGCGGCCGACAGTGGAGTCTCACCACGTCTCCATCACGGGTATGCAGGACTGTGTG
CAGCTGAATCAGTATACCCTGAAGGATGAAATTGGAAAGGGCTCCTATGGTGTCGTCAAG
TTGGCCTACAATGAAAATGACAATACCTACTATGCAATGAAGGTGCTGTCCAAAAAGAAG
CTGATCCGGCAGGCCGCTTTTCCACGTCGCCCTCCACCCCGAGGCACCCGGCCAGCTCCT
GGAGGCTGCATCCAGCCCAGGGGCCCCATTGAGCAGGTGTACCAGGAAATTGCCATCCTC
AAGAAGCTGGACCACCCCAATGTGGTGAAGCTGGTGGAGGTCCTGGATGACCCCAATGAG
GACCATCTGTACATGGTGTTCGAACTGGTCAACCAAGGGCCCGTGATGGAAGTGCCCACC
CTCAAACCACTCTCTGAAGACCAGGCCCGTTTCTACTTCCAGGATCTGATCAAAGGCATC
GAGTACTTACACTACCAGAAGATCATCCACCGTGACATCAAACCTTCCAACCTCCTGGTC
GGAGAAGATGGGCACATCAAGATCGCTGACTTTGGTGTGAGCAATGAATTCAAGGGCAGT
GACGCGCTCCTCTCCAACTACGTGGGCACGCCCGCCTTCATGGCTCCCGAGTCGCTCTCT
GAGACCCGCAAGATCTTCTCTGGGAAGGCCAAGGATGTTTGGGCCATGGGTGTGACACTA
TACTGCTTTGTCTTTGGCCAGTGCCCATTCATGGACGAGCGGATCATGTGTTTACACAGT
AAGATCAAGAGTCAGGCCCTGGAATTTCCAGACCAGCCCGACATAGCTGAGGACTTGAAG
GACCTGATCACCCGTATGCTGGACAAGAACCCCGAGTCGAGGATCGTGGTGCCGGAAATC
AAGCTGCACCCCTGGGTCACGAGGCATGGGGCGGAGCCGTTGCCGTCGGAGGATGAGAAC
TGCACGCTGGTCGAAGTGACTGAAGAGGAGGTCGAGAACTCAGTCAAACACATTCCCAGC
TTGGCAACCGTGATCCTGGTGAAGACCATGATACGTAAACGCTCCTTTGGGAACCCATTC
GAGGGCAGCCGGCGGGAGGAACGCTCACTGTCAGCGCCTGGAAACTTGCTCACCAAAAAA
CCAACCAGGCAATGTGAGTCCCTGTCTGAGCTCAAGGAAGCAAGGCAG[illegible]
CCAGGGCACCGACCCGCCCCCCGTGGGGAGGAGGAAGTGCTCTTGTGAGAGGCAGTCCC
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CCGGAGGAGGCCATGGAGCCCGAGTAG

SEQ ID NO: 67_5R69_17_2_H
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GCCATCCAAGTGGCTGAGTGGAGGGACCCTGCTCAAGTGCAGCTGCAGTGGCCGGGGTTT
CCCTCAGGTAGGGATCGGGGCGCCTTGTCGCCGCCAGCCACGTGTGGCGTCCGGTACAGT
CAGCAGAGTGCAGGGTGCGGGCACCAGGAAAGGGGGCGCAGGGGAACTCCCGCGGGCCTC
GCGTTTGCAAACTTCTCGCCTGGGCAGGAGGCGGTCGTGGGAAAGAAGGTGGAAGAGCGA
GCTTTTTGGAACTGTGCACGGGACAGATTGGACGCACACCCCTCGGGAGGCGCGAAGGCA
TGGAAAATTTGAAGCATATTATCACCCTTGGCCAGGTCATCCACAAACGGTGTGAAGAGA
TGAAATACTGCAAGAAACAGTGCCGGCGCCTGGGCCACCGCGTCCTCGGCCTGATCAAGC
CTCTGGAGATGCTCCAGGACCAAGGAAAGAGGAGCGTGCCCTCTGAGAAGTTAACCACAG
CCATGAACCGCTTCAAGGCTGCCCTGGAGGAGGCTAATGGGGAGATAGAAAAGTTCAGCA
ATAGATCCAATATCTGCAGGTTTCTAACAGCAAGCCAGGACAAAATACTCTTCAAGGACG
TGAACAGGAAGCTGAGTGATGTCTGGAAGGAGCTCTCGCTGTTACTTCAGGTTGAGCAAC
GCATGCCTGTTTCACCCATAAGCCAAGGAGCGTCCTGGGCACAGGAAGATCAGCAGGATG
CAGACGAAGACAGGCGAGCTTTCCAGATGCTAAGAAGAGATAATGAAAAAATAGAAGCTT
CACTGAGACGATTAGAAATCAACATGAAAGAAATCAAGGAAACTTTGAGGCAGTGTAAGT
TATCATGTGCCCTGCTGTTTCTGATGGCCCCCAAACTAGAAGTCATCAGTTTACTGGGAC

FIGURE 2CCC

CCCAGCCTCCCGCTACCCCTGCATTTGTCCATTTTCTGTGCTGGATGGCTGGAAGCAGCC
CACAGGTTTGGGGATCCATTCATGGCTAGCCCAGGCTTCTGTCCATGGAATAACATGTGG
AGAGAGCTTCTTGACCAGTAAGATACCTTCTAGCAGCTGTCAAAGTACTTAAAAACCTCT
ATGAATAGAATCAAAGCTTCAGTTCAGTTGCTGAATTTCCAAGAAGAAATTCAAATCAAA
TTTAAAATGCCCACTCATTCATTCATTCAACAAAACTGTGAGTATCTGGTTTATGCCAGA
GGCCATGCAAAGAGGTAACTAAGATGCAGAGAAGGACACTGCCTTCCAGGAGCTCACGGG
GTGGAGGAGGAAAGAGGAAAGACAGACAGTGAACACACAACAGCAAGGTTACTGAGCTTG
AACTATGTCCCTAACTACTAGATCTGAAATGACTACGCCAGATGCCAGATGCTCAAGTGC
CAAGCTCTGGGTAACAGGAATAGACATCCTTCCAGGATGAGAGAGATGAGTCTGGATGAG
GGTTAAGGCTGGAGGGACAGGCGGGATTTGAAGAGGAGGGAAAGGAAGTGGATGACACAT
TCTGTTAACTGTCCAGCTGTGTCTCTACTGGTCACTCAGAGGCAGGCCAGCCGCTCCCTT
GGGCTGAGTCCATCAGAAGCCCCAGCCACCACCAGCTCTGGTTCATGTAGTAGAGCTTCC
CACTCACACATCACAAATATGCCACCTCCCTTAGGACCCCTTCCTCTGCTCATTGACTCT
TTTGTCTTCTTTCCTCTCGGGGGTGAGGTCAGATTTACCACCAAAATGCATGCAGGAGAT
CCCGCAAGAGCAAATCAAGGAGATCAAGAAGGAGCAGCTTTCAGGATCCCCGTGGATTCT
GCTAAGGGAAAATGAAGTCAGCACACTTTATAAAGGAGAATACCACAGAGCTCCAGTGGC
CATAAAAGTATTCAAAAAACTCCAGGCTGGCAGCATTGCAATAGTGAGGCAGACTTTCAA
TAAGGAGATCAAAACCATGAAGAAATTCGAATCTCCCAACATCCTGCGTATATTTGGGAT
TTGCATTGATGAAACAGTGACTCCGCCTCAATTCTCCATTGTCATGGAGTACTGTGAACT
CGGGACCCTGAGGGAGCTGTTGGATAGGGAAAAAGACCTCACACTTGGCAAGCGCATGGT
CCTAGTCCTGGGGGCAGCCCGAGGCCTATACCGGCTACACCATTCAGAAGCACCTGAACT
CCACGGAAAAATCAGAAGCTCAAACTTCCTGGTAACTCAAGGCTACCAAGTGAAGCTTGC
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AGAAAACGATTCCAGTCATACAGGACACATCCCACTCCAAATGATATTTCCAAAAACATA
CCTCTGACAGTAACTTTGATAGATGGTTTGTCAAATGTATCTTTCTGGGTATCCACACCT
CTTGGCAATGAAATTTGCAGCTCCTCCCTTCCATAAATGAAGTCTCTTTCCCCACCATTT
GAATCTGGGCTGGCACTGTGACTTGATTTGATCAATAGAATGTGGAAGAAGTGACTGTAT
GCCAGTTCCAAGCCTAGGTTTCAAGAGGCCTTATAAATGTCTGTTGGAACCTTACCCAGC
CATGGACATGTTGAGTGAGCATGCTGGAGAATGAGAGACCACATGAAGCAGAAACATGCT
TTCCTAGCTGAAGTCATACTAGCCCAACCAACATGGCAGCTAACACATGAATGAGGCCAA
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GAGCTAAATAAATTACTGTTGTCTTTT

SEQ ID NO: 68_H85811_H
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CGATGGCCCCCGTGTACGAAGGTATGGCCTCACATGTGCAAGTTTTCTCCCCTCACACCC
TTCAATCAAGTGCCTTCTGTAGTGTGAAGAAACTGAAAATAGAGCCGAGTTCCAACTGGG
ACATGACTGGGTACGGCTCCCACAGCAAAGTGTATAGCCAGAGCAAGAACATCCCCCTGT
CGCAGCCAGCCACCACAACCGTCAGCACCTCCTTGCCGGTCCCAAACCCAAGCCTACCTT
ACGAGCAGACCATCGTCTTCCCAGGAAGCACCGGGCACATCGTGGTCACCTCAGCAAGCA

FIGURE 2DDD

GCACTTCTGTCACCGGGCAAGTCCTCGGCGGACCACACAACCTAATGCGTCGAAGCACTG
TGAGCCTCCTTGATACCTACCAAAAATGTGGACTCAAGCGTAAGAGCGAGGAGATCGAGA
ACACAAGCAGCGTGCAGATCATCGAGGAGCATCCACCCATGATTCAGAATAATGCAAGCG
GGGCCACTGTCGCCACTGCCACCACGTCTACTGCCACCTCCAAAAACAGCGGCTCCAACA
GCGAGGGCGACTATCAGCTGGTGCAGCATGAGGTACTGTGCTCCATGACCAACACCTACG
AGGTCTTAGAGTTCTTGGGCCGAGGGACGTTTGGGCAAGTGGTCAAGTGCTGGAAACGGG
GCACCAATGAGATCGTAGCCATCAAGATCCTGAAGAACCACCCATCCTATGCCCGACAAG
GTCAGATTGAAGTGAGCATCCTGGCCCGGTTGAGCACGGAGAGTGCCGATGACTATAACT
TCGTCCGGGCCTACGAATGCTTCCAGCACAAGAACCACACGTGCTTGGTCTTCGAGATGT
TGGAGCAGAACCTCTATGACTTTCTGAAGCAAAACAAGTTTAGCCCCTTGCCCCTCAAAT
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ACAGAGTCAAGGTCATCGACTTTGGTTCAGCCAGCCACGTCTCCAAGGCTGTGTGCTCCA
CCTACTTGCAGTCCAGATATTACAGGGCCCCTGAGATCATCCTTGGTTTACCATTTTGTG
AGGCAATTGACATGTGGTCCCTGGGCTGTGTTATTGCAGAATTGTTCCTGGGTTGGCCGT
TATATCCAGGAGATTCGGAGTATGATCAGATTCGGTATATTTCACAAACACAGGGTTTGC
CTGCTGAATATTTATTAAGCGCCGGGACAAAGACAACTAGGTTTTTCAACCGTGACACGG
ACTCACCATATCCTTTGTGGAGACTGAAGACACCAGATGACCATGAAGCAGAGACAGGGA
TTAAGTCAAAAGAAGCAAGAAAGTACATTTTCAACTGTTTAGATGATATGGCCCAGGTGA
ACATGACGACAGATTTGGAAGGGAGCGACATGTTGGTAGAAAAGGCTGACCGGCGGGAGT
TCATTGACCTGTTGAAGAAGATGCTGACCATTGATGCTGACAAGAGAATCACTCCAATCG
AAACCCTGAACCATCCCTTTGTCACCATGACACACTTACTCGATTTTCCCCACAGCACAC
ACGTCAAATCATGTTTCCAGAACATGGAGATCTGCAAGCGTCGGGTGAATATGTATGACA
CGGTGAACCAGAGCAAAACCCCTTTCATCACGCACGTGGCCCCCAGCACGTCCACCAACC
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GGCCTGACCCGTTCCAGCAAGCTCTCATCGTGTGTCCCCCCGGCTTCCAAGGCTTGCAGG
CCTCTGCC[illegible]AGCAGGCTC[illegible]TACTCGCTGCGAATGGAAAATGCAGTTGGC[illegible]A
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TGGCCCACGTGATGCGGCAGCAGCCAACCAGCACCACCTCCTCCCGGAAGAGTAAGCAGC
ACCAGTCATCTGTGAGAAATGTCTCCACCTGTGAGGTGTCCTCCTCTCAGGCCATCAGCT
CCCCACAGCGATCCAAGCGTGTCAAGGAGAACACACCTCCCCGCTGTGCCATGGTGCACA
GTAGCCCGGCCTGCAGCACCTCGGTCACCTGTGGGTGGGGCGACGTGGCCTCCAGCACCA
CCCGGGAACGGCAGCGGCAGACAATTGTCATTCCCGACACTCCCAGCCCCACGGTCAGCG
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CTGTCTCCAAGCAAAGAAAAAACGTCATCAGCTGTGTCACAGTCCACGACTCCCCCTACT
CCGACTCCTCCAGCAACACCAGCCCCTACTCCGTGCAGCAGCGTGCTGGGCACAACAATG
CCAATGCCTTTGACACCAAGGGGAGCCTGGAGAATCACTGCACGGGGAACCCCCGAACCA
TCATCGTGCCACCCCTGAAAACCCAGGCCAGCGAAGTATTGGTGGAGTGTGATAGCCTGG
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CCTCCACCAGCGGTCACTCTTCAGGGAGCTCATCTGGAGCCATCACCTACCGGCAGCAGC
GGCCGGGCCCCCACTTCCAGCAGCAGCAGCCACTCAATCTCAGCCAGGCTCAGCAGCACA
TCACCACGGACCGCACTGGGAGCCACCGAAGGCAGCAGGCCTACATCACTCCCACCATGG
CCCAGGCTCCGTACTCCTTCCCGCACAACAGCCCCAGCCACGGCACTGTGCACCCGCATC
TGGCTGCAGCCGCTGCCGCTGCCCACCTCCCCACCCAGCCCCACCTCTACACCTACACTG
CGCCGGCGGCCCTGGGCTCCACCGGCACCGTGGCCCACCTGGTGGCCTCGCAAGGCTCTG

FIGURE 2EEE

CGCGCCACACCGTGCAGCACACTGCCTACCCAGCCAGCATCGTCCACCAGGTCCCCGTGA
GCATGGCCCCCGGGTCCTGCCCTCGCCCACCATCCACCCGAGTCAGTATCCAGCCCAAT
TTGCCCACCAGACCTACATCAGCGCCTCGCCAGCCTCCACCGTCTACACTGGATACCCAC
TGAGCCCCGCCAAGGTCAACCAGTACCCTTACATATAAACACTGGAGGGGAGGGAGGGAG
GGAGGGAGGGAGAGAATGGCCCGAGGGAGGAGGGAGAGAAGGAGGGAGGCGCTCCTGGGA
CCGTGGGCGCTGGCCTTTTATACTGAAGATGCCGCACACAAACAATGCAAACGGGGCAGG
GGCGGGGGGGGGGGGCAGAGGGCAGGGGACGGGTCGGGACACCAGTGAAACTTGAACC
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GGTGGGAAATCTATGGTTTTTATTTTAAAAAAG

SEQ ID NO: 69_DYRK3_H
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TATGACACCTTCATGATGATAGATGAAACCAAATGTCCCCCCTGTTCAAATGTACTCTGC
AATCCTTCTGAACCACCTCCACCCAGAAGACTAAATATGACCGCTGAGCAGTTTACAGGA
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GAGATATGCCCAGAGATGCATATGTGTATATTTTTATGATCTTACAAACCTGCAAATGGA
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FIGURE 2FFF

SEQ ID NO: 70_AA589241_M DYRK3_M
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ACGGGAGGGTGGTGCTTCTCGGGGGTCGCTCACGCAGGGGTAAAAAGCGAGGCCCGCCAG
GCAGCAAAGACTGGGCAACCGCACTGAAGGGCTGTGGTGACTACTTGTTCATAGAGTTTC
TGAAACGATGCCTCCAGTGGACCCCTCTGCCCGCCTCACCCCGGCTCAAGCATTAAGAC
ATCCTTGGATTAGCAAGTCTACACCCAAACCTCTCACCATGGACAAGGTGCCAGGGAAGC
GGGTAGTTAACCCTACAAATGCTTTCCAGGGACTGGGTTCCAAGCTGCCTCCAGTCGTTG
GGATAGCCAGTAAGCTTAAAGCTAACCTAATGTCCGAAACCAGTGGTAGTATACCTCTGT
GCAGTGTATTGCCAAAGCTGATTAGCTAGTGGACCACTCAGAGACTGATACATATCATAT
GTATTTTTAATTACCTTGCAAACATGCAAATGGAAAACGGAATAATTGAAGCCCATTCAC
TGATGGATATGTTTTTGTTAGACTTTTTTTAACAAGGCAGAACTTTTTTATATGACTAT
AAAAGAACGCTTCAAGGGCTAATGTCAAACCAGCTTGTATTGGCCATCTGGAGTATACAT
TAAATGACTTTTTCATAGGTC

SEQ ID NO: 71_5R72_16_2_H
GTCGAGGCGCAGCGCTGCCATGGCTGGGGGCCGTGGGGCCCCCGGGCGCGGCCGGGACGA
GCCTCCGGAGAGCTACCCGCAACGACAGGACCACGAGCTACAGGCCCTGGAGGCCATCTA
CGGCGCGGACTTCCAAGACCTGCGGCCGGACGCTTGCGGACCGGTCAAAGAGCCCCCTGA
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CAAGAAACACTGTGGGGAGGTGATGATCTTTGAACTGGCTTACCACGTGCAGTCATTTCT
CAGCGAGCATAACAAGCCCCCTCCCAAGTCTTTTCATGAAGAAATGCTGGAAAGGCGGGC
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AATCCTGCATGAGATTCAGAGAAGGAAAGAAGAGATAAAAGAAGAGAAAAAAAGGAAAGA
AATGGCTAAGCAGGAACGTTTGGAAATTGCTAGTTTGTCAAACCAAGATCATACCTCTAA
GAAGGACCCAGGAGGACACAGAACGGCTGCCATTCTACATGGAGGCTCTCCTGACTTTGT
AGGAAATGGTAAACATCGGGCAAACTCCTCAGGAAGGTCTAGGCGAGAACGTCAGTATTC
TGTATGTAATAGTGAAGATTCTCCTGGCTCTTGTGAAATTCTGTATTTCAATATGGGGAG
TCCTGATCAGCTCATGGTGCACAAAGGGAAATGTATTGGCAGTGATGAACAACTTGGAAA
ATTAGTCTACAATGCTTTGGAAACAGCCACTGGTGGCTTTGTCTTGTTGTATGAGTGGGT
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TAAGTGCAAAAAGCAGATTCAAGGAACAGAAACAGAATTCAACTCACTGGTAAAATTGAG
CCATCCAAATGTAGTACGCTACCTTGCAATGAATCTCAAAGAGCAAGACGACTCCATCGT
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AGGCCCCATCCCTGTGCATCAGCTTCGCAGGTACACAGCTCAGCTCCTGTCAGGCCTTGA
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CAAGGAGGATGTGTTTGAGCAAACCCGAGTTCGTTTTAGTGACAATGCTCTGCCTTATAA
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GAAACACAGCTTTATAAATCCCCAGCCAAAAATGCCTCTAGTGGAACAAAGTCCTGAAGA
TTCTGGAGGACAAGATTATGTTGAGACTGTTATTCCTAGCAACCGGCTACCCAGTGCTGC
CTTCTTTAGTGAGACACAGAGACAGTTTTCCCGATACTTCATTGAGTTTGAAGAATTACA
ACTTCTTGGTAAAGGAGCTTTTGGAGCTGTCATCAAGGTGCAGAACAAGTTGGACGGCTG
CTGCTACGCAGTGAAGCGCATCCCCATCAACCCGGCCAGCCGGCAGTTCCGCAGGATCAA
GGGCGAAGTGACACTGCTGTCACGGCTGCACCATGAGAACATTGTGCGCTACTACAACGC
CTGGATCGAGCGGCACGAGCGGCCGGCGGGACCGGGGACGCCGCCCCCGGACTCCGGGCC

FIGURE 2GGG

CCTGGCCAAGGATGACCGAGCTGCACGCGGGCAGCCGGCGAGCGACACAGACGGCCTGGA
CAGCGTAGAGGCCGCCGCGCCGCCACCCATCCTCAGCAGCTCGGTGGAGTGGAGCACTTC
GGGCGAGCGCTCGGCCAGTGCCCGTTTCCCCGCCACCGGCCCGGGCTCCAGCGATGACGA
GGACGACGACGAGGACGAGCACGGTGGCGTCTTCTCCCAGTCCTTCCTGCCTGCTTCAGA
TTCTGAAAGTGATATTATCTTTGACAATGAAGATGAGAACAGTAAAAGTCAGAATCAGGA
TGAAGATTGCAATGAAAAGAATGGCTGCCATGAAAGTGAGCCATCAGTGACGACTGAGGC
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TGACCAGGGACTGTATCGAGACACCGTCAGACTCTGGAGGCTTTTTCGAGAGATTCTGGA
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AGCCTTTTCTGCTGACAGCAAACAAGACGATCAGACAGGAGACTTGATTAAGTCAGACCC
TTCAGGTCACTTAACTGGGATGGTTGGCACTGCTCTCTATTTAAGCCCAG[illegible]
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TGAGATGTCCTATCACCCCATGGTCACGGCTTCAGAAAGGATCTTTGTTCTCAACCAACT
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GAAATCAGTCATCTCCTGGCTGTTGAACCACGATCCAGCAAAACGGCCCACAGCCACAGA
GCTGCTCAAGAGTGAGCTGCTGCCCCCACCCCAGATGGAGGAGTCAGAGCTGCATGAAGT
GCTGCACCACACGCTGACCAACGTGGATGGGAAGGCCTACCGCACCATGATGGCCCAGAT
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GCTGACGAGGAGAGAAGTGGAAGCTAAATTTTGTAATCTGTCTTTGTCTTCTAATAGTCT
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CCTAGAGGAGGTTGTTGGACTGTTGAAGAAACTCGGCATCAAGTTACAGGTCTTGATCAA
TTTGGGCTTGGTTTACAAGGTGCAGCAGCACAATGGAATCATCTTCCAGTTTGTGGCTTT
CATCAAACGAAGGCAAAGGGCTGTACCTGAAATCCTCGCAGCTGGAGGCAGATATGACCT
GCTGATTCCCCAGTTTAGAGGGCCACAAGCTCTGGGGCCAGTTCCCACTGCCATTGGGGT
CAGCATAGCTATAGACAAGATATCTGCTGCTGTCCTCAACATGGAGGAATCTGTTACAAT
AAGCTCTTGTGACCTCCTGGTTGTAAGTGTTGGTCAGATGTCTATGTCCAGGGCCATCAA
CCTAACCCAGAAACTCTGGACAGCAGGCATCACAGCAGAAATCATGTACGACTGGTCACA
GTCCCAAGAGGAATTACAAGAGTACTGCAGACATCATGAAATCACCTATGTGGCCCTTGT
CTCGGATAAAGAAGGAAGCCATGTCAAGGTTAAGTCTTTCGAGAAGGAAAGGCAGACAGA
GAAGCGTGTGCTGGAGACTGAACTTGTGGACCATGTACTGCAGAAACTGAGGACTAAAGT
CACTGATGAAAGGAATGGCAGAGAAGCTTCCGATAATCTTGCAGTGCAAAATCTGAAGGG
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GAGTGTGCTAGCCCCGGAGAAGCTGTCAGCCAGCACTAGGAGGCGCTATGAAACTCAGGT
ACAAACTCGACTTCAGACCTCCCTTGCCAACTTACATCAGAAAAGCAGTGAAATTGAAAT
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ATACCTCAAATTAGTCTGTGATGAAATTTATAACATCAAAGTAGAAAAAAAGGTGTCTGT
GCTATTTCTGTACAGCTATAGAGATGACTACTACAGAATCTTATTTTAACCCTAAAGAAC
TGTCGTTAACCTCATTCAAACAGACAGAGGCTTATACTGGAATAATGGAATGTTGTACAT

FIGURE 2HHH

TCATCATAATTTAAAATTAAATTCTAAGAAGAGGCTGGGTGCAGTGGCTCACACCTTTAA
TCCCAGCACTTTGGGAAGCCAAGGCAGGAAGACTGCTTGAAACCAGGAGTTTGAGACCAG
CCT

SEQ ID NO: 73_R43524_H, HRI_H
ATGCTGGGGGGCAACTCCGGGGTCCGCAAGCGCGAAGAGGAGGGCGACGGGGCTGGGGCT
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TCTGATGTTCCAGCAGAAATCCAGGTGTTAAAAGAACCCCTACAACAGCCAACCTTCCCT
TTTGCAGTTGCAAACCAACTCTTGCTGGTTTCTTTGCTGGAGCACTTGAGCCACGTGCAT
GAACCAAACCCACTTCGTTCAAGACAGGTGTTTAAGCTACTTTGCCAGACGTTTATCAAA
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AACAGAGCTATTAGCACACTTAATGAGGTCTGCTAAAGAGAGAGTTTGTCAGGATCCTTGT
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TCACGTTACTTAAATGAATTTGAAGAACTTGTCATCTTAGGAAAAGGTGGATACGGAAGA
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GGGAAGAGAACACCAACACATACGTCCAGAGTGGGTACTTGTCTGTACGCTTCACCCGAA
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CAGCACTTAACGAGAAGGAACTCATCGCAGAGACCATCTGCCATTCAGCTGCTGCAGAGT
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FIGURE 2III

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GCTTACTGCATGCCAGGCATTGGGCTGGGAATTTTTATATTGGATCTAAAATAACTCTTA
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FIGURE 2JJJ

GTCGACCTCTATGTCCTGGAGAAGGCCTTCCTCAGCACGCACCCCCACACCGAGACCGCG
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AAGTTAGATGAGGTGCGCCTGAGAGGGCGAAAGCGGTCCATGGTCGGGTAGTGGAGCTGT
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SEQ ID NO: 76_17000139801197_H, IRAKM_H
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FIGURE 2KKK

TACATCAGACAGGGAAGACTTTCCGTTAAAACTGATGTCTACAGCTTCGGAATCGTGATC
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FIGURE 2LLL

AGCACTGCTGTTAGATACCCCTCAGGCAGTGTGGCCCTCCCAAGCCAGTGGCTGCTCATT
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GACGACCCTGAAGCTGAGCAACTCACCGTAGTGGGAAGATTTCCTTCAATCCCAAGGAC
GTGCTGGGCCGCGGGGCAGGCGGACTTTCGTTTTCCGGGGACAGTTTGAGGGACGGGCA
GTGGCTGTCAAGCGGCTCCTCCGCGAGTGCTTTGGCCTGGTTCGGCGGGAAGTTCAACTG
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CAGTTCCACTACATTGCCCTGGAGCTCTGCCGGGCCTCCTTGCAGGAGTACGTAGAAAAC
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FIGURE 2MMM

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FIGURE 2NNN

ATAGCTGCTGATGGAGTATTGAAGATCTGTGACTTTGGTGCCTCTCGGTTCCATAACCAT
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TGA

SEQ ID NO: 83_AI375137_H
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FIGURE 2OOO

GGCAAATTTGAAGTTGCCAAGGAAATCATCCAAATATCAGGAACAGAAAGTCTGACTAAG
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FIGURE 2PPP

TTTACAGGATGTCTTGCTTCATCGTAAACCTAAACTGGGACAGGAACTGGGCCGGGGCCA
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FIGURE 2QQQ

CAGTCAATAAGAGACCCAGCATCTATCCCTCCTGAAGAGATGTCTCCAGAATTCACAACT
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FIGURE 2RRR

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FIGURE 2SSS

ACAGTCGACAGGTCAAGGCTGAGCTGGCCCGGAAGAAGCGCGAGGAGCGGCGGCGGGAGA
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SEQ ID NO: 89_AA599286_H
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FIGURE 2TTT

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TGTGTGGGGGACGCTTACATCAGGCGCCTGGCTGCCGAGGCCACGGAGTGGCAACAGGCA
GGGGCGCCGCCCCCCTCCCGCTCCATAGTCAGCACTGCCCCCCAGGAGGTCTTGACCGGT
AAGCTGTCCAAAAACAAGAGGAAGAAGATGAGGCGCAAACGGAAACAGCAGAAGCGGCTG
CTGGAGGAGCGGCTGCGGGACCTGCAGAGGCTGGAGGCCATGGAGGCTGCCACCCAGGCT
GAGGACTCTGGCTTGAGACTAGACGGGGGCAGCGGCTCCACATCCTCTTCAGGCTTCTCC
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CTGGAGCCCCAAAATGCAGATAAGATCAAGATCAAGATCGCAGACCTGGGCAACGCCTGC
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TCAGGCCGCTATTCCCGGGAGTTCTTCAACCGGAGAGGAGAGCTGCGGCACATCCACAAT
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AGCATGGAGGACTTTCTGCTCTCCAATGGGTACCAGCTGGGCAAGACCATTGGGGAAGGG
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FIGURE 2UUU

ACCGGGACCTTAAGTGTGAGAACGCCTTGTTGCAGGGCTTCAACCTGAAGCTGACCGACT
TTGGCTTTGCCAAGGTGCTACCCAAGTCACGCAGGGAGCTGAGCCAGACCTTCTGTGGCA
GCACAGCCTATGCCGCCCCTGAGGTGCTACAGGGCATACCCCATGATAGCAAGAAAGGTG
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CTCAAGGTGTTGGCCTTTGGATAGGAGGCTTCCAAGTAGTAAAGCTCCCTGCTCTCAGCA
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TGAAAGTCTTGCGGCACAAGTACCTCATCAACTTCTATCGGGCCATTGAGAGCACATCTC
GAGTATACATCATTCTGGAACTGGCTCAGGGTGGTGATGTCCTTGAATGGATCCAGCGCT
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TCCCAGCTAACCATACCATCTCCCAGGAGTGCAAGGTCCAACTGCTCATTGCCTGTGTGG
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TGCTCAAGTTCCAGCCTGAGCAACCCACCCATGAGATCAGGCTGCTTGAGGCCATGTGCC
AGCTCCACAACACCACTAAACAGCACCAATCCTTGCAAATTACGACCTGAAAATGGCTGA
GGGAGGGGGCTAAGAGAGGAGCAAAGCAGGAGGTCTTGGGCTAAAAATCTTTTTTACCAA
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CCTGCATGAGGACGTGGCACGCAAGATGTTCCGACAGCTCTCCTCCGCCGTCAAGTACTG
CCACGACCTGGACATCGTCCACCGGGACCTCAAGTGCGAGAACCTTCTCCTCGACAAGGA
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GCGCATCATCCTCAGCAAGACCTTCTGCGGGTCGGCAGCATATGCAGCCCCCGAGGTGCT
GCAGAGCATCCCCTACCAGCCCAAGGTGTATGACATCTGGAGCCTGGGCGTGATCCTGTA

FIGURE 2VVV

CATCATGGTCTGCGGCTCCATGCCCTATGACGACTCCGACATCAGGAAGATGCTGCGTAT
CCAGAAGGAGCACCGTGTGGACTTCCCGCGCTCCAAGAACCTGACCTGCGAGTGCAAGGA
CCTCATCTACCGCATGCTGCAGCCCGACGTCAGCCAGCGGCTCCACATCGATGAGATCCT
CAGCCACTCGTGGCTGCAGCCCCCCAAGCCCAAAGCCACGTCTTCTGCCTCCTTCAAGAG
GGAGGGGGAGGGCAAGTACCGCGCTGAGTGCAAACTGGACACCAAGACAGGCTTGAGGCC
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CGAGAACGAGAACAGGATGGAGGACAGGCTGGCCGAGACCTCCAGGGCCAAAGACCATCA
CATCTCCGGAGCTGAGGTGGGGAAAGCAAGCACCTAGCATGACAATGGCCCCGTTGTGTG
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TT

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GTGCTGCTGAGCCCGGACGAGCGCCGCGTCAAGCTCACCGACTTCGGCTTCGGCCGCCAG
GCCCATGGCTACCCAGACCTGAGCACCACCTACTGCGGCTCAGCCGCCTACGCGTCACCC
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GTGCTCTACGTCATGGTCACCGGGTGCATGCCCTTCGACGACTCGGACATCGCCGGCCTG
CCCCGGCGCCAGAAACGCGGCGTGCTCTATCCCGAAGGCCTCGAGCTGTCCGAGCGCTGC
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GTAGCGCGCAACTGCTGGCTGCGCGCCGGGGACTCCGGCTAG

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CTTGATATCCAGTCTCACAGACTGCTCACAACAGTCCACAAGGCTGGTGGGGAGTGCTTC
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TCTGAGCATCTCGGCCGATTGCCAGGACCTGCTCAAGAGGCTCCTGGAACCCGATATGAT
CCTCCGGCCTTCAATTGAAGAAGTTAGTTGGCATCCATGGCTAGCAAGCACTTGATAAAA
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FIGURE 2WWW

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CGTGCAGTTTGAGGAGTGCGTCCTGCAGCGCAATGGGTTAGCCCAGCGCATGAGTCACGG
CAACAAGAGCTCGCAGCTTTACCTGCGCCTGGTGGAGACCTCGCTGAAAGGAGAAAGGAT
CCTGGGTTATGCTGAGGAGCCCTGCTATCTCTGGTTTGTCATGGAGTTCTGTGAAGGTGG
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GCTACAGCTGACGAGCGCCATTGCCTTCCTGCACAAAAACCATATTGTGCACAGGGACCT
GAAGCCAGACAACATCCTCATCACAGAGCGGTCTGGCACCCCCATCCTCAAAGTGGCCGA
CTTTGGACTAAGCAAGGTCTGTGCTGGGCTGGCACCCCGAGGCAAAGAGGGCAATCAAGA
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CATGGCTCCTGAAGTCTGGGAGGGACACTACACAGCCAAGGCGGACATCTTTGCCCTGGG
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FIGURE 2XXX

AAGCAGCTCTTGAAAGACATGTTAGCTGCTAACCCACAGGACCGACCTGATGCTTTTGAA
CTTGAAACCCGAATGGACCAGGTCACATGTGCTGCTTAAACTCCAGGGCTGAACGTCTTG
GGTGTTTTTAAACTAGGTCGATCCTTCGGGACCCACAGTCTCATCGTGTCTCGGACAGGA
TGGCAGAGGGTACAGGTGGTGGTGATCTCCTGACAGCTGGACCTCCCACAATGTGAAGCT
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SEQ ID NO: 99_AA215311_H
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GAAACCTCGACCTTGAAGATGGTGAGTACCCAGCCAAAGTACGATCTAATACGGAGGTA
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GCAGTGAAGAAAATTCGATGTCACGCACCTGAAAATGTTGAACTAGCCCTTCGTGAGTTC
TGGGCACTAAGCAGTATCAAGAGCCAACATCCAAATGTGATTCACTTGGAGGAATGCATC
CTACAAAAGGATGGATGGTGCAAAAGATGTCCCACGGCTCTAATTCTTCCCTTTATTTA
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TTGTGGTTTGTGATGGATTTTTGTGACGGAGGAGATATGAATGAGTATCTGTTGTCCAGG
AAGCCCAATCGTAAAACTAACACCAGCTTCATGCTTCAGCTGAGCAGTGCCCTGGCTTTC
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CATGCAGTCATATGGCAGCAGGTTGGTGATT

SEQ ID NO: 100_AA018361_H
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GGGCAGCGGCACGTACGCCACGGTGTACAAGGCCTACGCCAAGAAGGACACTCGTGAAGT

FIGURE 2YYY

GGTAGCCATAAAGTGTGTAGCCAAGAAAAGTCTGAACAAGGCATCGGTGGAGAACCTCCT
CACGGAGATTGAGATCCTCAAGGGCATTCGACATCCCCACATTGTGCAGCTGAAAGACTT
TCAGTGGGACAGTGACAATATCTACCTCATCATGGAGTTTTGCGCAGGGGGCGACCTGTC
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ATTAGCTAGCGCCCTGCAATTCCTGCATGAACGGAATATCTCTCACCTGGATCTGAAGCC
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CCGAGACTGCCGGGACCTACTGCAGCGGCTCCTGGAGCGGGACCCCAGCCGTCGCATCTC
CTTCCAGGACTTCTTTGCGCACCCCTGGGTGGACCTGGAGCACATGCCCAGTGGGCACAG
TCTGGGGCGAGCAACCGCCCTGGTGGTGCAGGCTGTGAAGAAAGACCAGGAGGGGGATTC
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TGAAGTGGATGCCCAGCGGAAGGAGGCAATTAAGGCAAAGGTGGGGCAGTACGTGTCCCG
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CTCTGCCCGAGACCTGCTCAGAGAGATGGCCCGGGACAAGCCACGCCTCCTAGCTGCCCT
GGAAGTGGCTTCAGCTGCCATGGCCAAGGAGGAGGCCGCCGGCGGGGAGCAGGATGCCCT
GGACCTGTACCAGCACAGCCTGGGGGAGCTACTGCTGTTGCTGCGGAGCCCCCGGGCCGG
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GAGCAGATGAGGGAATCTCGCTGGGAAGCTGACACCCTGGACAAAGAGGGACTGTCGGAA
TCTGTTCGTAGCTCTTGCACCCTTCAGTGACCCTAGAAGAATGATTGGACAGATGTGAGC
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CCCTGGCGAGCAGGCTTCTTGGATGGACAGTGCTGAGACCCCCATATCCCAGAGTCCCCA
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CCCTCTGGGCCCCACACTAGCCACAGCGCGGGCCTTGTGCTGGAGTTTGAGCCTGGGACA
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SEQ ID NO: 101_AA311714_H
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GAAAACCTCCCAGAAGATGTTGTGAGAGAATTTGGAATTGACCTGATTAGTGGATTACAT
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FIGURE 2ZZZ

GGGCCTGGCACACTGAAGTTTAGCAACTTTTGCTTGGCAAAAGTGGAAGGTGAAAATTTG
GAAGAGTTCTTTGCTTTGGTGGCAGCAGAGGAAGGAGGAGGTGATAATGGGGAAAATGTC
CTGAAGAAAAGCATGAAAAGTAGAGTCAAAGGATCTCCTGTATATACAGCACCAGAAGTT
GTGAGGGGTGCTGACTTTTCCATCTCCAGTGACCTCTGGTCTTTGGGCTGTCTGCTTTAT
GAAATGTTTTCAGGAAAACCTCCATTCTTCTCAGAAAGTGTTTCAGAATTAACTGAAAAG
ATCTTATGTGAAGATCCTTTGCCACCTATTCCGAAAGATTCTTCTCGTCCTAAAGCTTCT
TCAGATTTTATTAATTTGCTTGATGGGTTACTTCAAAGAGATCCTCAGAAAAGATTGACT
TGGACAAGGCTACTGCAGCATTCATTTTGGAAGAAAGCTTTTGCTGGAGCAGATCAGGAA
TCAAGCGTCGAAGATCTCAGTCTCAGCAGAAACACTATGGAGTGTTCTGGGCCACAAGAT
TCCAAGGAGCTTTTGCAGAACTCTCAGAGTAGACAAGCAAAAGGGCACAAGAGTGGTCAA
CCACTAGGTCACTCTTTCAGACTAGAAAATCCAACTGA[illegible]CCTAAGAGTACTCTT
GAGGGTCAATTGAATGAATCCATGTTTCTTCTCAGTTCTCGTCCTACTCCCAGAACTAGC
ACTGCAGTGGAAGTAAGTCCTGGTGAGGATATGACTCACTGTTCACCACAGAAGACTTCT
CCTCTGACCAAGATTACAAGTGGACACCTGAGTCAGCAGGACCTGGAATCCCAGATGAGA
GAGCTTATCTACACGGACTCAGATCTTGTTGTCACCCCCATTATCGACAATCCAAAGATA
ATGAAACAGCCACCAGTTAAATTTGATGCAAAAATATTGCATCTACCAACATATTCAGTG
GATAAGTTATTATTTCTGAAAGATCAAGATTGGAATGACTTTTTGCAACAAGTGTGCTCG
CAGATCGACTCCACTGAGAAGAGCATGGGGGCCTCCCGAGCCAAGCTGAATCTCCTTTGC
TATTTGTGCGTGGTGGCTGGTCACCAGGAGGTGGCCACCAGGCTCCTCCATTCCCCCCTG
TTCCAATTGCTAATCCAGCATTTGCGGATAGCTCCAAACTGGGATATACGGCCAAGGTT
GCTCACGTGATTGGTTTACTGGCTTCGCACACAACTGAGCTCCAGGAAAATACACCTGTT
GTTGAGACTACAAGCTCCATTGGAATCGGGATTTTGAACTGTCTTGTTCAACACTCCACT
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AAACTGTATCAGCATT

SEQ ID NO: 102_SGK384_H
TCTTTGGCCCACGTGCTGAGGGCGCGGCAGATCCTGACGGAGCCAGAAGTGCGCGACTAC
CTGCGG[illegible]CCTGGTCAGCGGCCTGCGCTACCTGCACCAGCGG[illegible]GCATCCTGCA[illegible]

SEQ ID NO: 103_AA210451_M SGK384_M
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GGTTGTGAGCTGCCATGTTGAACCAAGCAGGTCACTGAGGGACACAGGCATGTGGATGGA
AACCCTGCTGGGAGAAAAAAGAAACTGCTGAAGGGACTGACATGGGACAGCAACATGGAA
CCAGGAATGGTCTCACGCATAGAGAGCTCCCCCGGGGCGTGGGGCTGCTGCTCGCCATGG
CCCTTATGAACGTGGCGCTCTACCTCTGCCTTGATCAGCTTTTCATCTCCCCTGGACGAT
CCACCGCGGACTCTAGGCGCTGTCCTCCGGGCTACTTCAGAATGGGGCGGATGAGAAACT
GCTCACGCTGGCTGTCCTGTGAAGAGCTGAGGACAGAAGTCAGGCAGCTGAAGCGCGTTG
GGGAGGGAGCCGTGAAGAGAGTCTTTCTGTCTGAATGGAAGGAACACAAAGTCGCTCTCT
CCCGGCTCACCAGGCTGGAGATGAAGGAGGACTTCCTGCATGGGCTGCAGATGCTGAAGT
CTCTACAGAGTGAGCACGTGGTCACGCTGGTGGGCTACTGTGAGGAAGATGGCACTATTC
TCACCGAATATCACCCCTTAGGTTCCTTGAGCAACCTGGAAGAAACACTAAACCTTTCAA
AGTACCAAGACGTGAACACTTGGCAGCACAGGCTGCAGCTGGCCATGGAGTACGTCAGCA
TCATTAACTATCTGCATCACAGCCCCCTGGGCACGAGGGTCATGTGTGACTCTAACGACC
TGCCCAAAACATTGTCCCAGTACCTGCTAACAAGTAACTTCAGCATTGTGGCAAACGACC
TGGACGCTCTGCCCCTGGTAGACCATGACTCTGGGGTACTTATAAAGTGTGGCCACAGAG
AGCTCCATGGGGATTTTGTGGCTCCAGAGCAGCTGTGGCCCTACGGAGAAGACACGCCCT
TCCAAGACGATCTCATGCCTTCCTACAATGAGAAGGTTGACATCTGGAAGATTCCAGATG
TCTCCAGTTTCCTCTTGGGGCACGTGGAAGGGAGTGATATGGTTAGATTCCATTTGTTTG
ATATCCATAAGGCGTGCAAGAGCCAGATCCCGGCAGAAAGACCCACTGCTCAGAACGTGC

FIGURE 2AAAA

TAGACGCTTACCAGAGGGTTTTCCATTCACTCCGAGACACTGTGATGTCGCAGACGAAAG
AAATGCTGTAAAAATGAGCCATCGAGTGACGTGCTTGATGGCTGAATGGCATCCCAGCTG
TTCCGCTCTTGATGATGGAAGAGCTTTGCATGGATGGATGTTGACCCTGGCTGTTCAGCC
ACGTAGGCCTCCTCTACGTCTGCCTGCATGTTTGAGTGTTCTGCTCTCCTGGCAGCCCGG
ATGGAAGCTGCCAAGCGAGAAAGCCTGGCTTCAGGATGCTCCCTGGTGAAGATGCAGAGG
ATTCTGGATCTGCATAGTTTCAAGGGAGTGATCAAACGGTGACCTTGAAGACATGCTGCC
TGCCTTGGTAACTTTTTATAGACTAGTAGGAAACAGAAATCTTTTGGGGGAGGGGGGGAC
AACCCACTAGTTCCTCAGAGACAATTTCTTCTCATTCAGAAAGCCCTGTTGGAAGCTGGG
GATGTTTTAACTCCGTGGCAGGGCACTTGCCTAGTTGTGTGCAAAGCCTTGGATCTGACC
CATGGCATGTGCACACACACAAATGCTCAAAGAAAATCCCAGACGCCAGAAGTGTGCCCC
TTTCTTGTCAATAAGGTCATTGTCAGTACCGGAGATGATTTTTTTTATGAAGCCTTTATG
CTGACTCGTGTCACTGAGCCAAGTGTGCATGGTCGTTAGCTACTTTGTGGGTTCTTCTTT
CTTTCTACCCTACTTCTTCCCTTTCCACCCCCTAACACTAGATAGGAGAGAGGAGAGAGA
AAGGAAAGTGGGCACTGTTATATTGTTGGACGACTTCTTGCTGATTAAGGGGTGTCGAGT
TCCTTGGAGCAATGATCTTTGCTGCCAAGATATCTCATTTCTTCTTGTTTCTTCTTCGCC
CACGACCACTTCACAAACACCGACCAACAGCAAACAACAACCCACCCCGCTTCTCGGGGG
CCCTAGCACTTATGTACTTCTGAAAAGTCCCCAGAAATTCCAATCATCACACACTCAGAG
AAACTGTCTGCTGCTGGCAAAACTACACCCCTGCTAGAGCATGAGGCAAATCATAGTCAG
CTGCTGTGGACAGTCTGAAGCAGCCTGGCATCCCACACCTGAGATTAAAACAAAAACATT
CTTACCTGTGTTTTGTTTTTGTTTTAAGAAACCAAAGTGCACCAAGATAGCATGCTCTTG
AGATTGTGGCTGTCTAGAGATTTTTGGAACAGCAAGTTGAAGGAACTTTCTTACCTGCCT
TGAATGGTGCTTTGAACTTCCTGCTGACCTGGAGTTTCTGTGTGAATATTTCTATCCAGT
GTCCCCCTGTACCGGAAAGTACAAAGTCTGCTCTGGGCTTGCATGCCTGAACACTTTAAA
ACACTGTGGAGCCAGGAATAATGGTACCCACCTGTAATCCCAGCACCTGGGAGACAGGAG
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SEQ ID NO: 104_SGK071_2_H
GAGGTGGTGGCTGTGCAGATGATGGTGGAATGCATGGATGACCATTACGCCAGTCAGGCC
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CTGTTCATCACGTGGAATGGGGAGATCTCTTCTCTGTACCTCTGCCTGGTGATGGAGTTC
AATGAGCTCAGCTTCCAGGAGGTCATTGAGGATAAGAGGAAGGCAAAGAAAATCATTGAC
TCTGAGTGGATGCAGAATGTGCTGGGCCAGGTGCTGGACGCGCTGGAATACCTGCACCAT
TTGGACATCATCCACAGGAATCTCAAACCCTCCAACATCATCCTCATCAGCAGTGACCAC
TGCAAACTGCAGGACCTGAGTTCCAATGTGCTAATGACAGACAAAGCCAAATGGAATATT
CGTGCGGAGGAAGACCCCTTTCGTAAGTCCTGGATGGCCCCTGAAGCCCTCAACTTCTCC
TTCAGCCAGAAATCAGACATCTGGTCCCTGGGCTGCATCATTCTGGACATGACCAGCTGC
TCCTTCATGGATGGCACAGAAGCCATGCATCTGCGGAAGTCCCTCCGCCAGAGCCCAGGC
AGCCTGAAGGCCGTCCTGAAGACAATGGAGGAGAAGCAGATCCCGGATGTGGAAACCTTC
AGGAATCTTCTGCCCTTGATGCTCCAGATCGACCCCTCGGATCGAATAACGATAAAGGAC
GTGGTGCACATCACCTTCTTGAGAGGCTCCTTCAAGTCCTCGTGCGTCTCTCTGACCCTG
CACCGGCAGATGGTGCCTGCGTCCATCACCGACATGCTGTTAGAAGGCAACGTGGCCAGC
ATTTTAGGTGATGCTGGGGACACAAAGGGGGAGCGTGCCCTGAAGCTCCTGTCCATGGCC
TTGGCATCCTATTGTTTAGTTCCAGAGGGTTCATTATTTATGCCCCTGGCCTTGCTCCAC
ATGCACGACCAGTGGCTCAGCTGTGACCAGGACAGAGTCCCTGGGAAGAGAGACTTTGCC
TCCCTGGGGAAACTAGGGAAGCTGTTGGGCCCCATCCCAAAGGGTCTGCCGTGGCCCCCG
GAGCTGGTGGAGGTGGTGGTCACGACCATGGAGCTACATGACAGGGTCCTCGATGTCCAG
CTGTGTGCCTGCTCCCTGCTGCTGCACCTCCTGGGCCAAGCGCTGGTGCACCACCCGGAA
GCCAAGGCTCCCTGCAACCAAGCCATCACCTCCACCCTGCTGAGTGCTCTTCAGAGCCAC
CCCGAGGAGGAGCCACTTCTTGTCATGGTCTACAGCCTGCTAGCCATCACCACAACCCAG

FIGURE 2BBBB

GAGTCAGAGTCACTGTCAGAGGAGCTGCAGAACGCTGGGCTGCTGGAGCACATCCTGGAG
CACCTCAACAGCTCCCTCGAAAGCAGGGACGTCTGCGCCAGCGGCCTGGGCCTGCTCTGG
GCCCTCCTGCTGGACGACCCCATCTTGGCACTCCAGCGCCCCAGGAAAAAGAGAGCTCCA
AACCACGGAAAGCCCGGGAAACCCAAGAACCCTGCCAGCACCCAAAGTATCATTGTGAAC
AAGGCCCCCTTGGAGAAGGTCCCGGACCTCATCAGCCAGGTGTTGGCCACCTACCCTGCG
GATGGGGAAATGGCAGAAGCCAGCTGCGGAGTCTTCTGGCTGCTGTCCCTGCTGGGCTGC
ATCAAGGAGCAGCAGTTTGAACAAGTGGTGGCGCTGCTCCTGCAAAGCATCCGGCTGTGC
CAGGACAGAGCCCTGCTGGTGAACAATGCCTACCGGGGACTGGCCAGCCTGGTGAAGGTG
TCAGAGCTGGCGGCCTTCAAGGTGGTGGTGCAGGAGGAGGGCGGCAGTGGCCTCAGCCTC
ATCAAGGAGACCTACCAGCTCCACAGGGACGACCCGGAGGTGGTGGAGAACGTGGGCATG
CTGCTGGTCCACCTGGCTTCCTATGAGGAGATCCTGCCGGAGCTGGTGTCCAGTAGTATG
AAGGCCCTGCTCCAGGAGATCAAGGACCGCTTCACCTCCAGCCTGGTGAGTGACAGCAGC
GCCTTCAGCAAACCAGGCCTCCCTCCAGGTGGAAGCCCCCAGCTGGGGTGCACCACGTCT
GGGGGACTGGAATAG

SEQ ID NO: 105_AA118352_M SGK071_M
CAGAAGAAGACCCCTGCCAGAAGTCCTGGATGGCTCCTGAAGCTCTCAAATTCTCCTTCT
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TCCTGAACGACACAGAAGCCATGCAACTGCGGAAGGCCATCCGCCATCATCCAGGCAGCC
TGAAGCCCATCCTGAAAACCATGGAGGAGAAGCAAATCCCTGGTACAGATGTCTACTATT
TGCTTCTGCCCTTCATGTTGCATATCAACCCCTCCGATCGACTGGCAATCAAGGATGTGA
TGCAAGTCACCTTCATGAGCAACTCCTTCAAAAGCTCCTCTGTTGCGCTGAATATGCAGC
GGCAGAAGGTCCCCATCTTCATCACTGACGTGCTGCTTGAAGGCAACATGGCCAACATCT
TAGGCAGCTGGCTGTGTGCTTCCTTTGTGAACGACAGCAGGCACTGTGACTCAGGGATTG
GCTCGCAGAGACTTGGGTTTGATTTTCAGTCAGTCTCTTGGACAGAGCACCCTCTGAAAG
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TCAGCAGCATAAAGCAGCCTGGGCGGATCCTGGATATTCTGCTCAGCACCTGCTCCGTG
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GTTTGATCATCTCCTTCCTGATGGATACCTTGCGGAGCCATCCTAACTCTGAAAGGCTTG
TTAATGTGGTCTACAACGTGCTTGCCATTATTTCCAGCCAAGGACAGATCTCAGAAGAGC
TGGAAGAGGAGGGGTTGTTTCAGCTTGCCCAAGAGAACCTGGAGCACTTCCAAGAGGACA
GGGACATCTGCCTCTCTATCCTGAGCCTGCTCTGGTCCCTCCTGGTAGATGTTGTCACTG
TGGACAAAGAGCCCTTGGAGCAGCTCTCTGGCATGGTCACCTGGGTGCTGGCTACTCATC
CGGAGGACGTGGAAATAGCAGAGGCTGGCTGTGCGGTGCTCTGGCTGCTGTCCTTGTTGG
GCTGCATAAAGGAGAGTCAGTTTGAGCAGGTGGTAGTGCTGCTCCTGAGAAGCATCCAGC
TGTGCCCTGGCAGAGTACTGCTGGTGAACAATGCATTCCGTGGCTTGGCCAGCCTCGCAA
AGGTGTCCGAACTGGTGGCCTTCCGAATAGTAGTACTGGAAGAGGGCAGCAGCGGCCTCC
ACCTCATCCAAGATATCTACAAGCTCTACAAGGATGACCCTGAGGTGGTGGAGAACCTCT
GCATGCTGTTGGCCCATCTGACCTCCTACAAGGAGATCCTGCCAGAGATGGAGTCTGGAG
GCATCAAAGACCTAGTCCAGGTGATCCGGGGGCGCTTTACCTCCAGCCTGGAGCTGATTT
CTTACGCTGATGAGATACTCCAGGTACTGGAAGCAAATGCACAACCTGGCCTCCAGGAGG
ATCAGCTTGAGCCTCCTGCAGGGCAGGAAGCCCCACTGCAGGGAGAGCCCCTCTTCAGGC
CCTGACATGCTGCCCTTCTGGTCCTGTGGTAAGAGAAAGTATCACTAGGTCCAGTATTAA
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SEQ ID NO: 106_018653.9_H
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GCGGAGCCGCCTCGGAGCCTGAGCCGCCCGGGGCCGGGGCCGGGGAGCCGCGCGGGGCCG
GCCGGCCGGGGGGAGGGGAGCGATGCGGCGCCGGCGGGCGGCAGTGGCCGCGGGTTTCTG

FIGURE 2CCCC

CGCCTCCTTCCTGCTGGGCTCCGTCCTCAACGTGCTCTTCGCTCCGGGTCGGAGCCTCCG
AGGCCAGGCCAGTCCCCTGAGCCTTCGCCGGCCCCGGGTGCGGGCCGTCGCGGGGGCCGC
GGGGAGCTGGCCCGGCAGATCCGGGCGCGCTACGAGGAGGTGCAGCGCTATTCCCGCGGG
GGCCCCGGGCCCGGGGCGGGCCGGCCGGAGCGGCGGCGCCTGATGGACCTGGCTCCGGGC
GGGCCCGGCCTGCCGCGCCCCCGGCCCCCTTGGGCCCGGCCCCTGTCCGACGGCGCCCCA
GGCTGGCCCCCGGCTCCCGGCCCAGGCTCCCCCGGCCCGGGCCCGCGCCTGGGCTGCGCC
GCGCTTCGCAACGTGTCCGGCGCGCAGTACATGGGCTCAGGCTACACCAAGGCCGTGTAC
CGGGTCCGCCTGCCCGGCGGTGCCGCGGTGGCGCTCAAGGCGGTGGACTTTAGCGGCCAC
GATCTGGGCAGCTGCGTGCGCGAGTTCGGGGTACGGAGGGGCTGCTATCGGCTGGCGGCC
CACAAGCTGCTTAAGGAGATGGTGCTGCTGGAGCGGCTGCGGCACCCCAACGTGCTGCAG
CTCTATGGCTACTGCTACCAGGACAGCGAGGACATCCCAGACACCCTGACCACCATCACG
GAGCTGGGCGCCCCTCTAGAAATGATCCAGCTGCTGCAAACTT[illegible]TTC
CGAATCTGCCTGAGCCTGGGCCGCCTCCTCCACCACCTGGCCCACTCCCCACTGGGCTCC
GTCACTCTGCTGGACTTCCGCCCTCGGCAGTTTGTGCTGGTGGATGGGGAGCTCAAAGTG
ACGGACCTGGATGACGCACGTGTGGAGGAGACGCCGTGTGCAGGCAGCACCGACTGCATA
CTCGAGTTTCCGGCCAGGAACTTCACCCTGCCCTGCTCAGCCCAGGGCTGGTGCGAGGGC
ATGAACGAGAAGCGGAACCTCTATAATGCCTACAGGTTTTTCTTCACATACCTCCTGCCT
CACAGTGCCCCGCCTTCACTGCGTCCTCTGCTGGACAGCATCGTCAACGCCACAGGAGAG
CTCGCCTGGGGGGTGGACGAGACCCTGGCCCAGCTGGAGAAGGTGCTGCACCTGTACCGG
AGCGGGCAGTATCTGCAGAACTCCACGGCAAGCAGCAGTACCGAGTACCAGTGTATCCCA
GACAGCACCATCCCCCAGGAAGACTACCGCTGCTGGCCATCCTACCACCACGGGAGCTGC
CTCCTTTCAGTGTTCAACCTGGCTGAGGCTGTGGATGTCTGTGAGAGCCATGCCCAGTGT
CGGGCCTTTGTGGTCACCAACCAGACCACCTGGACAGGTCGGCAGCTGGTCTTTTTCAAG
ACTGGATGGAGCCAAGTGGTCCCTGATCCCAACAAGACCACATATGTGAAGGCCTCTGGC
TGACCTATCTGAGGGCTCGGCTGACCAGCTGACTATCCTCAGCAGCTGGGCTTGCCTGTG
GAGGGAGTGACTTGCACTGGCAGCACTGCATGTCACCTGGGAACCCCTGCAGACAAAGCT
AACATCCCAGACAGACAGATGTGACCAGGACAAACGTGCAATAATGCCAAATGTTAAAAT
GTGAGTTTACC[illegible]AGCTAT[illegible]ACTG[illegible]GGCTCCTAGTCCA[illegible]ATGGG[illegible]
GACTGCCTCTCCAACCCTGTGGGCTGTAAGCAAGCTCAGGCTAGTCTCCCCACTGGGGGC
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GGGACACTCCCAGGCCAGCCCAGGGGTCAGGGGCAGAGGTGCACACCTCAGCATGAGCCA
AGACTGGGGTCAGGGAGCAGGTGTGGTTTGAGCCAGGACCTGGGGCGGGGGTGGGGCCGG
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CCCTTCCTCGAGTTTGAATATCCAGAATCTTTTGTACTTCTTGTTGGTTAAATTGTTTAT
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SEQ ID NO: 107_AA396601_M
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CTTCCTGGAGGATCGATTCCGAATCTGCCTCAGCCTTGGCCGCCTCCTCCACCACCTGG
CCCACTCCCCGCTGGGCTCGGTCACCCTGCTTGACTTCCGCCCTCGGCAGTTTGTGCTAG
TGAACGGGGAGCTGAAAGTGACAGACCTGGATGATGCCCGCGTGGAAGAGACACCGTGCA

FIGURE 2DDDD

CCAGCAGTGCCGACTGCACGCTAGAGTTTCCAGCCAGGAACTTCAGCCTGCCCTGCTCGG
CCCAGGGCTGGTGCGAGGGCATGAATGAGAAACGGAACCTCTACAATGCCTACAGGTTCT
TCTTCACATACCTCCTGCCACACAGTGCCCCGCCTTCCCTCCGACCTCTCCTGGATAGCA
TCGTCAATGCCACGGGAGAGCTCGCCTGGGGGGTGGATGAGACCCTGGCCCAGCTGGAGA
CAGCGCTACACTTGTTCCGAAGTGGGCAGTACCTGCAGAACTCTACAAGCAGCAGGGCTG
AGTACCAGCGCATCCCGGACAGTGCCATCACACAGGAGGACTATCGCTGCTGGCCATCCT
ATCACCACGGCGGCTGCCTCCTGTCCGTGTTCAACCTGGCTGAGGCTATAGATGTCTGTG
AGAGCCATGCTCAGTGTCGTGCCTTTGTGGTCACCAACCAGACCACCTGGACAGGTCGGA
AGCTGGTCTTTTTTAAGACTGGATGGAACCAAGTGGTCCCTGATGCCGGCAAGACCACAT
ATGTGAAGGCCCCTGGTTGACTGGTTGTGGCTCAGCTGACCAGCTGGGCTTGCCTGCTG
CAGGCGTGACTTGCATCCCACCTGGGAACCCCTGCAGACAAAAGCTAGCTCCCAGAGCAA
CTGATGTCACCCACGGACAAAACGTGCAATATGCAA[illegible]AATGTTAAA[illegible]GTGAC[illegible]CCCACC
TTCAGTCCCAGACTGGTTGGAACCCGATTGCCTCTCTGGAGCTGTAGGCTGTGAGCAGGG
CTCAGGCTGGTCTTAACTGGGACAGTCCCGTGGGCAGCCCATTACTGCATTCATGCTTTG
AGAATGTAGCCAGAACACTGCTGCTGCATAAGCCACCGTGGGCAGGAGCTGCCTGGGGAC
AACCAGTCTCAGAGTGCTCTCTCAGCTCAGCTCCGCTCCAAATGGAGAGCGCGGGATGCG
GAGATGTGAGTGAACCAGCACTGGGAAGAAGGCTCTCGGGCCTCTCCCTAGAGGTTGCTC
CTAGGCCAGCCCCGAGGCCGTGGGCAGCAGTGCTCGCATCCATATGAGCCAAGACTAGAG
TGGAGGAGCAGATTGCATTTGAGCCAGGACTGGGGTGGGGGTAGGGTCGGGGCCTCTCTG
CCTCATTTGCTTTCAGTGAAAGCCAGGGAGCAGCCGCAGCCAGGCTCCTCCCACTCCTGG
AGGCCAGGCTCCTCCCCCTCCTGGAGGCCAGGCTCCTCCCCCTCCTGGAGTTTGCGTACC
CAGAAGCTTTTATACTTCTCGTTCATTAAATTGTTTATTTTTGTAAAAAAAAAAAATTAAT
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SEQ ID NO: 108_VRK3_H
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AAGAAAGTGAAATGGTCCAGCACCGTCACCTCTCCCCGATTATCCCTCTTCTCAGATGGT
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AAGCGGAGCCGAGTGACCACCTCACTTGAAGCTTTGCCCACAGGGACAGTGCTGACAGAC
AAGAGTGGGCGACAGTGGAAGCTGAAGTCCTTCCAGACCAGGGACAACCAGGGCATTCTC
TATGAAGCTGCACCCACCTCCACCCTCACCTGTGACTCAGGACCACAGAAGCAAAAGTTC
TCACTCAAACTGGATGCCAAGGATGGGCGCTTGTTCAATGAGCAGAACTTCTTCCAGCGG
GCCGCCAAGCCTCTGCAAGTCAACAAGTGGAAGAAGCTGTACTCGACCCCACTGCTGGCC
ATCCCTACCTGCATGGGTTTCGGTGTTCACCAGGACAAATACAGGTTCTTGGTGTTACCC
AGCCTGGGGAGGAGCCTTCAGTCGGCCCTGGATGTCAGCCCAAAGCATGTGCTGTCAGAG
AGGTCTGTGCTGCAGGTGGCCTGCCGGCTGCTGGATGCCCTGGAGTTCCTCCATGAGAAT
GAGTATGTTCATGGAAATGTGACAGCTGAAAATATCTTTGTGGATCCAGAGGACCAGAGT
CAGGTGACTTTGGCAGGCTATGGCTTCGCCTTCCGCTATTGCCCAAGTGGCAAACACGTG
GCCTACGTGGAAGGCAGCAGGAGCCCTCACGAGGGGGACCTTGAGTTCATTAGCATGGAC
CTGCACAAGGGATGCGGGCCCTCCCGCCGCAGCGACCTCCAGAGCCTGGGCTACTGCATG
CTGAAGTGGCTCTACGGGTTTCTGCCATGGACAAATTGCCTTCCCAACACTGAGGACATC
ATGAAGCAAAAACAGAAGTTTGTTGATAAGCCGGGGCCCTTCGTGGGACCCTGCGGTCAC
TGGATCAGGCCCTCAGAGACCCTGCAGAAGTACCTGAAGGTGGTGATGGCCCTCACGTAT
GAGGAGAAGCCGCCCTACGCCATGCTGAGGAACAACCTAGAAGCTTTGCTGCAGGATCTG
CGTGTGTCTCCATATGACCCCATTGGCCTCCCGATGGTGCCCTAG

FIGURE 2EEEE

SEQ ID NO: 109_S71575_M VRK3_M

CCATCCCCACCTGTATCGGCTTTGGCATTCACCAGGACAAGTACAGGTTCCTAGTATTCC
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AGAGATGTGTGCTTCAGGTGGCCTGCAGGCTGCTGGATGCTCTGGAGTATCTCCATGAAA
ATGAGTATGTTCACGGGAACCTGACAGCTGAGAATGTCTTTGTGAATCCAGAGGATCTGA
GCCAGGTGACCCTGGTGGGCTATGGCTTCACCTACCGATACTGCCCAGGTGGCAAACACG
TGGCCTACAAAGAAGGCAGCAGGAGTCCACACGATGGGGACTTGGAGTTCATTAGCATGG
ACCTGCACAAGGGATGCGGACCCTCCCGCCGCAGCGATCTCCAGACCTTGGGCTACTGTA
TGCTCAAGTGGCTTTATGGGTCCCTGCCATGGACAAATTGCCTTCCCAACACCGAAAAGA
TAACTAGGCAGAAGCAGAAGTATCTGGACAGCCCCGAGCGCCTCGTGGGACTGTGTGGCC
GCTGGAACAAGGCCTCAGAGACCCTGCGGGAGTACCTGAAGGTGGTGATGGCCCTCAATT
ATGAGGAGAAGCCACCCTATGCCACGCTGAGGAACAGCCTAGAAGCTCTGCTGCAGCTA
TGCGGGTGTCACCCTATGACCCTCTGGACCTCCAGATGGTGCCTTAGATGGAATCCAGAG
CTTCCGACTTGCAGCTTGAAGTAGAACATGAAGTAGTGTGACTGGAGGCCTGTTTGAACT
CATAGCTCCTAAAAGAATCCCTTGAATGTGCATTCTCACCGCTCCCTTAGGACATATGAA
TCAGCACTTGTGTTGGGGAACCTGAGTCATGTCATGTAATGTGAAACTCCTCCCTGTCTC
AGCTCTGGCAGCTGTGGATGGAGGTAAGTGGATGCTGGCGGCGGCGGCAGCAGCCAC
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SEQ ID NO: 110_AA45427_H

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GTGGCTTACTGTCTGAGGGAACGGGGTGCTAAGCATGAGGCCTGGCTGCTGCTACCATTC
TTCAAGAGAGGTACGCTGTGGAATGAGATAGAAAGGCTGAAGGACAAAGGCAACTTCCTG
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GCCAAGGGTTATGCCCACAGAGACTTGAAGCCCACCAATATATTGCTTGGAGATGAGGGG
CAGCCAGTTTTAATGGACTTGGGTTCCATCAATCAAGCATGCATCCATGTGGAGGGCTCC
CGCCAGGCTCTGACCCTGCAGGACTGGGCAGCCCAGCGGTGCACCATCTCCTACCGAGCC
CCAGAGCTCTTCTCTGTGCAGAGTCACTGTGTCATCGATGAGCGGACTGATGTCTGGTCC
CTAGGCTGCGTGCTATATGCCATGATGTTTGGGGAAGGCCCTTATGACATGGTGTTCCAA
AAGGGTGACAGTGTGGCCCTTGCTGTGCAGAACCAACTCAGCATCCCACAAAGCCCCAGG
CATTCTTCAGCATTGCGGCAGCTCCTGAACTCGATGATGACCGTGGACCCGCATCAGCGT
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SEQ ID NO: 111_H05721_H

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CGGCTTGGGGCGGCCGGGCCCGGCGGCGGGCTGTGTCCGCGGGGAGCGTCCAGGCTGGGC
CGCAGGACCGGGCGCGGAGCCTCGCAGGGTCGGGCTCGGGCTCCCTAACCGTCTCCGCTT
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CCTCATCGAGGAAAAACAGGCGGAGAGCCGGCGGGCGGTCTCGGCCTGTCAGGAGATCCA
GGCAATTTTTACCCAGAAAAGCAAGCCGGGGCCTGACCCGTTGGACACGAGACGCTTGCA
GGGCTTTCGGCTGGAGGAGTATCTGATAGGGCAGTCCATTGGTAAGGGCTGCAGTGCTGC
TGTGTATGAAGCCACCATGCCTACATTGCCCCAGAACCTGGAGGTGACAAAGAGCACCGG
GTTGCTTCCAGGGAGAGGCCCAGGTACCAGTGCACCAGGAGAAGGGCAGGAGCGAGCTCC

FIGURE 2FFFF

GGGGGCCCCTGCCTTCCCCTTGGCCATCAAGATGATGTGGAACATCTCGGCAGGTTCCTC
CAGCGAAGCCATCTTGAACACAATGAGCCAGGAGCTGGTCCCAGCGAGCCGAGTGGCCTT
GGCTGGGGAGTATGGAGCAGTCACTTACAGAAAATCCAAGAGAGGTCCCAAGCAACTAGC
CCCTCACCCCAACATCATCCGGGTTCTCCGCGCCTTCACCTCTTCCGTGCCGCTGCTGCC
AGGGGCCCTGGTCGACTACCCTGATGTGCTGCCCTCACGCCTCCACCCTGAAGGCCTGGG
CCATGGCCGGACGCTGTTCCTCGTTATGAAGAACTATCCCTGTACCCTGCGCCAGTACCT
TTGTGTGAACACACCCAGCCCCCGCCTCGCCGCCATGATGCTGCTGCAGCTGCTGGAAGG
CGTGGACCATCTGGTTCAACAGGGCATCGCGCACAGAGACCTGAAATCCGACAACATCCT
TGTGGAGCTGGACCCAGACGGCTGCCCCTGGCTGGTGATCGCAGATTTTGGCTGCTGCCT
GGCTGATGAGAGCATCGGCCTGCAGTTGCCCTTCAGCAGCTGGTACGTGGATCGGGGCGG
AAACGGCTGTCTGATGGCCCCAGAGGTGTCCACGGCCCGTCCTGGCCCCAGGGCAGTGAT
TGACTACAGCAAGGCTGATGCCTGGGCAGTGGGAGCCATCGCCTATGAAATCTTCGGCCT
TGTCAATCCCTTCTACGGCCAGGGCAAGGCCCACCTTGAAAGCCGCAGCTACCAAGAGGC
TCAGCTACCTGCACTGCCCGAGTCAGTGCCTCCAGACGTGAGACAGTTGGTGAGGGCACT
GCTCCAGCGAGAGGCCAGCAAGAGACCATCTGCCCGAGTAGCCGCAAATGTGCTTCATCT
AAGCCTCTGGGGTGAACATATTCTAGCCCTGAAGAATCTGAAGTTAGACAAGATGGTTGG
CTGGCTCCTCCAACAATCGGCCGCCACTTTGTTGGCCAACAGGCTCACAGAGAAGTGTTG
TGTGGAAACAAAAATGAAGATGCTCTTTCTGGCTAACCTGGAGTGTGAAACGCTCTGCCA
GGCAGCCCTCCTCCTCTGCTCATGGAGGGCAGCCCTGTGATGTCCCTGCATGGAGCTGGT
GAATTACTAAAAGAACATGGCATCCTCTGTGTCGTGATGGTCTGTGAATGGTGAGGGTGG
GAGTCAGGAGACAAGACAGCGCAGAGAGGGCTGGTTAGCCGGAAAAGGCCTCGGGCTTGG
CAAATGGAAGAACTTGAGTGAGAGTTCAGTCTGCAGTCCTCTGCTCACAGACATCTGAAA
AGTGAATGGCCAAGCTGGTCTAGTAGATGAGGCTGGACTGAGGAGGGGTAGGCCTGCATC
CACAGAGAGGATCCAGGCCAAGGCACTGGCTGTCAGTGGCAGAGTTTGGCTGTGACCTTT
GCCCCTAACACGAGGAACTCGTTTGAAGGGGGCAGCGTAGCATGTCTGATTTGCCACCTG
GATGAAGGCAGACATCAACATGGGTCAGCACGTTCAGTTACGGGAGTGGGAAATTACATG
AGGCCTGGGCCTCTGCGTTCCCAAGCTGTGCGTTCTGGACCAGCTACTGAATTATTAATC
TCACTTAGCGAAAGTGACGGATGAGCAGTAAGTAACTAACTGTGGGATTTAAACTTGAG
GGTTTCCCTCCTGACTAGCCTCTCTTACAGGAATTGTGAAATATTAAATGCAAATTTACA
ACTGCAGATGACGTATGTGCCTTGAACTGAATATTTGGCTTTAAGAATGATTCTTCTTAT
ACTCTGAAGGTGAGAATATTTTGTGGGCAGGTATCAACATTGGGGAAGAGATTTCATGTC
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CAGTAAAGGTTGTCTTCAACTGACAAAA

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CAGATGACCAAGGAAGAGCGGCAGGCAGCCCAGAATGAGTGCCAGGTCCTCAAGCTGCTC
AACCACCCCAATGTCATTGAGTACTACGAGAACTTCCTGGAAGACAAAGCCCTTATGATC
GCCATGGAATATGCACCAGGCGGCACTCTGGCTGAGTTCATCCAAAAGCGCTGTAATTCC
CTGCTGGAGGAGGAGACCATCCTGCACTTCTTCGTGCAGATCCTGCTTGCACTGCATCAT
GTGCACACCCACCTCATCCTGCACCGAGACCTCAAGACCCAGAACATCCTGCTTGACAAA
CACCGCATGGTCGTCAAGATCGGTGATTTCGGCATCTCCAAGATCCTTAGCAGCAAGAGC
ACCCCATGCTATATCTCCCCTGAGCTGTGTGAGGGCAAGCCCTACAACCAGAAGAGTGAC
ATCTGGGCCCTGGGCTGTGTCCTCTACGAGCTGGCCAGCCTCAAGAGGGCTTTCGAGGCT
GCGAACTTGCCAGCACTGGTGCTGAAGATCATGAGTGGCACCTTTGCACCTATCTCTGAC
CGGTACAGCCCTGAGCTTCGCCAGCTGGTCCTGAGTCTACTCAGCCTGGAGCCTGCCCAG
CGGCCACCACTCAGCCACATCATGGCACAGCCCCTCTGCATCCGTGCCCTCCTCAACCTC
CACACCGACGGCAGAGAAGTCCGTGGCCCCCAGCAACACAGGGAGCAGGACCACCAGTGT
CCGCTGCAGAGAGGCATCATCATGACATTCGGCAGCGGCAGCAATGGGTGCCTAGGCCAT

FIGURE 2GGGG

GGCAGCCTCACTGACATCAGCCAGCCCACCATTGTGGAGGCTTTGTTGGGCTATGAAATG
GTGCAGCAAGTGGAGGAGGCCCTGAGCTTCACACTACTAGGCTCTGCACCCCTGGACCAG
GAGCCTCTGCTGAGTATAGACCTGGGCACTGCTCACTCAGCTGCTGTGACTGGTGAGGAG
GACTTGGGCTCTGGAGATGTAAACAGGTTACCCAGCTGGGAGAGAGGACATCTGCTGGCT
GGTGTGGCGTCCAGCACTGATGTGTCTACCTTCTCTGAAGGTGACTGCAAGGAGCCTGAC
AAGTGCTGCTGGAGACACAAGCAGTGCACTGGGCACATCATCTACCCTTTCGCCTCTGAC
TGTGTCCGCCACAGCCTGCACCTACACTCTGTCAACCACTGCAACTGTAATTCTAGGCTG
AAGGACTCTTCAGAGGATAGCAGCAGCTCCCGGGGCGCGGGCCCAACCTGCTCCCATGTC
ATCGAGTCCCCTTGCTTTGAGCTCACACCGGAGGAGGAGCATGTGGAGCGATTCCGGTAT
GGCTGGTGCAAAAGCTACAGACCTGTCTCTGTGGCAGTGATCCACCATCCACTCTACCAT
GAGTGTGGGGCAGATGATCTAAATGXXAAGAAGAGGAAGAGGAGGAGGAGGAAAAGCAAG
CCCCCCATCCCGACACAGGTCGGGCCCGCCACCGCCTCCCCTGACCTAGGCACCAGCATG
GCCACTGGTACCCCTGACTCCACAGCGCCCATCACCATCTGGCGCTCTGAGAGCCCCACA
GGGAAGGGTCAGGGCAGCAAGGTGATCAAGAAGGTAAAGAAGAAAAAGGAAAAAGAGAAA
GACAAGGAGGAGATGGATGAGAAGGCAAAGCTGAAGAAAAAAGCCAAGAAAGGCCAGTTG
ACTAAGAAGAAAAGCCCGGTTAAATTGGAGCCTTCCCCGCCAGACGTGAGCCGATCATTA
AGCGCAAGACAGCTGGCCAGGATGTCCGAGTCCAGCCCAGAAAGCCGGGAAGAGCTGGAG
AGCGAGGACAGTTACAATGGCCGGGGGCAGGGAGAACTGTCCAGCGAGGATATTGTGGAA
TCATCATCGCCCAGGAAGAGAGAGAACACAGTCCAGGCCAAAAAGACAGGGGCAAAGCCC
TCACAAGCCAGGAAGGTAAACAAGAGAAAATCTCCCCCAGGATCAAACCCCAACCTCAGT
TGAGGCCAGGGTGGTCAGGGTGCAGAATAAATGCCATCGAGCCTGTGGCTGGCCCTCTGC
TGCTGTTCTCTCCCTCCAACCTGGCTGTTTCTTGCGGGGCAAGGGGTGGGCTCAGGGCTG
CAGGGGTTTCTCAAAGGCAATCCAGCTTTCACAAAGGAAGCCCATGGAAGGCAGGTGGG
AGGGAAAGGAAGGGGCACAGCCCTATTTCTTCCTACCTGCTAGGACAAGGTGGAAGAGTG
TATCTGGGGTGGGAAGGAGGGCTTCCCCTCTCTGCTGCGAGAGACTGGTCTGTGTGAAAT
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CCC

SEQ ID NO: 113_AA836348_H
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GGCGGCGGCGCGGCGGAGCAGGAGGAACTGCACTACATCCCCATCCGCGTCCTGGGCCGC
GGCGCCTTCGGGGAAGCCACGCTGTACCGCCGCACCGAGGATGACTCACTGGTTGTGTGG
AAGGAAGTCGATTTGACCCGGCTGTCTGAGAAGGAACGTCGTGATGCCTTGAATGAGATA
GTTATTCTGGCACTGCTGCAGCACGACAACATTATTGCCTACTACAATCACTTCATGGAC
AATACCACGCTGCTGATTGAGCTGGAATATTGTAATGGAGGGAACCTGTATGACAAAATC
CTTCGTCAGAAGGACAAGTTGTTTGAGGAAGAGATGGTGGTGTGGTACCTATTTCAGATT
GTTTCAGCAGTGAGCTGCATCCATAAAGCTGGAATCCTTCATAGAGATATAAAGACATTA
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ATTTTTGAACTGCTTACCTTAAAGAGGACGTTTGATGCTACAAACCCACTTAACCTGTGT
GTGAAGATCGTGCAAGGAATTCGGGCCATGGAAGTTGACTCTAGCCAGTACTCTTTGGAA
TTGATCCAAATGGTTCATTCGTGCCTTGACCAGGATCCTGAGCAGAGACCTACTGCAGAT
GAACTTCTAGATCGCCCTCTTCTCAGGAAACGCAGGAGGTCAAGCACTGTGACTGAAGCA
CCCATTGCTGTAGTAACATCACGAACCAGTGAAGTCTATGTTTGGGGTGGTGGAAAATCC
ACCCCCCAGAAACTGGATGTTATCAAGAGTGGCTGTAGTGCCCGGCAGGTCTGTGCAGGG
AATACCCACTTTGCTGTGGTCACAGTGGAGAAGGAACTGTACACTTGGGTGAACATGCAA
GGAGGCACTAAACTCCATGGTCAGCTGGGCCATGGAGACAAAGCCTCCTATCGACAGCCA
AAGCATGTGGAAAAGTTGCAAGGCAAAGCTATCCGTCAGGTGTCATGTGGTGATGATTTC

FIGURE 2HHHH

ACTGTCTGTGTGACTGATGAGGGTCAGCTCTATGCCTTCGGATCAGATTATTATGGCTGC
ATGGGGGTGGACAAAGTTGCTGGCCCTGAAGTGCTAGAACCCATGCAGCTGAACTTCTTC
CTCAGCAATCCAGTGGAGCAGGTCTCCTGTGGAGATAATCATGTGGTGGTTCTGACACGA
AACAAGGAAGTCTATTCTTGGGGCTGTGGCGAATATGGACGACTGGGTTTGGATTCAGAA
GAGGATTATTATACACCACAAAAGGTGGATGTTCCCAAGGCCTTGATTATTGTTGCAGTT
CAATGTGGCTGTGATGGGACATTTCTGTTGACCCAGTCAGGCAAAGTGCTGGCCTGTGGA
CTCAATGAATTCAATAAGCTGGGTCTGAATCAGTGCATGTCGGGAATTATCAACCATGAA
GCATACCATGAAGTTCCCTACACAACGTCCTTTACCTTGGCCAAACAGTTGTCCTTTTAT
AAGATCCGTACCATTGCCCCAGGCAAGACTCACACAGCTGCTATTGATGAGCGAGGCCGG
CTGCTGACCTTTGGCTGCAACAAGTGTGGGCAGCTGGGCGTTGGGAACTACAAGAAGCGT
CTGGGAATCAACCTGTTGGGGGACCCCTTGGTGGGAAGCAAGTGATCAGGGTCTCCTGC
GCTGATGAGTTTACCATTGCTGCCACTGATGAGAAAGTATTGAATTCTAGGACCATCCGT
TCCAATAGCAGTGGCTTATCCATTGGAACTGTGTTTCAGAGCTCTAGCCCGGGAGGAGGC
GGCGGGGGCGGCGGTGGTGAAGAAGAGGACAGTCAGCAGGAATCTGAAACTCCTGACCCA
AGTGGAGGCTTCCGAGGAACAATGGAAGCAGACCGAGGAATGGAAGGTTTAATCAGTCCC
ACAGAGGCCATGGGGAACAGTAATGGGGCCAGCAGCTCCTGTCCTGGCTGGCTTCGAAAG
GAGCTGGAAAATGCAGAATTTATCCCCATGCCTGACAGCCCATCTCCTCTCAGTGCAGCG
TTTTCAGAATCTGAGAAAGATACCCTGCCCTATGAAGAGCTGCAAGGACTCAAAGTGGCC
TCTGAAGCTCCTTTGGAACACAAACCCCAAGTAGAAGCCTCGGTAACTGAGCTTTTTGCC
TTTGAATCACAACTAGTCACCTCGGCTGAATCCTGCAGTAACCTGTGCTGGGAAGGGAAC
ACCACTGACTCCTCCTGCGTGTGCGTGCAGCTCTCTGCAGGTGGAGGTTGA

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GCAGCTGTGCTCCTCATTGCTGCCGGGCAGCACTTTGAGGATTCCAAAGAGCTCCGGCTA
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TACTGGGATGTGGGTTTCTACCTGGGAGCCCAGATCCTCGCCAATGACCCCACCCAGGTG
GTGCTGGCTGCAGAGCAGCTGTATAAGCTCAATGCCCCCATATGGTACCTGGTGTCCGTG
ATGGAGACCTTCCTGCTCTACCAGCACTTCAGGCCCACGCCAGAGCCCCCTGGAGGGCCA
CCACGCCGTGCCCACTTCTGGCTCCACTTCTTGCTACAGTCCTGCCAACCATTCAAGACA
GCCTGTGCCCAGGGCGACCAGTGCTTGGTGCTGGTCCTGGAGATGAACAAGGTGCTGCTG
CCTGCAAAGCTCGAGGTTCGGGGTACTGACCCAGTAAGCACAGTGACCCTGAGCCTGCTG
GAGCCTGAGACCCAGGACATTCCCTCCAGCTGGACCTTCCCAGTCGCCTCCATATGCGGA
GTCAGCGCCTCAAAGCGCGACGAGCGCTGCTGCTTCCTCTATGCACTCCCCCCGGCTCAG
GACGTCCAGCTGTGCTTCCCCAGCGTAGGGCACTGCCAGTGGTTCTGCGGCCTGATCCAG
GCCTGGGTGACGAACCCGGATTCCACGGCGCCCGCGGAGGAGGCGGAGGGCGCGGGGGAG
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CTTAAGATCTTCATGGAGGAAGTGCCTGGAGGCAGCCTGTCCTCCTTGCTGCGGTCGGTG
TGGGGACCCCTGAAGGACAACGAGAGCACCATCAGTTTCTACACCCGCCAGATCCTGCAG
GGACTTGGCTACTTGCACGACAACCACATCGTGCACAGGGACATAAAAGGGGACAATGTG
CTGATCAACACCTTCAGTGGGCTGCTCAAGATTTCTGACTTCGGCACCTCCAAGCGGCTG
GCAGGCATCACACCTTGCACTGAGACCTTCACAGGAACTCTGCAGTATATGGCCCCAGAA

FIGURE 2IIII

ATCATTGACCAGGGCCCACGCGGGTATGGGAAAGCAGCTGACATCTGGTCACTGGGCTGC
ACTGTCATTGAGATGGCCACAGGTCGCCCCCCCTTCCACGAGCTCGGGAGCCCACAGGCT
GCCATGTTTCAGGTGGGTATGTACAAGGTCCATCCGCCAATGCCCAGCTCTCTGTCGGCC
GAGGCCCAAGCCTTTCTCCTCCGAACTTTTGAGCCAGACCCCCGCCTCCGAGCCAGCGCC
CAGACACTGCTGGGGGACCCCTTCCTGCAGCCTGGGAAAAGGAGCCGCAGCCCCAGCTCC
CCACGACATGCTCCACGGCCCTCAGATGCCCCTTCTGCCAGTCCCACTCCTTCAGCCAAC
TCAACCACCCAGTCTCAGACATTCCCGTGCCCTCAGGCACCCTCTCAGCACCCACCCAGC
CCCCCGAAGCGCTGCCTCAGTTATGGGGCACCAGCCAGCTCCGGGTGCCCGAGGAGCCT
GCGGCCGAGGAGCCTGCGTCTCCGGAGGAGAGTTCGGGGCTGAGCCTGCTGCACCAGGAG
AGCAAGCGTCGGGCCATGCTGGCCGCAGTATTGGAGCAGGAGCTGCCAGCGCTGGCGGAG
AATCTGCACCAGGAGCAGAAGCAAGAGCAGGGGGCCCGTCTGGCCAG[illegible]ACCATGTGGAA
GAGCTCCTGCGCTGCC[illegible]CGGCCACACATCCACACTCCCAACCGCCGGCAGCT[illegible]G
GAGCTGCGGGCGCTGCAAGGACGGCTGAGGGCCCAGGGCCTTGGGCCTGCGCTTCTGCAC
AGACCGCTGTTTGCCTTCCCGGATGCGGTGAAGCAGATCCTCCGCAAGCGCCAGATCCGT
CCACACTGGATGTTCGTTCTGGACTCACTGCTCAGCCGTGCTGTGCGGGCAGCCCTGGGT
GTGCTAGGACCGGAGGTGGAGAAGGAGGCGGTCTCACCGAGGTCAGAGGAGCTGAGTAAT
GAAGGGGACTCCCAGCAGAGCCCAGGCCAGCAGAGCCCGCTTCCGGTGGAGCCCGAGCAG
GGCCCCGCTCCTCTGATGGTGCAGCTGAGCCTCTTGAGGGCAGAGACTGATCGGCTGCGC
GAAATCCTGGCGGGGAAGGAACGGGAGTACCAGGCCCTGGTGCAGCGGGCTCTACAGCGG
CTGAATGAGGAAGCCCGGACCTATGTCCTGGCCCCAGAGCCTCCAACTGCTCTTTCAACG
GACCAGGGCCTGGTGCAGTGGCTACAGGAACTGAATGTGGATTCAGGCACCATCCAAATG
CTGTTGAACCATAGCTTCACCCTCCACACTCTGCTCACCTATGCCACTCGAGATGACCTC
ATCTACACCCGCATCAGGGGAGGGATGGTATGCCGCATCTGGAGGGCCATCTTGGCACAG
CGAGCAGGATCCACACCAGTCACCTCTGGACCCTGA

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TCCATCAACGGCCTGCTAGAGGATTTTGACAACATCTCGGTGACTCGCTCCAACTCCCTA
AGGAAAGAAAGCCCACCCACCCCAGATCAGGGAGCCTCCAGCCACGGTCCAGGCCACGCG
GAAGAAAATGGCTTCATCACCTTCTCCCAGTATTCCAGCGAATCCGATACTACTGCTGAC
TACACGACCGAAAAGTACAGGGAGAAGAGTCTCTATGGAGATGATCTGGATCCGTATTAT
AGAGGCAGCCACGCAGCCAAGCAAAATGGGCACGTAATGAAAATGAAGCACGGGGAGGCC
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AGAGCCTCGAGTAGCTCCCCTCTGGATTATTCATTCCAATTCACACCTTCTAGAACTGCA
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CTGGATGACTATGACAGGAGGCCAAAGTCTTCGTACCTGAATCAGACAAGCCCTCAGCCC
ACCATGCGGCAGAGGTCCAGGTCAGGCTCGGGACTCCAGGAACCGATGATGCCATTTGGA
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CAAAGCAAATCGGGCTATTCCTCAAGCAGTCACCAGTACCCGTCTGGGTACCACAAAGCC
ACCTTGTACCATCACCCCTCCCTGCAGAGCAGTTCGCAGTACATCTCCACGGCTTCCTAC
CTGAGCTCCCTCAGCCTCTCATCCAGCACCTACCCGCCGCCCAGCTGGGGCTCCTCCTCC
GACCAGCAGCCCTCCAGGGTGTCCCATGAACAGTTTCGGGCGGCCCTGCAGCTGGTGGTC
AGCCCAGGAGACCCCAGGGAATACTTGGCCAACTTTATCAAAATCGGGGAAGGCTCAACC
GGCATCGTATGCATCGCCACCGAGAAACACACAGGGAAACAAGTTGCAGTGAAGAAAATG

FIGURE 2JJJJ

GACCTCCGGAAGCAACAGAGACGAGAACTGCTTTTCAATGAGGTCGTGATCATGCGGGAT
TACCACCATGACAATGTGGTTGACATGTACAGCAGCTACCTTGTCGGCGATGAGCTCTGG
GTGGTCATGGAGTTTCTAGAAGGTGGTGCCTTGACAGACATTGTGACTCACACCAGAATG
AATGAAGAACAGATAGCTACTGTCTGCCTGTCAGTTCTGAGAGCTCTCTCCTACCTTCAT
AACCAAGGAGTGATTCACAGGGACATAAAAAGTGACTCCATCCTCCTGACAAGCGATGGC
CGGATAAAGTTGTCTGATTTTGGTTTCTGTGCTCAAGTTTCCAAAGAGGTGCCGAAGAGG
AAATCATTGGTTGGCACTCCCTACTGGATGGCCCCTGAGGTGATTTCTAGGCTACCTTAT
GGGACAGAGGTGGACATCTGGTCCCTCGGGATCATGGTGATAGAAATGATTGATGGCGAG
CCCCCCTACTTCAATGAGCCTCCCCTCCAGGCGATGCGGAGGATCCGGGACAGTTTACCT
CCAAGAGTGAAGGACCTACACAAGGTTTCTTCAGTGCTCCGGGGATTCCTAGACTTGATG
TT[illegible]GCAGCCCTCTCAGAGAGCAACAGCCCAGGAACTCCTCGGAC[illegible]CCAT[illegible]
AAACTAGCAGGTCCACCGTCTTGCAT[illegible]GTCCCCCTCA[illegible]CATCAC[illegible]

SEQ ID NO: 116_SURTK106_H
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AAACTAGGAAGGCAAGGAATGGCAAGGTCAGGAATTACTCACAGCTGTGCTGTGTGCATT
CTCTGTGGGCCTAGCAGGGAAGGGGACAGCCCTGTGGCAATGGGCATGACACGGATGCTC
CTGGAATGCAGTCTCAGTGACAAGTTGTGTGTCATCCAGGAGAAGCAGTATGAAGTGATT
ATCGTCCCAACTTTGTTGGTTACTATCTTCCTCATCCTTCTTGGGGTCATCCTGTGGCTT
TTTATCAGAGAACAAAGAACTCAACAGCAGCGTTCTGGACCTCAAGGCATTGCCCCTGTT
CCTCCACCTAGGGACCTAAGCTGGGAAGCAGGACATGGAGGAAATGTGGCTTTGCCACTT
AAGGAGACATCCGTGGAAAACTTTCTGGGAGCTACCACACCTGCCCTGGCTAAGCTGCAG
GTGCCGCGGGAGCAACTCTCTGAAGTTCTGGAGCAGATTTGCAGTGGTAGCTGTGGGCCC
ATCTTTCGAGCCAATATGAACACTGGGGACCCTTCTAAGCCCAAGAGTGTTATTCTCAAG
GCTTTAAAAGAACCAGCTGGGCTCCATGAGGTACAAGATTTCTTAGGGCGAATCCAATTC
CATCAATACCTGGGGAAACACAAAAACCTGGTGCAGCTGGAAGGCTGCTGCACTGAAAAG
C[illegible]ATGG[illegible]TTGGAGGA[illegible]GTGGCCCAGG[illegible]GAC[illegible]TGCTC[illegible]
ACCTGTCGGCGGGATGTGATGACTATGGATGGTCTTCTCTATGATCTCACAGAAAAACAA
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GATGTCTGGTCTTTTGGGATCCTGCTCTATGAGATGGTGACTCTAGGAGCACCACCGTAT
CCTGAAGTCCCTCCTACCAGCATCCTAGAGCATCTCCAAAGAAGGAAAATCATGAAGAGA
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GATGACGAGGCTGTGTTACAAGTACCAGAGTTGGTGGTACCTGAACTGTATGCAGCTGTG
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AAGAAACATTCATGCATGAGTATATGTTCTTGGAATCAATTCCTCTAAGAACAGAGAATG
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TTTCTCGGGAAATCTGAAATGATGCTGGATGGGACTCTACACATCCTGAGCTAAGACATA
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TGCAAAGGAGGTTTTAGAACTCTGCAGTATTTGTTGGGGCATGGCACAAATAAGCTCATC
CCTCCCGTCCGAGGCTAGTTTCCTCTGGAACCACATTTTTATCTAGATGAAAATTTGGAA
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CTTGCTCAGGATTACAGATATGGACCAACACCTCCTTCAAGAAAAGGTGGTAGGACACAA
AGTTCTTCAGTCCTGAGCCCTACATGTGGGGCTGGAGGAGAACTATAACGGAAAAACCTC
TGAGTTTCACCTTAGGTATAGATAAAAGAAAGATGGTCCCCTTTTATCTGATTCTGAGAC
AGGTAAATTCTGTTTGTTACTACGTTTAATTAGAAGGTGGAGGAGTCATTTCATGATTAA

FIGURE 2KKKK

GAACATTCAACATGTATTGTTCATTAAGCTAGCTTCCTAGTTCCGATTAGACTAAGGAGA
CTAAGCCTAGAGAGTCAATGTTAGAACAGTGAAAAGAATTCTGTGTGTGTGTGTGTGTGT
GTGTGTGTGTGCACAATAAATAGGAAATGTAGAAACCAAGCAAGAAGGCTTAGTAGCTCA
GTCTTTAACAAGGGCTAGAAAAGAATGTAATCTGATATGGAAGGATAGCAGCTTCTAATT
TTCAATCATCTGTTGATATACTGTGAAACTTATTTATTAAATTAATATTTATTAAATGG

SEQ ID NO: 117_AA098024_M
CTGCAGGAGAAGCACCTGTTTCATGGGGATGTGGCTGCCAGGAACATCCTGATCCAAAGT
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ATCTCCTCTGCTCGATCCAGCACCATCCCTCTCAAGTGGCTTGCTCCAGAAAGGCTTCTC
CTGAGACCTGCAAGCATCAGGGGAGATATTTGGTCCTTTGGGATCCTGCTTTATGAGATG
GTGACTCTAGGAGCACCACCATACCCTGAAGTCCCTCCCACCAGCATCCTACAATATCTT
CAGAGAAAGAAAATCATGAAGAGACCCAGCAGCTGCTCACATGCCATGTACAACATCATG
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CTAGAAGCTGCTTCTAGATCTGCCGATGACAAGGCTGTGTTGCAAGTGCCAGAGTTGGTG
GTGCCTGAACTGTATGCAGATGTGGCTGGCATCAGGGCAGAAAGCATTTCCTATAGCTTC
AGTGTCCTTTGAAGATGGTCCTAGACAAATGACTATATATGGGTGGAATTAGTTCCTTCA
AGAACAGAGAGAAGGAACTTTCTGTGGCCCACCAAGGGAGAAAAAAGGACATGGATCTTG
CATCTTTCCCTAAACATTTTCCTAGACATCTGAAATGCTGCTGGATGAAGCTCTACCTCT
ACATACCATGTACTCTTGAGCTAAGAATCACCATCAATTGTAGTTTGCTTTCCAGTCCCA
AGGGCTGAAGTATAAGTGGTGGACCGTGTCATTCTAAAGGAGGTTTTTAAAATCTGCAAT
GATTGTAAGGGAATTAGGCAAAAGGGCTGGTCCCACTCACTCCAGGCTGGTTTACTACTG
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TCGTTTCATTGAACTCTGAGGCAGGTGGACCATGCATGATACTAAGTTTAATTAGAAGCTG
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GTTATTTTACTAGGAAAATTAGAGAACCTATAGTTTCCAAAAAGAGATTCTTTATGTGCA
AAATGAGATAACTCTCTACCTCACAGGGTTGGTGTGAGGAACAATGAGAATATGTATTTG
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SEQ ID NO: 118_SGK2ALPHA_H
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TTAAAGAAGAAAGAGCAGAGCCACATCATGGCAGAGCGCAGTGTGCTTCTGAAGAACGTG
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TCCCTCAACATCATTTACAGGGATCTGAAACCAGAGAACATTCTCTTGGACTGCCAGGGA
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FIGURE 2LLLL

TCCACATTCTGTGGTACCCCTGAGTACTTGGCACCTGAAGTGCTTCGGAAAGAGCCTTAT
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GACCAGAGGCAGCGGCTGGGCTCCAAAGCAGACTTTCTTGAGATTAAGAACCATGTATTC
TTCAGCCCCATAAACTGGGATGACCTGTACCACAAGAGGCTAACTCCACCCTTCAACCCA
AATGTGACAGGACCTGCTGACTTGAAGCATTTTGACCCAGAGTTCACCCAGGAAGCTGTG
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AAGAAAAATAATGTTTCGGAGTCCAGGACTGGCAGGACAGGTCATCAGATACTCAGAGGC
TGTATCTCTGCCCTGCCAACCTTGACAAATGGCTTCCAATGTTAGGTTTGCTACAAGATG
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GTTGGGTAGGCAGCCAGCCCTCTTTTACCATAGGGCCTCCTGGTGTTTGGATTTTGATCT
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TATGTTGAAAAA

SEQ ID NO: 120_CCRK_H
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AATCAGTATGTGGTACAACTGAAGGCTGTGTTCCCACACGGTGGAGGCTTTGTGCTGGCC
TTTGAGTTCATGCTGTCGGATCTGGCCGAGGTGGTGCGCCATGCCCAGAGGCCACTAGCC
CAGGCACAGGTCAAGAGCTACCTGCAGATGCTGCTCAAGGGTGTCGCCTTCTGCCATGCC
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SEQ ID NO: 121_TESK2_H
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FIGURE 2MMMM

CCCACCGCCTCCGCAGGCTAAGGAGCCGCTGCCACCAACGAGCTGTGAGGGTTACTATGC
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CATACTACCGGCCACGAGATGGTGCTGCCCGCACCCCCAAAGTCAACCCTTTTAGTGCTC
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AGTCAGTGTTACAGGT